



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:41 PM GMT

PDB ID : 1BZX
Title : THE CRYSTAL STRUCTURE OF ANIONIC SALMON TRYPSIN IN COM-
PLEX WITH BOVINE PANCREATIC TRYPSIN INHIBITOR
Authors : Helland, R.; Leiros, I.; Berglund, G.I.; Willassen, N.P.; Smalas, A.O.
Deposited on : 1998-11-05
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

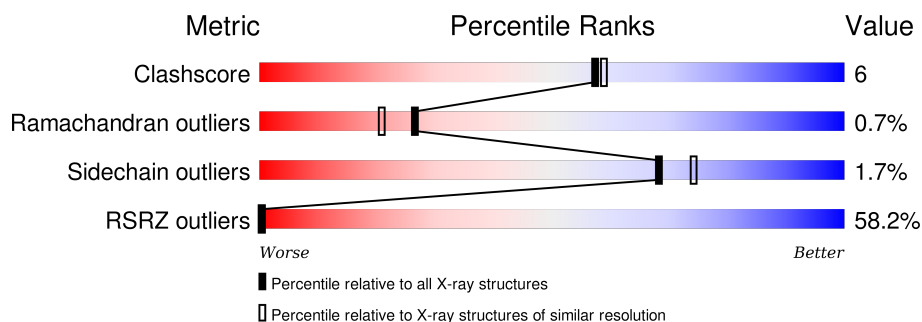
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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. 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	E	222	
2	I	58	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2219 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 PROTEIN (TRYPSIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	222	Total	C	N	O	S	58	3	0
			1675	1046	280	330	19			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	24	PRO	ALA	CONFLICT	UNP P35031
E	28	PRO	THR	CONFLICT	UNP P35031

- Molecule 2 is a protein called PROTEIN (BOVINE PANCREATIC TRYPSIN INHIBITOR).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	58	Total	C	N	O	S	19	1	0
			458	287	84	79	8			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	1	Total	Ca	0	0
			1	1		

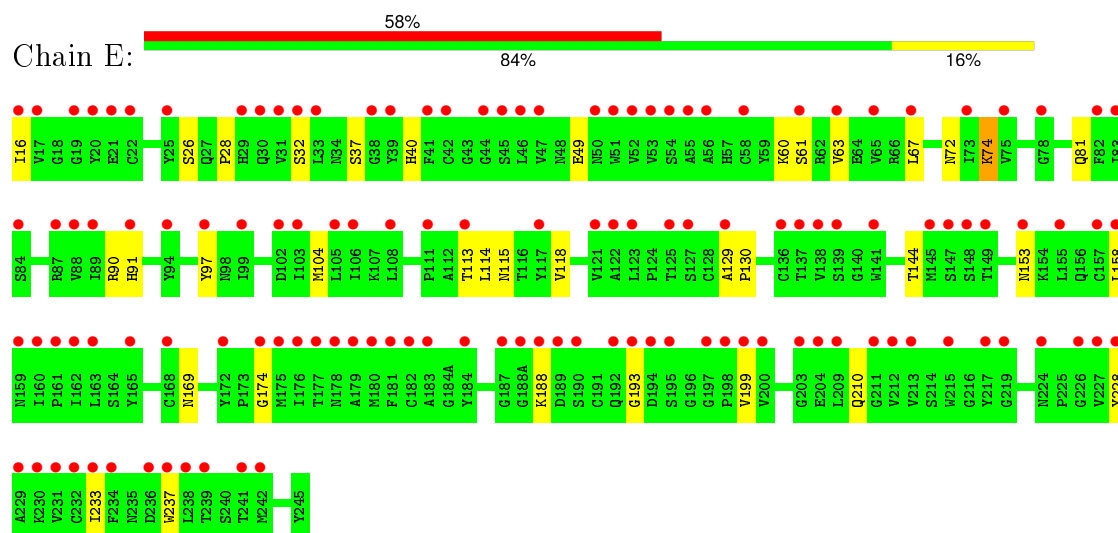
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	66	Total	O	0	0
			66	66		
4	I	19	Total	O	0	0
			19	19		

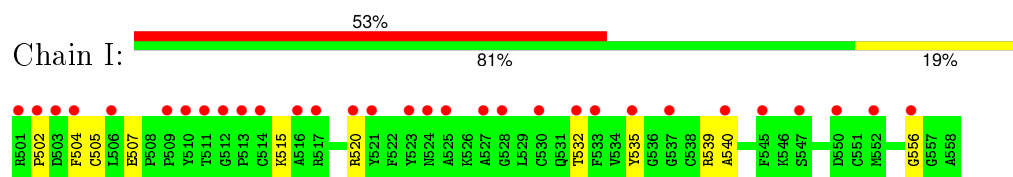
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ($RSRZ > 2$). 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: PROTEIN (TRYPSIN)



• Molecule 2: PROTEIN (BOVINE PANCREATIC TRYPSIN INHIBITOR)



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	84.12Å 84.12Å 222.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.10 27.33 – 2.13	Depositor EDS
% Data completeness (in resolution range)	97.3 (8.00-2.10) 95.4 (27.33-2.13)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 2.14Å)	Xtriage
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.206 , 0.238 0.440 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	38.3	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 95.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 25738 reflections	Xtriage
F_o, F_c correlation	0.73	EDS
Total number of atoms	2219	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: CA

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	E	0.49	0/1728	0.70	0/2351
2	I	0.59	1/473 (0.2%)	0.71	0/632
All	All	0.52	1/2201 (0.0%)	0.71	0/2983

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	515	LYS	C-N	-6.07	1.20	1.34

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	E	1675	0	1582	20	0
2	I	458	0	439	5	0
3	E	1	0	0	0	0
4	E	66	0	0	1	0
4	I	19	0	0	0	0
All	All	2219	0	2021	24	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 6.

All (24) 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:E:74:LYS:HE3	1:E:74:LYS:HA	1.69	0.74
2:I:504:PHE:O	2:I:507:GLU:HG2	2.00	0.62
2:I:502:PRO:HG2	2:I:505:CYS:SG	2.40	0.60
1:E:169:ASN:HD21	1:E:174:GLY:H	1.53	0.55
2:I:535:TYR:CZ	2:I:540:ALA:HB2	2.42	0.55
1:E:114:LEU:HA	1:E:118:VAL:O	2.11	0.49
1:E:97:TYR:O	2:I:539:ARG:NH2	2.46	0.49
1:E:210:GLN:NE2	4:E:781:HOH:O	2.46	0.49
1:E:90:ARG:HA	1:E:104:MET:HB2	1.95	0.49
1:E:26:SER:C	1:E:28:PRO:HD3	2.32	0.48
1:E:32:SER:OG	1:E:40:HIS:HD2	1.97	0.47
1:E:113:THR:O	1:E:115:ASN:ND2	2.48	0.47
1:E:60:LYS:HB2	1:E:63[B]:VAL:CG1	2.47	0.45
1:E:129:ALA:HA	1:E:130:PRO:HD3	1.67	0.45
1:E:74:LYS:HE3	1:E:74:LYS:CA	2.43	0.44
1:E:67:LEU:HD12	1:E:81:GLN:O	2.18	0.44
1:E:91:HIS:HA	1:E:237:TRP:CZ2	2.53	0.43
2:I:520:ARG:O	2:I:532:THR:HA	2.18	0.43
1:E:158:LEU:HD11	1:E:188:LYS:HB3	2.01	0.43
1:E:16:ILE:O	1:E:144:THR:HA	2.19	0.42
1:E:72:ASN:HA	1:E:153:ASN:O	2.19	0.42
1:E:40:HIS:HE1	1:E:193:GLY:O	2.02	0.42
1:E:199:VAL:HG21	1:E:228:TYR:CD2	2.54	0.42
1:E:169:ASN:ND2	1:E:174:GLY:H	2.16	0.40

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	E	223/222 (100%)	215 (96%)	7 (3%)	1 (0%)	39	37
2	I	57/58 (98%)	56 (98%)	0	1 (2%)	11	5
All	All	280/280 (100%)	271 (97%)	7 (2%)	2 (1%)	26	21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	49	GLU
2	I	556	GLY

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	E	190/187 (102%)	186 (98%)	4 (2%)	61	66
2	I	47/46 (102%)	47 (100%)	0	100	100
All	All	237/233 (102%)	233 (98%)	4 (2%)	68	74

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

Mol	Chain	Res	Type
1	E	37	SER
1	E	61	SER
1	E	74	LYS
1	E	233	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	30	GLN
1	E	40	HIS
1	E	169	ASN
1	E	192	GLN
1	E	202	ASN

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Mol	Chain	Res	Type
1	E	210	GLN
1	E	224	ASN
2	I	531	GLN

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 1 ligands modelled in this entry, 1 is 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 ⓘ

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, 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(Å ²)	Q<0.9
1	E	219/222 (98%)	2.47	129 (58%) 0 0	18, 35, 57, 75	8 (3%)
2	I	56/58 (96%)	2.27	31 (55%) 0 0	17, 32, 57, 67	3 (5%)
All	All	275/280 (98%)	2.43	160 (58%) 0 0	17, 34, 57, 75	11 (4%)

All (160) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	22	CYS	6.7
1	E	242	MET	6.0
1	E	172	TYR	5.9
1	E	229	ALA	5.4
2	I	525	ALA	5.4
1	E	203	GLY	5.3
1	E	117	TYR	5.2
1	E	165	TYR	5.2
1	E	53	VAL	5.1
2	I	540	ALA	4.8
2	I	530	CYS	4.8
2	I	514	CYS	4.7
1	E	89	ILE	4.6
1	E	193	GLY	4.6
1	E	55	ALA	4.6
1	E	153	ASN	4.5
2	I	552[A]	MET	4.5
1	E	228	TYR	4.5
1	E	181	PHE	4.5
1	E	197	GLY	4.5
2	I	523	TYR	4.4
1	E	61	SER	4.3
1	E	215	TRP	4.3
1	E	16	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
1	E	162	ILE	4.3
1	E	121	VAL	4.3
1	E	239	THR	4.2
1	E	175[A]	MET	4.2
1	E	195	SER	4.2
1	E	148	SER	4.2
1	E	234	PHE	4.1
1	E	187	GLY	4.1
1	E	51	TRP	4.1
1	E	237	TRP	4.1
1	E	94	TYR	4.0
1	E	212	VAL	4.0
1	E	213	VAL	4.0
1	E	67	LEU	4.0
1	E	217	TYR	4.0
1	E	84	SER	3.9
1	E	183	ALA	3.9
1	E	136	CYS	3.9
1	E	125	THR	3.9
1	E	209	LEU	3.9
1	E	219	GLY	3.9
2	I	506	LEU	3.8
2	I	509	PRO	3.8
1	E	163	LEU	3.8
1	E	97	TYR	3.8
2	I	502	PRO	3.8
1	E	155	LEU	3.7
1	E	47	VAL	3.7
1	E	113	THR	3.7
2	I	527	ALA	3.6
1	E	63[A]	VAL	3.6
1	E	231	VAL	3.6
1	E	20	TYR	3.5
1	E	179	ALA	3.5
1	E	139	SER	3.5
1	E	190	SER	3.5
1	E	108	LEU	3.5
1	E	184	TYR	3.4
1	E	39	TYR	3.4
2	I	545	PHE	3.3
1	E	33	LEU	3.3
1	E	182	CYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	E	147	SER	3.3
1	E	226	GLY	3.3
1	E	19	GLY	3.2
1	E	204	GLU	3.2
1	E	25	TYR	3.2
2	I	535	TYR	3.2
2	I	550	ASP	3.2
1	E	188	LYS	3.2
1	E	211	GLY	3.2
1	E	194	ASP	3.2
1	E	29	HIS	3.2
1	E	41	PHE	3.2
1	E	158	LEU	3.2
1	E	188(A)	GLY	3.1
1	E	138	VAL	3.1
2	I	537	GLY	3.1
2	I	511	THR	3.1
1	E	52	VAL	3.1
1	E	103	ILE	3.1
2	I	524	ASN	3.1
1	E	111	PRO	3.1
1	E	137	THR	3.1
1	E	78	GLY	3.0
1	E	199	VAL	3.0
1	E	233	ILE	3.0
1	E	105	LEU	2.9
2	I	516	ALA	2.9
2	I	501	ARG	2.9
2	I	556	GLY	2.9
1	E	56	ALA	2.9
1	E	160	ILE	2.9
1	E	232	CYS	2.9
2	I	510	TYR	2.9
1	E	91	HIS	2.8
1	E	38	GLY	2.8
1	E	241	THR	2.8
1	E	180	MET	2.7
1	E	32	SER	2.7
1	E	123	LEU	2.7
1	E	46	LEU	2.7
1	E	174	GLY	2.6
1	E	145	MET	2.6

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Mol	Chain	Res	Type	RSRZ
1	E	176	ILE	2.6
1	E	17	VAL	2.6
1	E	99	ILE	2.6
1	E	161	PRO	2.5
2	I	503	ASP	2.5
2	I	533	PHE	2.5
1	E	200	VAL	2.5
1	E	149	THR	2.5
1	E	87	ARG	2.5
1	E	31	VAL	2.5
1	E	227	VAL	2.4
1	E	54	SER	2.4
1	E	122	ALA	2.4
1	E	65	VAL	2.4
1	E	75	VAL	2.4
2	I	512	GLY	2.4
1	E	58	CYS	2.4
1	E	168	CYS	2.4
1	E	82	PHE	2.4
1	E	127	SER	2.4
1	E	50	ASN	2.4
1	E	83	ILE	2.3
1	E	73	ILE	2.3
1	E	44	GLY	2.3
2	I	547	SER	2.3
2	I	532	THR	2.3
1	E	189	ASP	2.3
1	E	88	VAL	2.3
1	E	102	ASP	2.3
1	E	129	ALA	2.3
1	E	30	GLN	2.2
1	E	106	ILE	2.2
1	E	45	SER	2.2
1	E	238	LEU	2.2
1	E	224	ASN	2.2
1	E	157	CYS	2.2
1	E	177	THR	2.2
1	E	230	LYS	2.2
2	I	521	TYR	2.2
2	I	513	PRO	2.2
1	E	236	ASP	2.2
1	E	159	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	141	TRP	2.1
2	I	504	PHE	2.1
1	E	192	GLN	2.1
2	I	528	GLY	2.1
1	E	198	PRO	2.0
1	E	21	GLU	2.0
1	E	42	CYS	2.0
2	I	517	ARG	2.0
2	I	520	ARG	2.0
1	E	178	ASN	2.0

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. 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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	CA	E	700	1/1	0.47	0.14	-3.72	52,52,52,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.