wwPDB X-ray Structure Validation Summary Report (i)

May 13, 2020 – 09:52 am BST

PDB ID	:	2XVG
Title	:	crystal structure of alpha-xylosidase (GH31) from Cellvibrio japonicus
Authors	:	Larsbrink, J.; Izumi, A.; Ibatullin, F.; Nakhai, A.; Gilbert, H.J.; Davies, G.J.; Brumer, H.
Deposited on	:	2010-10-26
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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

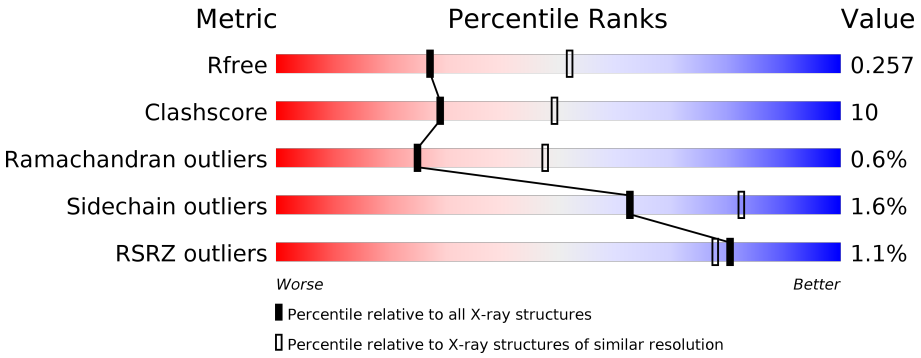
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.60 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 >=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	1020	% 73% 19% • 7%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7703 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 ALPHA XYLOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	944	7577	4843	1294	1425	15	54	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	989	LYS	-	expression tag	UNP B3PBD9
A	990	VAL	-	expression tag	UNP B3PBD9
A	991	VAL	-	expression tag	UNP B3PBD9
A	992	ILE	-	expression tag	UNP B3PBD9
A	993	ASN	-	expression tag	UNP B3PBD9
A	994	SER	-	expression tag	UNP B3PBD9
A	995	LYS	-	expression tag	UNP B3PBD9
A	996	LEU	-	expression tag	UNP B3PBD9
A	997	GLU	-	expression tag	UNP B3PBD9
A	998	GLY	-	expression tag	UNP B3PBD9
A	999	LYS	-	expression tag	UNP B3PBD9
A	1000	PRO	-	expression tag	UNP B3PBD9
A	1001	ILE	-	expression tag	UNP B3PBD9
A	1002	PRO	-	expression tag	UNP B3PBD9
A	1003	ASN	-	expression tag	UNP B3PBD9
A	1004	PRO	-	expression tag	UNP B3PBD9
A	1005	LEU	-	expression tag	UNP B3PBD9
A	1006	LEU	-	expression tag	UNP B3PBD9
A	1007	GLY	-	expression tag	UNP B3PBD9
A	1008	LEU	-	expression tag	UNP B3PBD9
A	1009	ASP	-	expression tag	UNP B3PBD9
A	1010	SER	-	expression tag	UNP B3PBD9
A	1011	THR	-	expression tag	UNP B3PBD9
A	1012	ARG	-	expression tag	UNP B3PBD9
A	1013	THR	-	expression tag	UNP B3PBD9
A	1014	GLY	-	expression tag	UNP B3PBD9
A	1015	HIS	-	expression tag	UNP B3PBD9

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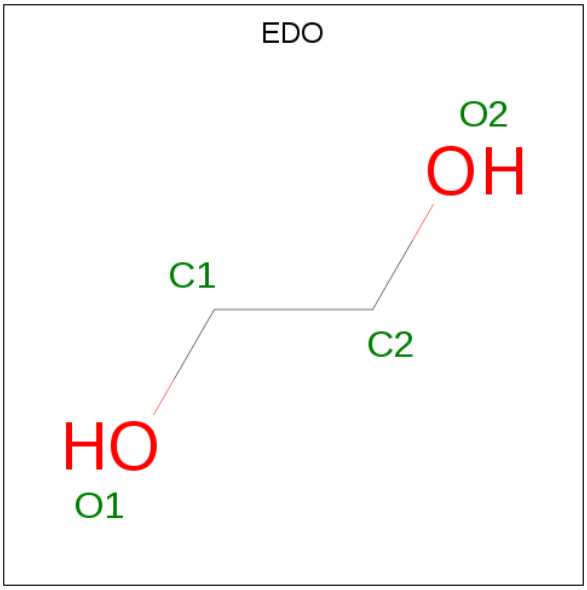
Chain	Residue	Modelled	Actual	Comment	Reference
A	1016	HIS	-	expression tag	UNP B3PBD9
A	1017	HIS	-	expression tag	UNP B3PBD9
A	1018	HIS	-	expression tag	UNP B3PBD9
A	1019	HIS	-	expression tag	UNP B3PBD9
A	1020	HIS	-	expression tag	UNP B3PBD9

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

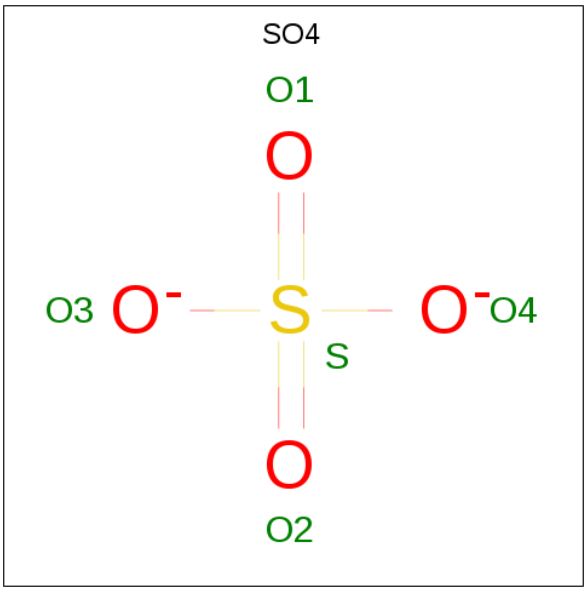
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Cl 4 4	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 5 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Ni 2 2	0	0

- Molecule 6 is water.

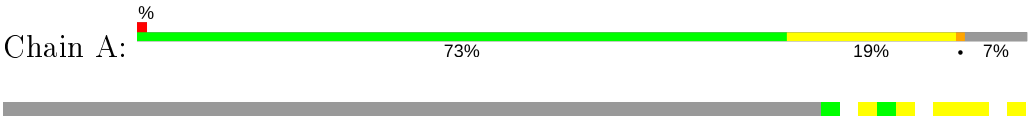
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	103	Total O 103 103	0	0

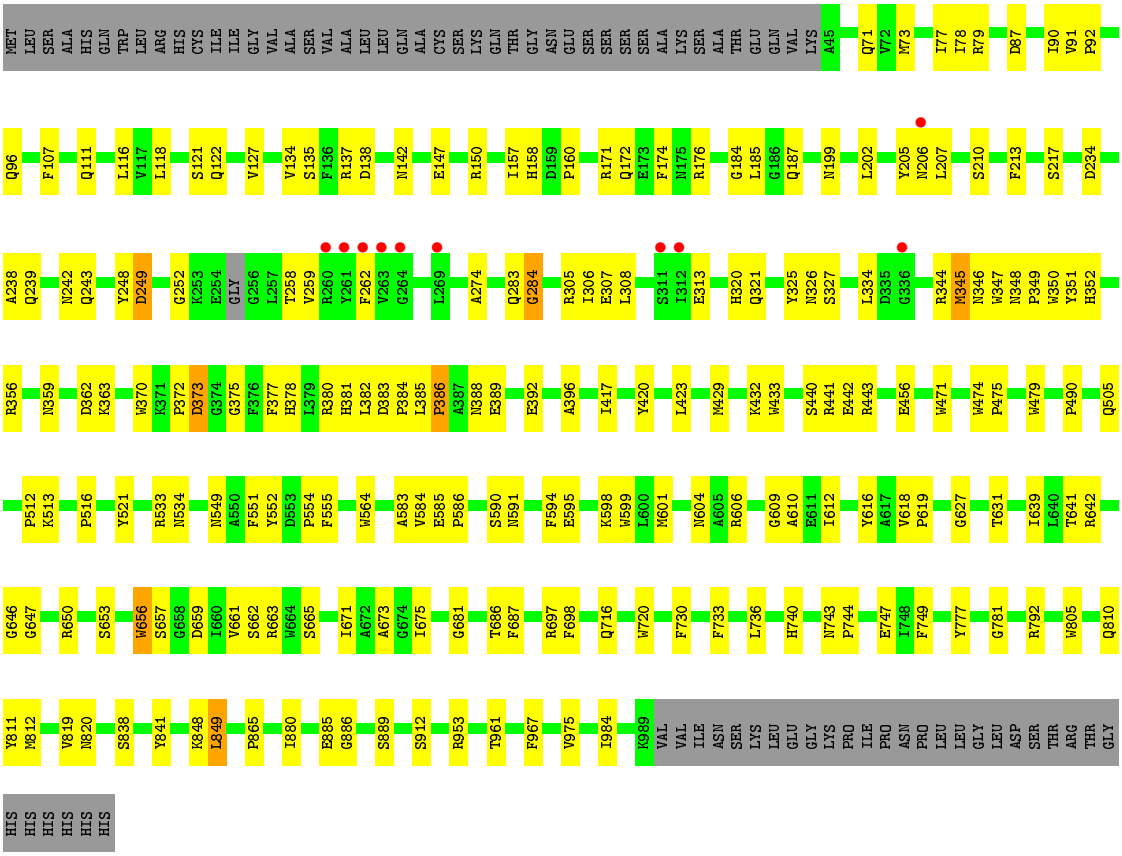
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: ALPHA XYLOSIDASE

Chain A:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α, β, γ	156.19Å 156.19Å 227.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.88 – 2.60 49.88 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.88-2.60) 99.9 (49.88-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.49 (at 2.61Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.204 , 0.259 0.200 , 0.257	Depositor DCC
R_{free} test set	2587 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	58.6	Xtriage
Anisotropy	0.178	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 41.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7703	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.17% 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: NI, CL, EDO, 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	0.44	0/7785	0.58	0/10573

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

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	7577	0	7275	142	0
2	A	4	0	0	0	0
3	A	12	0	18	1	0
4	A	5	0	0	0	0
5	A	2	0	0	0	0
6	A	103	0	0	2	0
All	All	7703	0	7293	142	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 10.

The worst 5 of 142 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:880:ILE:HG22	1:A:885:GLU:HG2	1.59	0.84
1:A:555:PHE:CZ	1:A:612:ILE:HD12	2.21	0.76
1:A:586:PRO:HD2	1:A:601:MET:CE	2.20	0.72
1:A:262:PHE:HB2	1:A:305:ARG:HG2	1.71	0.72
1:A:554:PRO:HG3	1:A:616:TYR:CZ	2.26	0.71

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	940/1020 (92%)	886 (94%)	48 (5%)	6 (1%)	25 47

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	373	ASP
1	A	662	SER
1	A	249	ASP
1	A	345	MET
1	A	386	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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	792/856 (92%)	779 (98%)	13 (2%)	62 82

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	656	TRP
1	A	665	SER
1	A	849	LEU
1	A	552	TYR
1	A	838	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	239	GLN
1	A	320	HIS
1	A	321	GLN
1	A	326	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 6 are monoatomic - leaving 4 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		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	SO4	A	1995	-	4,4,4	0.13	0	6,6,6	0.16	0
3	EDO	A	1996	-	3,3,3	0.74	0	2,2,2	0.21	0
3	EDO	A	1994	-	3,3,3	0.59	0	2,2,2	0.19	0
3	EDO	A	1997	-	3,3,3	0.55	0	2,2,2	0.22	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	EDO	A	1996	-	-	1/1/1/1	-
3	EDO	A	1994	-	-	0/1/1/1	-
3	EDO	A	1997	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1996	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1996	EDO	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues

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	944/1020 (92%)	-0.36	10 (1%) 80 78	38, 70, 128, 188	15 (1%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	263	VAL	4.0
1	A	261	TYR	3.9
1	A	312	ILE	3.2
1	A	269	LEU	3.0
1	A	336	GLY	2.8

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 carbohydrates 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
3	EDO	A	1994	4/4	0.83	0.77	86,88,90,91	0
3	EDO	A	1997	4/4	0.87	0.68	98,98,99,101	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	EDO	A	1996	4/4	0.91	0.17	47,52,60,62	0
4	SO4	A	1995	5/5	0.97	0.13	130,133,135,136	0
2	CL	A	1992	1/1	0.99	0.14	56,56,56,56	0
2	CL	A	1993	1/1	0.99	0.14	69,69,69,69	0
5	NI	A	1999	1/1	0.99	0.13	66,66,66,66	0
5	NI	A	1998	1/1	1.00	0.13	44,44,44,44	0
2	CL	A	1991	1/1	1.00	0.13	64,64,64,64	0
2	CL	A	1990	1/1	1.00	0.14	56,56,56,56	0

6.5 Other polymers (i)

There are no such residues in this entry.