wwPDB X-ray Structure Validation Summary Report (i)

May 16, 2020 – 08:41 pm BST

PDB ID	:	6GOA
Title	:	Structural basis for OXA-48 dimerization - R189A mutant
Authors	:	Lund, B.A.; Thomassen, A.M.; Leiros, H.K.S.
Deposited on	:	2018-06-01
Resolution	:	2.55 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 (i)) 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 ⓘ

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

The reported resolution of this entry is 2.55 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.
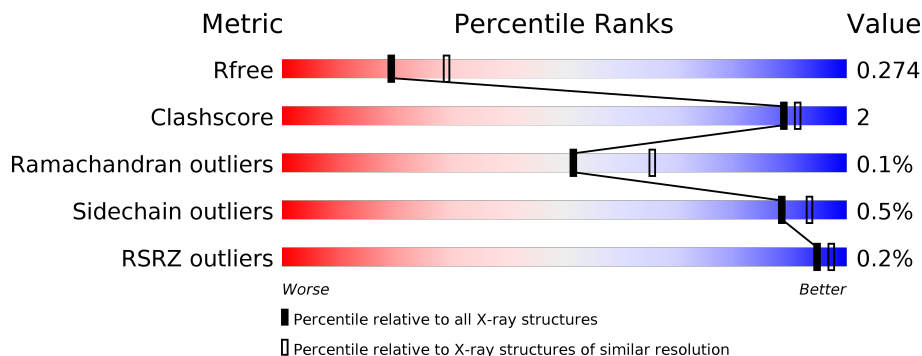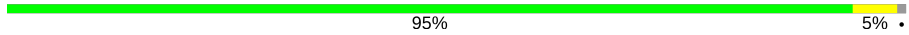

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	244	93% ... 6% ·
1	B	244	97% ... · ·
1	C	244	94% ... 5% ·
1	D	244	93% ... 7% ·
1	E	244	93% ... 6% ·
1	F	244	95% ... · ·

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	244	95% ⬛ 5% ·
1	H	244	2% ⬛ 87% ⬛ 11% ·

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 31547 atoms, of which 15323 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 Beta-lactamase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	242	Total 3897	C 1259	H 1921	N 346	O 364	S 7	0	0	0
1	B	242	Total 3882	C 1256	H 1910	N 345	O 364	S 7	0	0	0
1	C	242	Total 3897	C 1259	H 1921	N 346	O 364	S 7	0	0	0
1	D	242	Total 3897	C 1259	H 1921	N 346	O 364	S 7	0	0	0
1	E	242	Total 3882	C 1256	H 1910	N 345	O 364	S 7	0	0	0
1	F	242	Total 3898	C 1259	H 1922	N 346	O 364	S 7	0	0	0
1	G	242	Total 3880	C 1256	H 1908	N 345	O 364	S 7	0	0	0
1	H	242	Total 3882	C 1256	H 1910	N 345	O 364	S 7	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	GLY	-	expression tag	UNP Q6XEC0
A	189	ALA	ARG	engineered mutation	UNP Q6XEC0
B	22	GLY	-	expression tag	UNP Q6XEC0
B	189	ALA	ARG	engineered mutation	UNP Q6XEC0
C	22	GLY	-	expression tag	UNP Q6XEC0
C	189	ALA	ARG	engineered mutation	UNP Q6XEC0
D	22	GLY	-	expression tag	UNP Q6XEC0
D	189	ALA	ARG	engineered mutation	UNP Q6XEC0
E	22	GLY	-	expression tag	UNP Q6XEC0
E	189	ALA	ARG	engineered mutation	UNP Q6XEC0
F	22	GLY	-	expression tag	UNP Q6XEC0
F	189	ALA	ARG	engineered mutation	UNP Q6XEC0
G	22	GLY	-	expression tag	UNP Q6XEC0

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	189	ALA	ARG	engineered mutation	UNP Q6XEC0
H	22	GLY	-	expression tag	UNP Q6XEC0
H	189	ALA	ARG	engineered mutation	UNP Q6XEC0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	2	Total 2 Cl 2	0	0
2	E	1	Total 1 Cl 1	0	0
2	H	1	Total 1 Cl 1	0	0
2	B	1	Total 1 Cl 1	0	0
2	C	2	Total 2 Cl 2	0	0
2	A	1	Total 1 Cl 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	63	Total 63 O 63	0	0
3	B	58	Total 58 O 58	0	0
3	C	40	Total 40 O 40	0	0
3	D	56	Total 56 O 56	0	0
3	E	49	Total 49 O 49	0	0
3	F	68	Total 68 O 68	0	0
3	G	51	Total 51 O 51	0	0
3	H	39	Total 39 O 39	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: Beta-lactamase

Chain A:

93%   6% •

- Molecule 1: Beta-lactamase

Chain B:

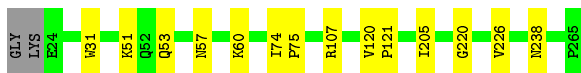97%   • •

- Molecule 1: Beta-lactamase

Chain C:

94%   5% •

- Molecule 1: Beta-lactamase

Chain D:

93%   7% •

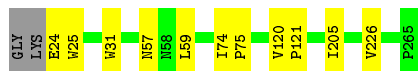- Molecule 1: Beta-lactamase

Chain E:

93%   6% •

- Molecule 1: Beta-lactamase

Chain F:

95%   • •

```
GLY LYS E24 W25 W31 N57 I74 P75 I205 G220 V226 N238 D245 P265
```

• Molecule 1: Beta-lactamase

Chain G:

95%   5% •

```
GLY LYS E24 W25 W31 N57 N58 L59 I74 P75 V120 P121 I205 V226 P265
```

• Molecule 1: Beta-lactamase

Chain H:

2%

87%   11% •

```
GLY LYS E24 W25 W31 N32 A33 E37 H38 Q53 N57 N58 L59 D101 I102 S118 V119 V120 P121 E132 M138 F142 I149 N152 V153 D154 S155 I164 S165 E168 T209 P217 G220 W221 W222 V226 W233 M237 N238 P265
```
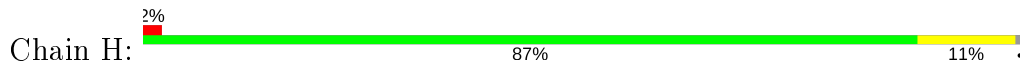
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	107.73Å 85.55Å 125.81Å 90.00° 90.08° 90.00°	Depositor
Resolution (Å)	24.67 – 2.55 24.67 – 2.55	Depositor EDS
% Data completeness (in resolution range)	96.3 (24.67-2.55) 82.7 (24.67-2.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.92 (at 2.53Å)	Xtriage
Refinement program	PHENIX dev_3150	Depositor
R, R_{free}	0.239 , 0.275 0.239 , 0.274	Depositor DCC
R_{free} test set	2200 reflections (3.05%)	wwPDB-VP
Wilson B-factor (Å^2)	22.0	Xtriage
Anisotropy	1.025	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 24.3	EDS
L-test for twinning[2]	$< |L| > = 0.52, < L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.126 for h,-k,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	31547	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.66 % 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 2.6467e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

---

[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: KCX, CL

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	0.26	0/2012	0.45	0/2722
1	B	0.26	0/2008	0.44	0/2718
1	C	0.26	0/2012	0.45	0/2722
1	D	0.26	0/2012	0.44	0/2722
1	E	0.30	0/2008	0.47	0/2718
1	F	0.26	0/2012	0.45	0/2722
1	G	0.25	0/2008	0.44	0/2718
1	H	0.27	0/2008	0.45	0/2718
All	All	0.27	0/16080	0.45	0/21760

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	1976	1921	1921	8	0
1	B	1972	1910	1910	2	0
1	C	1976	1921	1921	7	0
1	D	1976	1921	1921	8	0
1	E	1972	1910	1910	7	0

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1976	1922	1921	4	0
1	G	1972	1908	1910	6	0
1	H	1972	1910	1910	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	E	1	0	0	0	0
2	G	2	0	0	0	0
2	H	1	0	0	0	0
3	A	63	0	0	3	0
3	B	58	0	0	0	0
3	C	40	0	0	0	0
3	D	56	0	0	0	0
3	E	49	0	0	0	0
3	F	68	0	0	0	0
3	G	51	0	0	1	0
3	H	39	0	0	0	0
All	All	16224	15323	15324	59	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 59 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:259:LYS:HE2	1:D:265:PRO:OXT	1.89	0.73
1:C:259:LYS:HE3	1:C:265:PRO:OXT	1.93	0.67
1:H:164:ILE:HA	1:H:168:GLU:OE1	1.99	0.62
1:E:51:LYS:HE3	1:E:53:GLN:OE1	1.99	0.62
1:C:48:ASN:ND2	1:C:51:LYS:HD3	2.16	0.61

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	239/244 (98%)	233 (98%)	6 (2%)	0	100	100
1	B	239/244 (98%)	233 (98%)	6 (2%)	0	100	100
1	C	239/244 (98%)	234 (98%)	5 (2%)	0	100	100
1	D	239/244 (98%)	234 (98%)	5 (2%)	0	100	100
1	E	239/244 (98%)	233 (98%)	6 (2%)	0	100	100
1	F	239/244 (98%)	231 (97%)	7 (3%)	1 (0%)	34	46
1	G	239/244 (98%)	234 (98%)	5 (2%)	0	100	100
1	H	239/244 (98%)	234 (98%)	5 (2%)	0	100	100
All	All	1912/1952 (98%)	1866 (98%)	45 (2%)	1 (0%)	51	65

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	25	TRP

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	208/210 (99%)	207 (100%)	1 (0%)	88	93
1	B	207/210 (99%)	205 (99%)	2 (1%)	76	84
1	C	208/210 (99%)	208 (100%)	0	100	100
1	D	208/210 (99%)	208 (100%)	0	100	100
1	E	207/210 (99%)	206 (100%)	1 (0%)	88	93
1	F	208/210 (99%)	207 (100%)	1 (0%)	88	93
1	G	207/210 (99%)	207 (100%)	0	100	100
1	H	207/210 (99%)	204 (99%)	3 (1%)	67	79
All	All	1660/1680 (99%)	1652 (100%)	8 (0%)	88	93

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	107	ARG
1	H	237	MET
1	H	101	ASP
1	B	170	ILE
1	F	245	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues 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	$\#|Z| > 2$
1	KCX	C	73	1	7,11,12	0.84	0	4,12,14	0.63	0
1	KCX	E	73	1	7,11,12	0.81	0	4,12,14	0.72	0
1	KCX	G	73	1	7,11,12	0.87	0	4,12,14	0.65	0
1	KCX	H	73	1	7,11,12	0.85	0	4,12,14	0.78	0
1	KCX	B	73	1	7,11,12	0.82	0	4,12,14	0.54	0
1	KCX	F	73	1	7,11,12	0.79	0	4,12,14	0.72	0
1	KCX	D	73	1	7,11,12	0.79	0	4,12,14	0.77	0
1	KCX	A	73	1	7,11,12	0.83	0	4,12,14	0.73	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
1	KCX	C	73	1	-	0/7/10/12	-
1	KCX	E	73	1	-	0/7/10/12	-
1	KCX	G	73	1	-	0/7/10/12	-
1	KCX	H	73	1	-	0/7/10/12	-
1	KCX	B	73	1	-	0/7/10/12	-
1	KCX	F	73	1	-	0/7/10/12	-
1	KCX	D	73	1	-	0/7/10/12	-
1	KCX	A	73	1	-	0/7/10/12	-

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.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

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 (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, 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(Å²)	Q<0.9
1	A	241/244 (98%)	-0.22	0	100	100	24, 37, 55, 82	0
1	B	241/244 (98%)	-0.21	0	100	100	25, 37, 56, 78	0
1	C	241/244 (98%)	-0.21	0	100	100	22, 37, 55, 68	0
1	D	241/244 (98%)	-0.03	0	100	100	27, 45, 66, 83	0
1	E	241/244 (98%)	-0.11	0	100	100	26, 41, 62, 74	0
1	F	241/244 (98%)	-0.30	0	100	100	22, 33, 50, 72	0
1	G	241/244 (98%)	-0.17	0	100	100	17, 39, 57, 75	0
1	H	241/244 (98%)	0.19	4 (1%)	70	76	39, 57, 87, 105	0
All	All	1928/1952 (98%)	-0.13	4 (0%)	95	97	17, 40, 65, 105	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	102	ILE	2.6
1	H	153	VAL	2.4
1	H	38	HIS	2.2
1	H	217	PRO	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, 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(Å²)	Q<0.9
1	KCX	G	73	12/13	0.96	0.15	35,40,58,58	0
1	KCX	E	73	12/13	0.97	0.13	26,28,32,34	0

Continued on next page...

wwPDB X-ray Structure Validation Summary Report

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	KCX	C	73	12/13	0.97	0.12	24,31,37,39	0
1	KCX	H	73	12/13	0.97	0.15	44,52,62,76	0
1	KCX	B	73	12/13	0.97	0.14	28,36,54,66	0
1	KCX	F	73	12/13	0.97	0.12	23,28,35,39	0
1	KCX	D	73	12/13	0.97	0.12	33,39,61,74	0
1	KCX	A	73	12/13	0.97	0.13	34,41,47,49	0

6.3 Carbohydrates (i)

There are no carbohydrates 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(Å^2)	Q<0.9
2	CL	C	302	1/1	0.76	0.13	51,51,51,51	0
2	CL	G	302	1/1	0.91	0.18	52,52,52,52	0
2	CL	H	301	1/1	0.94	0.20	58,58,58,58	0
2	CL	E	301	1/1	0.95	0.12	54,54,54,54	0
2	CL	B	301	1/1	0.95	0.14	49,49,49,49	0
2	CL	A	301	1/1	0.97	0.11	38,38,38,38	0
2	CL	G	301	1/1	0.99	0.05	30,30,30,30	0
2	CL	C	301	1/1	0.99	0.06	37,37,37,37	0

6.5 Other polymers (i)

There are no such residues in this entry.