

# Full wwPDB X-ray Structure Validation Report (i)

#### May 23, 2020 – 03:53 pm BST

PDB ID : 4IZU

Title: The E41Q mutant of the amidase from Nesterenkonia sp. AN1 showing the

result of Michael addition of acrylamide at the active site cysteine

Authors: Kimani, S.W.; Sewell, B.T.

Deposited on : 2013-01-30

Resolution : 1.40 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 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

 $\begin{array}{rcl} {
m CCP4} & : & 7.0.044 \; ({
m Gargrove}) \\ {
m roteins}) & : & {
m Engh} \; \& \; {
m Huber} \; (2001) \end{array}$ 

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

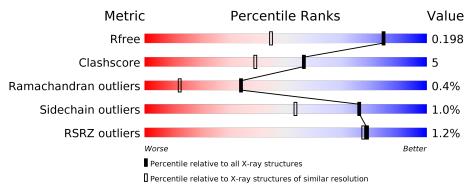
Validation Pipeline (wwPDB-VP) : 2.11

# 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 1.40 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \ resolution} \\ (\#{\rm Entries, \ resolution \ range(\AA)}) \end{array}$		
$R_{free}$	130704	1714 (1.40-1.40)		
Clashscore	141614	1812 (1.40-1.40)		
Ramachandran outliers	138981	1763 (1.40-1.40)		
Sidechain outliers	138945	1762 (1.40-1.40)		
RSRZ outliers	127900	1674 (1.40-1.40)		

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	Quality of chain						
			% ■							
1	A	283	75%	13%	٠	10%				

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ROP	A	301	-	X	-	-
3	1HC	A	303	-	X	X	-



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2301 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 Amidase.

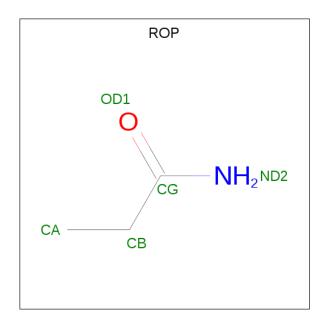
$\mathbf{Mol}$	Chain	Residues	Atoms				ZeroOcc	${f AltConf}$	Trace		
1	A	254	Total 1973	C 1243	N 351	O 373	S 6	0	14	0	

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	=	INITIATING METHIONINE	UNP D0VWZ1
A	-18	GLY	-	EXPRESSION TAG	UNP D0VWZ1
A	-17	SER	_	EXPRESSION TAG	UNP D0VWZ1
A	-16	SER	-	EXPRESSION TAG	UNP D0VWZ1
A	-15	HIS	_	EXPRESSION TAG	UNP D0VWZ1
A	-14	HIS	-	EXPRESSION TAG	UNP D0VWZ1
A	-13	HIS	_	EXPRESSION TAG	UNP D0VWZ1
A	-12	HIS	_	EXPRESSION TAG	UNP D0VWZ1
A	-11	HIS	-	EXPRESSION TAG	UNP D0VWZ1
A	-10	HIS	-	EXPRESSION TAG	UNP D0VWZ1
A	-9	SER	-	EXPRESSION TAG	UNP D0VWZ1
A	-8	SER	-	EXPRESSION TAG	UNP D0VWZ1
A	-7	GLY	_	EXPRESSION TAG	UNP D0VWZ1
A	-6	LEU	-	EXPRESSION TAG	UNP D0VWZ1
A	-5	VAL	=	EXPRESSION TAG	UNP D0VWZ1
A	-4	PRO	-	EXPRESSION TAG	UNP D0VWZ1
A	-3	ARG	-	EXPRESSION TAG	UNP D0VWZ1
A	-2	GLY	=	EXPRESSION TAG	UNP D0VWZ1
A	-1	SER	-	EXPRESSION TAG	UNP D0VWZ1
A	0	HIS	-	EXPRESSION TAG	UNP D0VWZ1
A	41	GLN	GLU	ENGINEERED MUTATION	UNP D0VWZ1

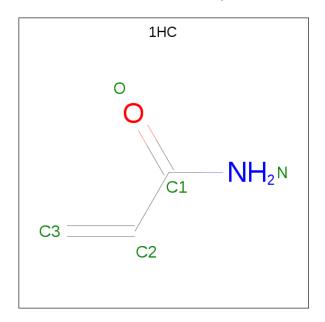
• Molecule 2 is PROPIONAMIDE (three-letter code: ROP) (formula: C<sub>3</sub>H<sub>7</sub>NO).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 5				0	0
2	A	1	Total 5	C 3		O 1	0	0

• Molecule 3 is prop-2-enamide (three-letter code: 1HC) (formula:  $C_3H_5NO$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 5	C 3	N 1	O 1	0	0

• Molecule 4 is water.

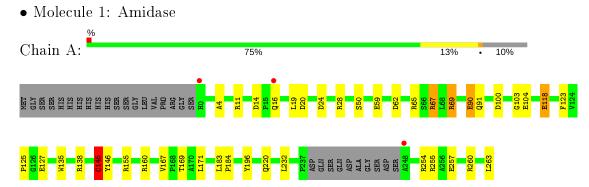


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	313	Total O 313 313	0	0



# 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.





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	76.10Å 115.45Å 65.93Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.05 - 1.40	Depositor
Resolution (A)	38.05 - 1.40	EDS
% Data completeness	99.5 (38.05-1.40)	Depositor
(in resolution range)	99.5 (38.05-1.40)	EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.62 (at 1.40Å)	Xtriage
Refinement program	REFMAC	Depositor
D D.	0.173 , 0.199	Depositor
$R, R_{free}$	0.172 , $0.198$	DCC
$R_{free}$ test set	2908 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.5	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.38 , 45.7	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.51, < L^2>=0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	2301	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.49% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: ROP, 1HC

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	${ m nd\ lengths}$	Bond angles		
			RMSZ	# Z  > 5	RMSZ	# Z >5	
	1	Α	1.53	$17/2073 \ (0.8\%)$	1.43	$29/2825 \; (1.0\%)$	

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	${ m Observed}( m \AA)$	$Ideal(\AA)$
1	A	160	ARG	CZ-NH1	8.22	1.43	1.33
1	A	257	GLU	CG-CD	8.05	1.64	1.51
1	A	67	ARG	CZ-NH1	7.39	1.42	1.33
1	A	255	ARG	CG-CD	-6.87	1.34	1.51
1	A	260	ARG	CZ-NH1	6.36	1.41	1.33
1	A	118[A]	GLU	CD-OE2	-6.24	1.18	1.25
1	A	118[B]	GLU	CD-OE2	-6.24	1.18	1.25
1	A	138	ARG	CB-CG	-6.11	1.36	1.52
1	A	145	CYS	CB-SG	6.06	1.92	1.82
1	A	67	ARG	CZ-NH2	5.96	1.40	1.33
1	A	127	GLU	CD-OE1	5.92	1.32	1.25
1	A	260	ARG	CB-CG	-5.66	1.37	1.52
1	A	263	LEU	C-O	5.65	1.34	1.23
1	A	255	ARG	CZ-NH1	5.64	1.40	1.33
1	A	260	ARG	CG-CD	5.30	1.65	1.51
1	A	59	GLU	CG-CD	5.26	1.59	1.51
1	A	135	TRP	CE2-CZ2	5.02	1.48	1.39

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	A	160	ARG	NE-CZ-NH2	-14.77	112.92	120.30
1	A	260	ARG	NE-CZ-NH2	-14.29	113.15	120.30
1	A	67	ARG	NE-CZ-NH1	-11.54	114.53	120.30
1	A	260	ARG	NE-CZ-NH1	11.50	126.05	120.30

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
1	A	160	ARG	NE-CZ-NH1	11.18	125.89	120.30
1	A	254	ARG	NE-CZ-NH2	-10.20	115.20	120.30
1	A	254	ARG	NE-CZ-NH1	9.93	125.27	120.30
1	A	69[A]	ARG	NE-CZ-NH1	-8.70	115.95	120.30
1	A	69[B]	ARG	NE-CZ-NH1	-8.70	115.95	120.30
1	A	14	ASP	CB-CG-OD2	-8.36	110.78	118.30
1	A	20	ASP	CB-CG-OD2	-6.66	112.31	118.30
1	A	24	ASP	CB-CG-OD2	-6.64	112.32	118.30
1	A	69[A]	ARG	CG-CD-NE	-6.64	97.86	111.80
1	A	69[B]	ARG	CG-CD-NE	-6.64	97.86	111.80
1	A	65	ARG	NE-CZ-NH2	-6.62	116.99	120.30
1	A	146	TYR	CB-CG-CD2	-6.33	117.20	121.00
1	A	62	ASP	CB-CG-OD2	-6.10	112.81	118.30
1	A	19	LEU	CB-CG-CD2	5.90	121.02	111.00
1	A	69[A]	ARG	CD-NE-CZ	5.87	131.82	123.60
1	A	69[B]	ARG	CD-NE-CZ	5.87	131.82	123.60
1	A	100	ASP	CB-CG-OD2	-5.77	113.11	118.30
1	A	155	ARG	NE-CZ-NH2	-5.71	117.44	120.30
1	A	20	ASP	CB-CG-OD1	5.57	123.31	118.30
1	A	123	PHE	CB-CG-CD1	-5.46	116.98	120.80
1	A	28[A]	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	A	28[B]	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	A	28[A]	ARG	NE-CZ-NH1	5.29	122.95	120.30
1	A	28[B]	ARG	NE-CZ-NH1	5.29	122.95	120.30
1	A	104	GLU	CG-CD-OE1	5.07	128.45	118.30

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	1973	0	1965	20	0
2	A	10	0	12	1	0
3	A	5	0	5	6	0
4	A	313	0	0	1	0

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Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
All	All	2301	0	1982	20	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 5.

All (20) 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	${ m distance} \; ({ m \AA})$	overlap (Å)
1:A:16[B]:GLN:OE1	3:A:303:1HC:H2	1.64	0.96
1:A:145:CYS:SG	1:A:169[A]:THR:OG1	2.38	0.80
1:A:90:GLU:OE2	1:A:91:GLN:HG3	1.84	0.78
1:A:171:LEU:HD22	1:A:196[B]:TYR:OH	1.84	0.77
1:A:67:ARG:HH21	3:A:303:1HC:C3	1.99	0.75
1:A:169[B]:THR:HG21	1:A:196[B]:TYR:CD1	2.39	0.58
1:A:67:ARG:HH21	3:A:303:1HC:H2	1.71	0.54
1:A:50[A]:SER:OG	1:A:118[A]:GLU:HG3	2.10	0.52
1:A:171:LEU:CD2	1:A:196[B]:TYR:OH	2.56	0.51
1:A:169[B]:THR:HG21	1:A:196[B]:TYR:CE1	2.46	0.51
1:A:67:ARG:NH2	3:A:303:1HC:H2	2.27	0.49
1:A:167:VAL:HG12	1:A:169[B]:THR:HG22	1.94	0.49
1:A:11[A]:ARG:NE	4:A:654:HOH:O	2.45	0.48
1:A:16[B]:GLN:OE1	3:A:303:1HC:C3	2.49	0.47
1:A:67:ARG:NH2	3:A:303:1HC:C3	2.75	0.45
1:A:69[B]:ARG:HG3	1:A:103:GLY:O	2.19	0.42
1:A:145:CYS:HB3	2:A:302:ROP:OD1	2.19	0.42
1:A:4:ALA:HA	1:A:232:LEU:O	2.21	0.41
1:A:183:LEU:HB2	1:A:184:PRO:HD3	2.02	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	
1	A	$264/283 \ (93\%)$	261 (99%)	2 (1%)	1 (0%)	34 12	

#### All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	145	CYS

#### 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	$209/219 \ (95\%)$	207 (99%)	2 (1%)	76 53	

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

Mol	Chain	Res	Type
1	A	90	GLU
1	A	125	PRO

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)

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

## 5.5 Carbohydrates (i)

There are no carbohydrates in this entry.



## 5.6 Ligand geometry (i)

3 ligands 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	Res Link	Bond lengths			Bond angles		
MIOI					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	1HC	A	303	_	4,4,4	1.78	1 (25%)	2,4,4	2.18	1 (50%)
2	ROP	A	302	1	4,4,4	1.31	0	4,4,4	1.23	1 (25%)
2	ROP	A	301	1	4,4,4	1.88	2 (50%)	4,4,4	2.10	1 (25%)

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	1HC	A	303	-	-	2/2/2/2	-
2	ROP	A	302	1	-	0/2/2/2	-
2	ROP	A	301	1	-	2/2/2/2	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	${f Atoms}$	$\mathbf{Z}$	${f Observed(\AA)}$	$\mathbf{Ideal}(\mathbf{\AA})$
3	A	303	1HC	O-C1	3.01	1.32	1.24
2	A	301	ROP	OD1-CG	-2.60	1.16	1.24
2	A	301	ROP	CA-CB	2.21	1.61	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	${f Atoms}$	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}(^{o})$
2	A	301	ROP	CA-CB-CG	-3.55	106.17	112.79
3	A	303	1HC	O-C1-N	3.06	129.10	122.58
2	A	302	ROP	OD1-CG-CB	-2.06	115.54	121.98

There are no chirality outliers.



All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	303	1HC	N-C1-C2-C3
2	A	301	ROP	CA-CB-CG-OD1
2	A	301	ROP	CA-CB-CG-ND2
3	A	303	1HC	O-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	303	1HC	6	0
2	A	302	ROP	1	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 (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.

$\mathbf{M}$	ol Chain	ain Analysed	<RSRZ $>$	$ ext{RSRZ}{>}$ #RSRZ ${>}2$		>2	$OWAB(Å^2)$	Q < 0.9
1	A	$254/283 \; (89\%)$	-0.05	3 (1%)	79	77	9, 13, 21, 33	11 (4%)

#### All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	A	0	HIS	5.4	
1	A	248	ALA	2.6	
1	A	16[A]	GLN	2.2	

### 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 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,  $95^{th}$  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
3	1HC	A	303	5/5	0.66	0.26	33,33,38,39	0
2	ROP	A	301	5/5	0.83	0.16	17,24,29,31	3
2	ROP	A	302	5/5	0.92	0.09	13,14,14,15	0



# 6.5 Other polymers (i)

There are no such residues in this entry.

