



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:24 AM GMT

PDB ID : 2ACT  
Title : CRYSTALLOGRAPHIC REFINEMENT OF THE STRUCTURE OF ACTINIDIN AT 1.7 ANGSTROMS RESOLUTION BY FAST FOURIER LEAST-SQUARES METHODS  
Authors : Baker, E.N.  
Deposited on : 1979-11-27  
Resolution : 1.70 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

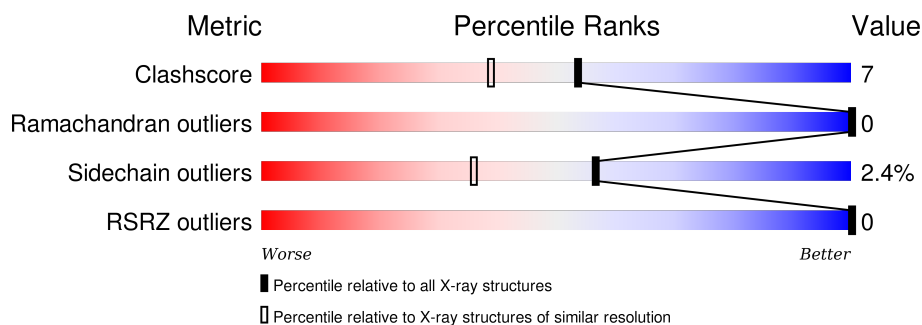
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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))
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$ . 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	220	

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	NH4	A	221	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1931 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.

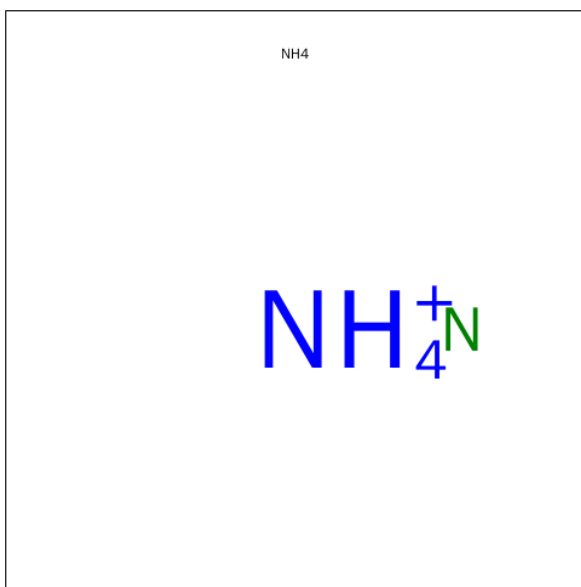
- Molecule 1 is a protein called ACTINIDIN PRECURSOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	5	0
			1658	1039	270	340	9			

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	THR	VAL	CONFLICT	UNP P00785
A	42	SER	THR	CONFLICT	UNP P00785
A	44	SER	VAL	CONFLICT	UNP P00785
A	66	ASP	ASN	CONFLICT	UNP P00785
A	80	ASP	ASN	CONFLICT	UNP P00785
A	97	ASP	GLU	CONFLICT	UNP P00785
A	99	ASP	ASN	CONFLICT	UNP P00785
A	100	VAL	LEU	CONFLICT	UNP P00785
A	101	ALA	ASP	CONFLICT	UNP P00785
A	104	ASP	ASN	CONFLICT	UNP P00785
A	105	GLN	GLU	CONFLICT	UNP P00785
A	146	GLN	HIS	CONFLICT	UNP P00785
A	148	ALA	SER	CONFLICT	UNP P00785
A	160	VAL	ILE	CONFLICT	UNP P00785
A	164	ILE	VAL	CONFLICT	UNP P00785
A	165	VAL	THR	CONFLICT	UNP P00785
A	175	VAL	ILE	CONFLICT	UNP P00785

- Molecule 2 is AMMONIUM ION (three-letter code: NH4) (formula: H<sub>4</sub>N).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total N 1 1	0	0

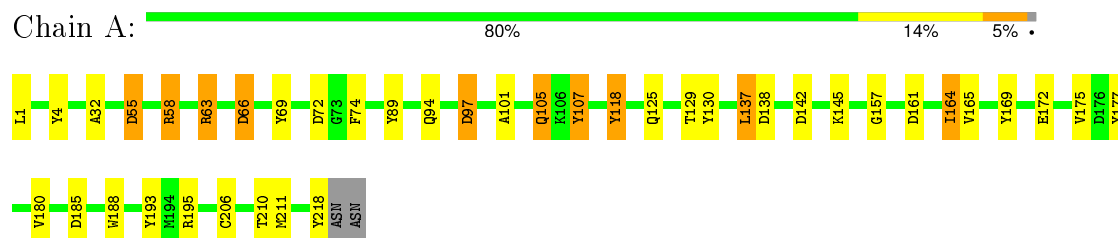
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	272	Total O 272 272	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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: ACTINIDIN PRECURSOR



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.20 Å 81.80 Å 33.03 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.70 40.90 – 1.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-1.70) 100.0 (40.90-1.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.30 (at 1.70 Å)	Xtriage
Refinement program	FAST-FOURIER LEAST-SQUARES REFINEMENT	Depositor
R, $R_{free}$	0.171 , (Not available) 0.159 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	10.6	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 45.6	EDS
Estimated twinning fraction	0.027 for k,h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 24142 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	1931	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.01% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: CSD, NH4

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	0.86	0/1713	1.90	47/2338 (2.0%)

There are no bond length outliers.

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	58[A]	ARG	NE-CZ-NH1	-13.88	113.36	120.30
1	A	58[B]	ARG	NE-CZ-NH1	-13.88	113.36	120.30
1	A	63	ARG	NE-CZ-NH1	12.38	126.49	120.30
1	A	97	ASP	CB-CG-OD2	-11.99	107.50	118.30
1	A	58[A]	ARG	CD-NE-CZ	-10.98	108.23	123.60
1	A	58[B]	ARG	CD-NE-CZ	-10.98	108.23	123.60
1	A	58[A]	ARG	NE-CZ-NH2	10.69	125.65	120.30
1	A	58[B]	ARG	NE-CZ-NH2	10.69	125.65	120.30
1	A	130	TYR	CB-CG-CD1	-10.36	114.78	121.00
1	A	185	ASP	CB-CG-OD1	-9.53	109.73	118.30
1	A	169	TYR	CB-CG-CD1	-9.24	115.46	121.00
1	A	97	ASP	CA-CB-CG	-9.02	93.56	113.40
1	A	107	TYR	CB-CG-CD1	-8.69	115.79	121.00
1	A	195	ARG	NE-CZ-NH1	-8.36	116.12	120.30
1	A	4	TYR	CB-CG-CD2	-8.24	116.05	121.00
1	A	4	TYR	CB-CG-CD1	8.01	125.80	121.00
1	A	218	TYR	CZ-CE2-CD2	-7.76	112.81	119.80
1	A	172	GLU	N-CA-CB	-7.68	96.78	110.60
1	A	185	ASP	CB-CG-OD2	7.11	124.69	118.30
1	A	177	TYR	CG-CD1-CE1	-7.09	115.63	121.30
1	A	69	TYR	CB-CG-CD1	-6.93	116.84	121.00
1	A	107	TYR	CA-CB-CG	-6.87	100.36	113.40
1	A	218	TYR	CG-CD1-CE1	-6.72	115.92	121.30
1	A	66	ASP	CA-CB-CG	-6.69	98.67	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	138	ASP	CB-CG-OD1	-6.61	112.35	118.30
1	A	72	ASP	CB-CG-OD2	-6.59	112.37	118.30
1	A	172	GLU	CB-CG-CD	6.57	131.93	114.20
1	A	94	GLN	CB-CA-C	-6.52	97.37	110.40
1	A	193	TYR	CB-CG-CD1	-6.31	117.21	121.00
1	A	94	GLN	CA-CB-CG	6.19	127.02	113.40
1	A	118	TYR	CB-CG-CD2	-6.14	117.32	121.00
1	A	145	LYS	CA-CB-CG	-6.08	100.02	113.40
1	A	177	TYR	CD1-CE1-CZ	6.04	125.24	119.80
1	A	63	ARG	CD-NE-CZ	6.03	132.04	123.60
1	A	66	ASP	CB-CG-OD2	-5.89	113.00	118.30
1	A	55	ASP	CB-CG-OD1	-5.65	113.22	118.30
1	A	218	TYR	CG-CD2-CE2	5.57	125.75	121.30
1	A	161	ASP	CB-CG-OD2	-5.56	113.29	118.30
1	A	175	VAL	CA-CB-CG1	-5.51	102.63	110.90
1	A	74	PHE	CB-CG-CD1	-5.34	117.06	120.80
1	A	211	MET	CG-SD-CE	5.30	108.68	100.20
1	A	193	TYR	CG-CD2-CE2	-5.23	117.12	121.30
1	A	130	TYR	CB-CA-C	-5.21	99.99	110.40
1	A	69	TYR	CD1-CG-CD2	5.19	123.61	117.90
1	A	188	TRP	CB-CG-CD2	-5.14	119.92	126.60
1	A	142	ASP	CA-CB-CG	-5.12	102.13	113.40
1	A	105	GLN	N-CA-CB	-5.07	101.47	110.60

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	1658	0	1548	21	0
2	A	1	0	0	0	0
3	A	272	0	0	6	2
All	All	1931	0	1548	21	2

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 7.

All (21) 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:101:ALA:HB2	3:A:313:HOH:O	1.16	1.29
1:A:58[B]:ARG:CZ	3:A:413:HOH:O	2.20	0.89
1:A:32:ALA:HB3	1:A:165:VAL:HG21	1.55	0.89
1:A:164:ILE:HG13	1:A:180:VAL:HG13	1.55	0.86
1:A:55:ASP:HA	1:A:58[B]:ARG:HH12	1.49	0.77
1:A:58[B]:ARG:NH1	3:A:413:HOH:O	2.21	0.72
1:A:164:ILE:HG13	1:A:180:VAL:CG1	2.21	0.71
1:A:125:GLN:O	1:A:129[B]:THR:HG23	1.94	0.68
1:A:55:ASP:HA	1:A:58[B]:ARG:NH1	2.14	0.61
1:A:58[B]:ARG:NH1	3:A:412:HOH:O	2.35	0.59
1:A:118:TYR:HB2	1:A:210:THR:O	2.04	0.57
1:A:32:ALA:CB	1:A:165:VAL:HG21	2.31	0.57
1:A:137:LEU:HG	1:A:164:ILE:CD1	2.41	0.51
1:A:58[A]:ARG:CG	1:A:58[A]:ARG:NH1	2.71	0.51
1:A:97:ASP:N	1:A:97:ASP:OD2	2.48	0.46
1:A:1:LEU:HD22	1:A:129[B]:THR:HG21	1.98	0.45
1:A:101:ALA:CB	3:A:313:HOH:O	2.03	0.44
1:A:105:GLN:HG2	1:A:107:TYR:CE2	2.53	0.43
1:A:157:GLY:O	1:A:206:CYS:HA	2.20	0.42
1:A:137:LEU:HD21	1:A:164:ILE:HD12	2.02	0.41
1:A:63:ARG:HB2	3:A:446:HOH:O	2.20	0.41

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:425:HOH:O	3:A:493:HOH:O[2_655]	0.85	1.35
3:A:338:HOH:O	3:A:465:HOH:O[2_655]	2.18	0.02

## 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	220/220 (100%)	214 (97%)	6 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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	175/173 (101%)	171 (98%)	4 (2%)	58	37

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	ASP
1	A	89	TYR
1	A	137	LEU
1	A	164	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
1	CSD	A	25	1	3,7,8	0.63	0	3,8,10	5.05	2 (66%)

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	CSD	A	25	1	-	0/2/6/8	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	25	CSD	OD1-SG-CB	-8.17	91.79	105.40
1	A	25	CSD	O-C-CA	-2.95	117.80	125.49

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 1 ligands modelled in this entry, 1 is modelled with single atom - 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

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 [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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	217/220 (98%)	-0.50	0 100 100	5, 9, 23, 33	0

There are no RSRZ outliers to report.

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	CSD	A	25	8/9	0.97	0.09	-	5,7,15,22	2

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NH4	A	221	1/1	0.99	0.22	12.09	8,8,8,8	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.