

Full wwPDB X-ray Structure Validation Report (i)

Aug 20, 2023 – 06:43 AM EDT

PDB ID : 2FDK

Title: Crystal Structure of AlkB in complex with Fe(II), 2-oxoglutarate, and methy-

lated trinucleotide T-meA-T (air 9 days)

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Structural Genomics Consortium (NESG)

Deposited on : 2005-12-14

Resolution : 2.30 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 (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 : 2.35

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

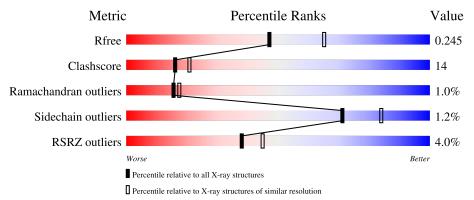
Validation Pipeline (wwPDB-VP) : 2.35

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 2.30 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	Similar resolution
Metric	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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					
			33%	•				
1	В	3	33%	67%				
			3%					
2	A	211	69% 26%					



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 1822 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 DNA chain called 5'-D(P*TP*(MA7)P*T)-3'.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	R	3	Total	С	N	О	Р	0	0	0
1	ע	3	63	31	9	20	3	0	U	

• Molecule 2 is a protein called Alkylated DNA repair protein alkB.

Mo	ol (Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2		A	199	Total 1548	C 986	N 281	O 273	S 8	0	0	1

There are 6 discrepancies between the modelled and reference sequences:

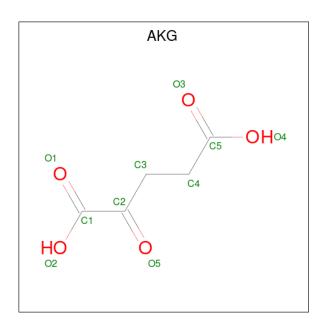
Chain	Residue	Modelled	Actual	Comment	Reference
A	11	MET	-	initiating methionine	UNP P05050
A	217	ASN	-	cloning artifact	UNP P05050
A	218	LEU	-	cloning artifact	UNP P05050
A	219	TYR	-	cloning artifact	UNP P05050
A	220	PHE	-	cloning artifact	UNP P05050
A	221	GLN	-	cloning artifact	UNP P05050

• Molecule 3 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Fe 1 1	0	0

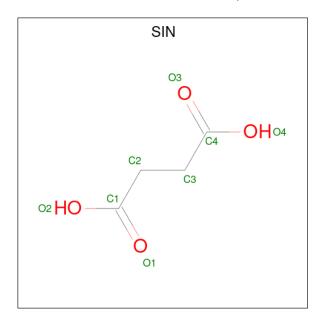
• Molecule 4 is 2-OXOGLUTARIC ACID (three-letter code: AKG) (formula: $C_5H_6O_5$).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 10	C 5	O 5	0	1

 \bullet Molecule 5 is SUCCINIC ACID (three-letter code: SIN) (formula: $\mathrm{C_4H_6O_4}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 8 4 4	0	1

• Molecule 6 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	В	15	Total O 15 15	0	0
6	A	177	Total O 177 177	0	1



3 Residue-property plots (i)

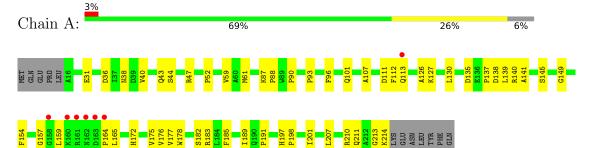
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

 \bullet Molecule 1: 5'-D(P*TP*(MA7)P*T)-3'

Chain B: 33% 67%



• Molecule 2: Alkylated DNA repair protein alkB





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants	40.58Å 40.58Å 117.05Å	Donogitor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 - 2.30	Depositor
Resolution (A)	29.26 - 2.00	EDS
% Data completeness	93.2 (19.99-2.30)	Depositor
(in resolution range)	87.1 (29.26-2.00)	EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.40 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
D.D.	0.171 , 0.242	Depositor
R, R_{free}	0.168 , 0.245	DCC
R_{free} test set	1206 reflections (10.46%)	wwPDB-VP
Wilson B-factor (Å ²)	21.0	Xtriage
Anisotropy	0.455	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38 , 73.4	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.097 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	1822	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.56% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: SIN, FE2, AKG, MA7

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	Bo	nd lengths	Bond angles		
MIOI		RMSZ	# Z > 5	RMSZ	# Z >5	
1	В	1.34	1/43 (2.3%)	0.76	0/60	
2	A	0.38	0/1593	0.55	0/2168	
All	All	0.43	1/1636 (0.1%)	0.55	0/2228	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
1	В	501	DT	OP3-P	-7.16	1.52	1.61

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)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	В	63	0	39	5	0
2	A	1548	0	1517	42	0
3	A	1	0	0	0	0
4	A	10	0	4	0	0
5	A	8	0	4	0	0
6	A	177	0	0	14	0
6	В	15	0	0	3	0
All	All	1822	0	1564	46	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 14.

All (46) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${f distance}({ m \AA})$	overlap (Å)
2:A:149:GLY:H	2:A:172:HIS:HD2	1.17	0.88
2:A:149:GLY:H	2:A:172:HIS:CD2	2.03	0.76
1:B:502:MA7:HN2	6:A:792[B]:HOH:O	1.88	0.73
2:A:130:LEU:HD11	2:A:165:LEU:HD11	1.74	0.68
2:A:141:ALA:HB3	6:A:679:HOH:O	1.93	0.67
2:A:93:PRO:HG2	2:A:96:PHE:CD1	2.34	0.62
2:A:31:GLU:HG3	6:A:624:HOH:O	2.01	0.60
2:A:107:ALA:HB2	2:A:177:VAL:HG21	1.83	0.60
1:B:501:DT:OP3	2:A:52:PRO:HD2	2.04	0.58
2:A:176:VAL:HG11	2:A:178:TRP:CZ2	2.38	0.57
2:A:182:SER:HA	2:A:185:PHE:CD1	2.44	0.53
2:A:87:LYS:HB3	6:A:664:HOH:O	2.10	0.52
2:A:38:ASN:HB3	6:A:706:HOH:O	2.10	0.52
2:A:127:LYS:HD3	2:A:191:PRO:HG3	1.93	0.51
1:B:501:DT:H5'	6:B:748:HOH:O	2.12	0.50
2:A:145:SER:O	2:A:175:VAL:HA	2.10	0.50
2:A:137:PRO:HG3	2:A:213:GLY:O	2.12	0.49
2:A:183:ARG:HH11	2:A:183:ARG:HG3	1.77	0.48
2:A:211:GLN:HB3	6:A:683:HOH:O	2.13	0.47
2:A:139:LEU:HG	6:A:652:HOH:O	2.15	0.47
2:A:159:LEU:HD12	2:A:159:LEU:N	2.29	0.47
2:A:61:MET:HG3	6:A:603:HOH:O	2.16	0.46
2:A:43:GLN:HB3	2:A:90:PRO:HG3	1.97	0.46
2:A:145:SER:HA	2:A:207:LEU:O	2.16	0.46
2:A:101:GLN:HG3	6:A:763:HOH:O	2.17	0.45
2:A:138:ASP:OD1	2:A:140:ARG:HB2	2.14	0.45
2:A:111:ASP:O	2:A:113:GLN:HG2	2.16	0.45
2:A:59:VAL:HG23	2:A:127:LYS:O	2.16	0.45
2:A:88:PRO:HD2	6:A:664:HOH:O	2.16	0.44
2:A:157:GLY:CA	2:A:165:LEU:HD23	2.47	0.44
2:A:36:ASP:O	2:A:40:VAL:HG23	2.18	0.44
2:A:135:ASP:HA	6:A:756:HOH:O	2.18	0.43
2:A:93:PRO:HG2	2:A:96:PHE:CG	2.53	0.43
1:B:501:DT:H71	6:B:765:HOH:O	2.18	0.43
2:A:126:ALA:O	2:A:191:PRO:HA	2.20	0.42
6:B:602:HOH:O	2:A:59:VAL:HG23	2.19	0.42
2:A:157:GLY:HA3	2:A:165:LEU:HD23	2.02	0.42

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Continued	trom	mmoninonic	maaa
COHABABACA		DIEUIUU	DUIUE
0 0 1000100000			

Atom-1	Atom-2	Interatomic	Clash
7100111-1	1100111-2	${ m distance}({ m \AA})$	overlap (Å)
2:A:172:HIS:HE1	6:A:622:HOH:O	2.01	0.42
2:A:44:SER:OG	2:A:90:PRO:HD3	2.20	0.42
2:A:157:GLY:HA3	6:A:625:HOH:O	2.20	0.42
2:A:183:ARG:HG3	2:A:183:ARG:NH1	2.35	0.42
2:A:112:PHE:CE1	2:A:211:GLN:HG3	2.54	0.41
1:B:502:MA7:H62	1:B:502:MA7:HN1	1.68	0.41
2:A:154:PHE:HA	2:A:189:ILE:HD13	2.01	0.41
2:A:214:LYS:N	6:A:746:HOH:O	2.54	0.41
2:A:197:HIS:HA	2:A:198:PRO:HD3	1.94	0.41

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	
2	A	197/211 (93%)	191 (97%)	4 (2%)	2 (1%)	15 17	

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	201	ILE
2	A	164	PRO

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	
2	A	161/174 (92%)	159 (99%)	2 (1%)	71 84	

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

Mol	Chain	Res	Type
2	A	47	ARG
2	A	210	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	28	ASN
2	A	43	GLN
2	A	120	ASN
2	A	155	GLN
2	A	172	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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	Pog	Link	Bo	ond leng	$ ag{ths}$	В	ond ang	les
MIOI	туре	Chain	rtes	Lilik	Counts RMSZ		# Z > 2	Counts	RMSZ	# Z > 2
1	MA7	В	502	1	18,24,25	0.84	1 (5%)	14,35,38	1.40	1 (7%)

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
1	MA7	В	502	1	-	0/3/21/22	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
1	В	502	MA7	C2-N3	2.02	1.34	1.30

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
1	В	502	MA7	C2-N3-C4	-4.87	110.50	116.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	В	502	MA7	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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		
MIOI					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
4	AKG	A	400[A]	3	9,9,9	1.22	1 (11%)	11,11,11	1.45	2 (18%)
5	SIN	A	401[B]	3	7,7,7	0.68	0	8,8,8	1.47	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
4	AKG	A	400[A]	3	-	3/9/9/9	-
5	SIN	A	401[B]	3	-	5/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\mid \operatorname{Ideal}(ext{Å}) \mid$
4	A	400[A]	AKG	C2-C1	-3.00	1.49	1.53

All (2) bond angle outliers are listed below:

	Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
	4	A	400[A]	AKG	O2-C1-C2	2.13	119.79	113.97
ľ	4	A	400[A]	AKG	C3-C2-C1	2.11	119.89	115.97

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms	
4	A	400[A]	AKG	O2-C1-C2-C3	
5	A	401[B]	SIN	C1-C2-C3-C4	
5	A	401[B]	SIN	C2-C3-C4-O4	
4	A	400[A]	AKG	C3-C4-C5-O4	
5	A	401[B]	SIN	O2-C1-C2-C3	
5	A	401[B]	SIN	O1-C1-C2-C3	
5	A	401[B]	SIN	C2-C3-C4-O3	
4	A	400[A]	AKG	C3-C4-C5-O3	

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^{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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	В	2/3~(66%)	2.26	1 (50%) 0 0	50, 50, 50, 85	0
2	A	199/211 (94%)	0.05	7 (3%) 44 51	11, 22, 51, 81	0
All	All	201/214 (93%)	0.07	8 (3%) 38 45	11, 22, 51, 85	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	162	ASN	5.8
1	В	501	DT	4.3
2	A	163	ASP	3.1
2	A	164	PRO	2.8
2	A	158	GLY	2.7
2	A	113	GLN	2.6
2	A	160	LYS	2.5
2	A	161	ARG	2.1

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. 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{ ilde{A}}^2)$	Q<0.9
1	MA7	В	502	22/23	0.85	0.24	38,43,68,69	22

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^{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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
5	SIN	A	401[B]	8/8	0.91	0.35	6,12,19,22	8
4	AKG	A	400[A]	10/10	0.93	0.35	36,37,37,37	10
3	FE2	A	300	1/1	0.99	0.09	32,32,32,32	0

6.5 Other polymers (i)

There are no such residues in this entry.

