



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:04 PM UTC

PDB ID : 7PC9 / pdb_00007pc9
Title : The PDZ domain of SYNJ2BP complexed with the PDZ-binding motif of HTLV1-TAX1
Authors : Cousido-Siah, A.; Trave, G.; Gogl, G.
Deposited on : 2021-08-03
Resolution : 2.40 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Xtrriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

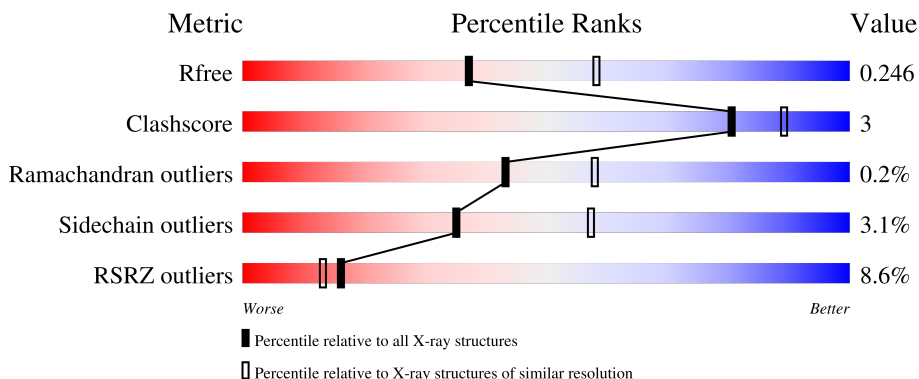
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 of 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 $\leq 5\%$. 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	415	 4% 90% 8%
1	B	415	 13% 87% 9%
2	C	10	 70% 10% 20%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6854 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 Synaptojanin-2-binding protein,Annexin A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	397	3160	1973	553	623	11	0	0	0
1	A	407	3247	2026	569	641	11	0	1	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	2	GLY	-	expression tag	UNP P57105
B	3	SER	-	expression tag	UNP P57105
B	4	HIS	-	expression tag	UNP P57105
B	5	MET	-	expression tag	UNP P57105
B	104	GLY	-	linker	UNP P57105
B	105	SER	-	linker	UNP P57105
B	143	GLU	ALA	conflict	UNP P07355
A	2	GLY	-	expression tag	UNP P57105
A	3	SER	-	expression tag	UNP P57105
A	4	HIS	-	expression tag	UNP P57105
A	5	MET	-	expression tag	UNP P57105
A	104	GLY	-	linker	UNP P57105
A	105	SER	-	linker	UNP P57105
A	143	GLU	ALA	conflict	UNP P07355

- Molecule 2 is a protein called Protein Tax-1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	8	74	46	14	14	0	0	0

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	5	Total Ca 5 5	0	0
3	A	5	Total Ca 5 5	0	0

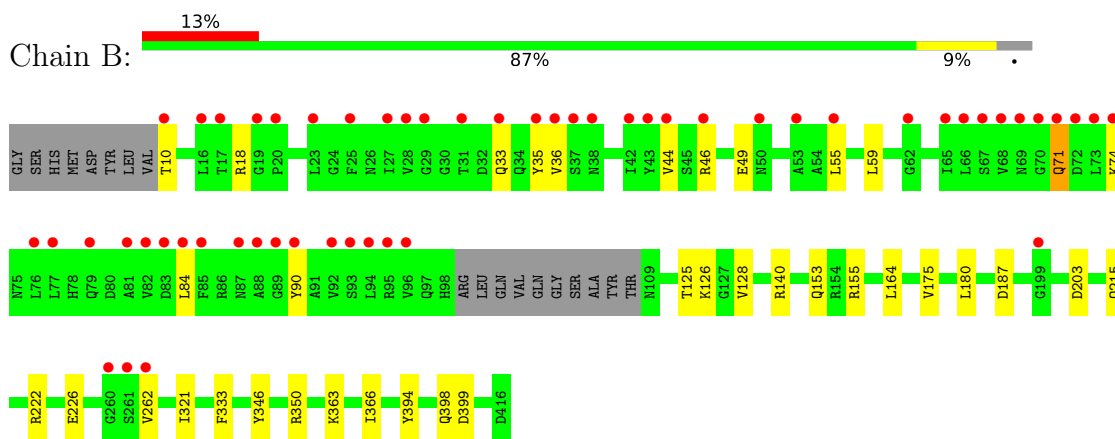
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	187	Total O 187 187	0	0
4	A	173	Total O 173 173	0	0
4	C	3	Total O 3 3	0	0

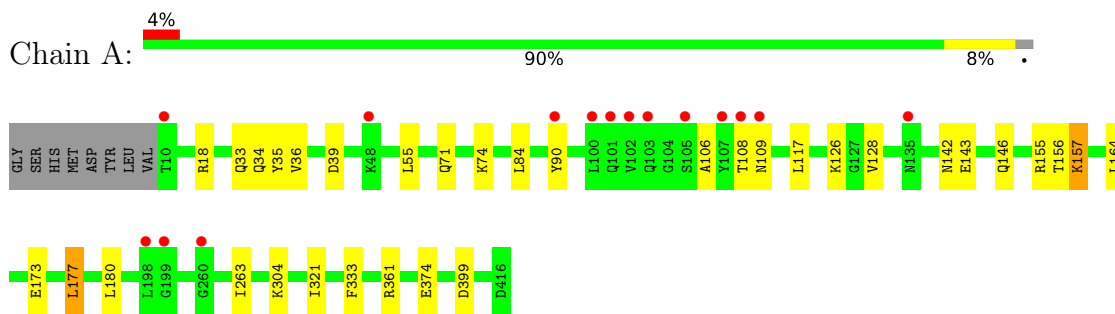
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

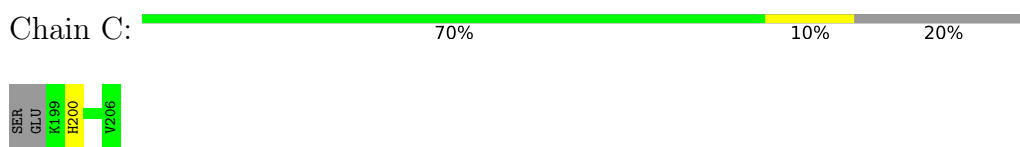
- Molecule 1: Synaptojanin-2-binding protein,Annexin A2



- Molecule 1: Synaptojanin-2-binding protein,Annexin A2



- Molecule 2: Protein Tax-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.99Å 99.85Å 173.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.33 – 2.40 49.33 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.3 (49.33-2.40) 99.3 (49.33-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 2.39Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.203 , 0.243 0.205 , 0.246	Depositor DCC
R_{free} test set	2068 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	38.9	Xtrriage
Anisotropy	0.172	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6854	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.55% 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, 0.333 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: 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	A	0.16	0/3288	0.34	0/4418
1	B	0.15	0/3199	0.32	0/4296
2	C	0.17	0/75	0.37	0/97
All	All	0.16	0/6562	0.33	0/8811

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	3247	0	3256	15	0
1	B	3160	0	3172	20	0
2	C	74	0	69	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	173	0	0	1	0
4	B	187	0	0	9	0
4	C	3	0	0	0	0
All	All	6854	0	6497	34	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 3.

All (34) 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:B:18:ARG:HB3	1:B:90:TYR:HA	1.80	0.64
1:A:106:ALA:HB3	1:A:109:ASN:HB2	1.82	0.60
1:B:155:ARG:NH1	4:B:604:HOH:O	2.21	0.56
1:B:90:TYR:OH	1:A:117:LEU:HG	2.06	0.55
1:B:10:THR:N	4:B:612:HOH:O	2.41	0.52
1:A:117:LEU:HD13	1:A:155:ARG:NE	2.24	0.52
1:B:126:LYS:NZ	4:B:610:HOH:O	2.34	0.52
1:A:18:ARG:HB3	1:A:90:TYR:HA	1.90	0.51
1:A:142:ASN:N	1:A:374:GLU:OE2	2.41	0.50
1:A:156:THR:O	1:A:157:LYS:HG2	2.12	0.49
1:A:142:ASN:O	1:A:146:GLN:HG2	2.13	0.48
1:A:164:LEU:HD12	1:A:180:LEU:HD11	1.95	0.48
1:B:262:VAL:O	4:B:601:HOH:O	2.20	0.48
1:B:222:ARG:NH1	1:B:226:GLU:OE2	2.47	0.48
1:B:363:LYS:NZ	4:B:616:HOH:O	2.42	0.47
1:B:350:ARG:NH1	4:B:613:HOH:O	2.41	0.47
1:B:187:ASP:OD1	4:B:602:HOH:O	2.20	0.47
1:B:394:TYR:O	1:B:398:GLN:HG2	2.15	0.47
1:B:44:VAL:HG21	1:B:59:LEU:HD11	1.98	0.46
1:A:173:GLU:HG2	1:A:177:LEU:HD22	1.98	0.46
1:B:74:LYS:HE3	1:B:74:LYS:HB2	1.79	0.45
1:A:74:LYS:HE3	1:A:74:LYS:HB2	1.82	0.45
1:A:33:GLN:O	1:A:35:TYR:N	2.44	0.44
1:B:175:VAL:HG22	1:B:366:ILE:HG23	1.98	0.44
1:B:215:GLN:OE1	4:B:603:HOH:O	2.21	0.44
1:A:321:ILE:HD13	1:A:333:PHE:HB3	1.99	0.43
1:A:143:GLU:HG3	4:A:663:HOH:O	2.19	0.43
1:B:71:GLN:O	1:B:71:GLN:HG3	2.18	0.43
1:B:321:ILE:HD13	1:B:333:PHE:HB3	2.00	0.42
1:A:34:GLN:HA	1:A:39:ASP:O	2.20	0.42
1:B:164:LEU:HD12	1:B:180:LEU:HD11	2.02	0.41
1:B:346:TYR:HA	4:B:622:HOH:O	2.20	0.41
1:B:33:GLN:C	1:B:35:TYR:H	2.28	0.40
1:A:263:ILE:HD13	1:A:304:LYS:HE2	2.04	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	A	406/415 (98%)	397 (98%)	8 (2%)	1 (0%)	43	58
1	B	393/415 (95%)	385 (98%)	7 (2%)	1 (0%)	36	50
2	C	6/10 (60%)	6 (100%)	0	0	100	100
All	All	805/840 (96%)	788 (98%)	15 (2%)	2 (0%)	43	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	128	VAL
1	B	128	VAL

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	353/359 (98%)	343 (97%)	10 (3%)	38	60
1	B	344/359 (96%)	333 (97%)	11 (3%)	34	56
2	C	8/10 (80%)	7 (88%)	1 (12%)	4	6
All	All	705/728 (97%)	683 (97%)	22 (3%)	35	57

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	36	VAL

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Mol	Chain	Res	Type
1	B	46	ARG
1	B	49	GLU
1	B	55	LEU
1	B	71	GLN
1	B	84	LEU
1	B	125	THR
1	B	140	ARG
1	B	153	GLN
1	B	203	ASP
1	B	399	ASP
1	A	36	VAL
1	A	55	LEU
1	A	71	GLN
1	A	84	LEU
1	A	108	THR
1	A	126	LYS
1	A	157	LYS
1	A	177	LEU
1	A	361	ARG
1	A	399	ASP
2	C	200	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	341	GLN
1	B	405	GLN
1	A	405	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 10 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

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	A	407/415 (98%)	-0.07	15 (3%) 45 41	17, 43, 75, 96	1 (0%)
1	B	397/415 (95%)	0.31	55 (13%) 6 5	26, 45, 145, 167	0
2	C	8/10 (80%)	0.85	0 100 100	56, 66, 78, 85	0
All	All	812/840 (96%)	0.12	70 (8%) 16 13	17, 44, 128, 167	1 (0%)

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	73	LEU	4.8
1	B	65	ILE	4.7
1	B	69	ASN	4.7
1	B	90	TYR	4.7
1	B	94	LEU	4.6
1	B	35	TYR	4.4
1	A	90	TYR	4.4
1	B	36	VAL	4.3
1	B	70	GLY	4.2
1	B	68	VAL	4.2
1	A	102	VAL	3.9
1	B	77	LEU	3.9
1	B	44	VAL	3.8
1	B	10	THR	3.8
1	B	92	VAL	3.7
1	A	107	TYR	3.7
1	A	100	LEU	3.6
1	B	55	LEU	3.5
1	B	20	PRO	3.3
1	B	67	SER	3.3
1	B	71	GLN	3.3
1	A	103	GLN	3.3
1	B	42	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	28	VAL	3.2
1	B	66	LEU	3.1
1	B	27	ILE	3.1
1	A	260	GLY	3.1
1	B	43	TYR	3.0
1	B	37	SER	3.0
1	B	87	ASN	3.0
1	B	23	LEU	3.0
1	B	19	GLY	3.0
1	B	89	GLY	3.0
1	A	108	THR	2.9
1	B	74	LYS	2.9
1	B	76	LEU	2.9
1	A	101	GLN	2.9
1	B	72	ASP	2.7
1	A	109	ASN	2.7
1	B	29	GLY	2.7
1	B	17	THR	2.7
1	A	10	THR	2.7
1	B	96	VAL	2.6
1	B	95	ARG	2.6
1	B	82	VAL	2.5
1	B	31	THR	2.5
1	B	83	ASP	2.5
1	A	199	GLY	2.4
1	B	84	LEU	2.4
1	B	199	GLY	2.4
1	B	261	SER	2.3
1	B	262	VAL	2.3
1	B	38	ASN	2.3
1	B	81	ALA	2.3
1	B	85	PHE	2.3
1	A	48	LYS	2.2
1	B	46	ARG	2.2
1	B	53	ALA	2.2
1	B	33	GLN	2.2
1	B	93	SER	2.2
1	B	79	GLN	2.2
1	A	105	SER	2.2
1	B	260	GLY	2.2
1	B	62	GLY	2.1
1	A	198	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	16	LEU	2.1
1	A	135	ASN	2.1
1	B	25	PHE	2.0
1	B	50	ASN	2.0
1	B	88	ALA	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 oligosaccharides 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
3	CA	B	501	1/1	0.79	0.12	127,127,127,127	0
3	CA	A	502	1/1	0.81	0.09	102,102,102,102	0
3	CA	A	503	1/1	0.94	0.06	69,69,69,69	0
3	CA	B	503	1/1	0.95	0.06	77,77,77,77	0
3	CA	B	502	1/1	0.96	0.04	68,68,68,68	0
3	CA	A	501	1/1	0.97	0.05	64,64,64,64	0
3	CA	B	505	1/1	0.99	0.02	36,36,36,36	0
3	CA	B	504	1/1	0.99	0.04	50,50,50,50	0
3	CA	A	504	1/1	0.99	0.04	41,41,41,41	0
3	CA	A	505	1/1	0.99	0.03	35,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.