



wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 08:56 am BST

PDB ID : 5MFQ
Title : Crystal structure of the GluK1 ligand-binding domain in complex with kainate and BPAM-344 at 1.90 Å resolution
Authors : Larsen, A.P.; Frydenvang, K.; Kastrup, J.S.
Deposited on : 2016-11-18
Resolution : 1.90 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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

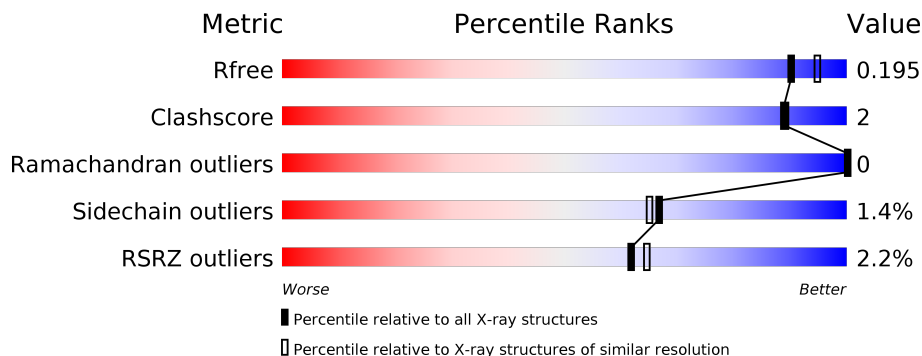
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 $\leq 5\%$. 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	257	 93% 5%
1	B	257	 94% 5%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4788 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.

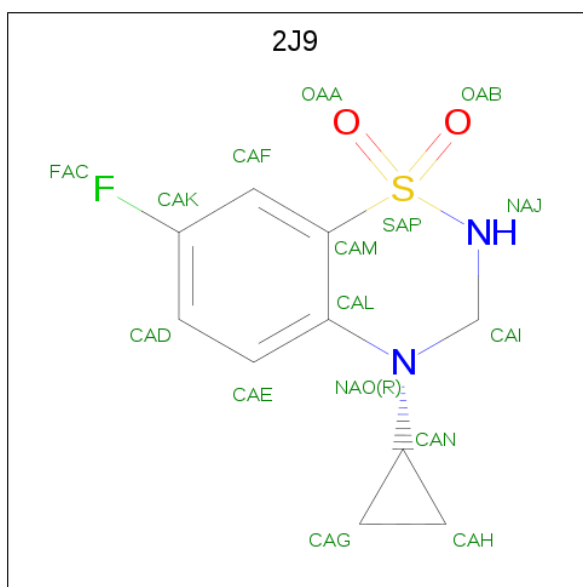
- Molecule 1 is a protein called Glutamate receptor ionotropic, kainate 1, Glutamate receptor ionotropic, kainate 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	253	2048	1308	340	388	12	0	6	0
1	B	254	2067	1322	341	392	12	0	8	0

There are 8 discrepancies between the modelled and reference sequences:

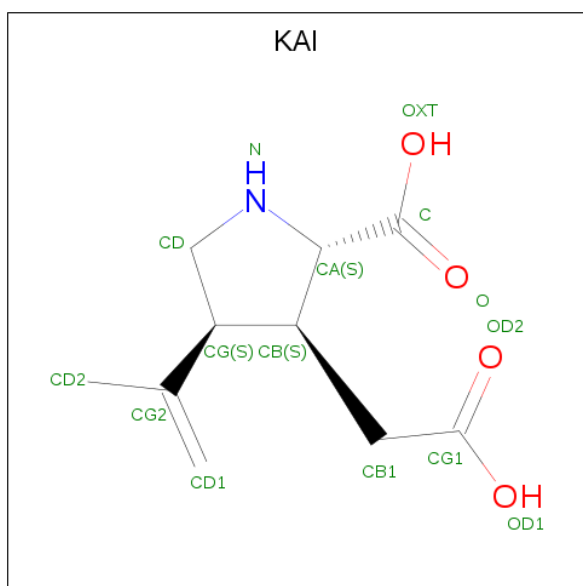
Chain	Residue	Modelled	Actual	Comment	Reference
A	429	GLY	-	cloning artifact	UNP P22756
A	462	GLY	ALA	conflict	UNP P22756
A	545	GLY	-	linker	UNP P22756
A	546	THR	-	linker	UNP P22756
B	429	GLY	-	cloning artifact	UNP P22756
B	462	GLY	ALA	conflict	UNP P22756
B	545	GLY	-	linker	UNP P22756
B	546	THR	-	linker	UNP P22756

- Molecule 2 is 4-cyclopropyl-7-fluoro-3,4-dihydro-2H-1,2,4-benzothiadiazine 1,1-dioxide (three-letter code: 2J9) (formula: C₁₀H₁₁FN₂O₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf		
			Total	C	F	N	O			S	
2	A	1	Total	16	10	1	2	2	1	0	0
2	A	1	Total	16	10	1	2	2	1	0	0

- Molecule 3 is 3-(CARBOXYMETHYL)-4-ISOPROPENYLPROLINE (three-letter code: KAI) (formula: C₁₀H₁₅NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			
3	A	1	Total	15	10	1	4	0	0

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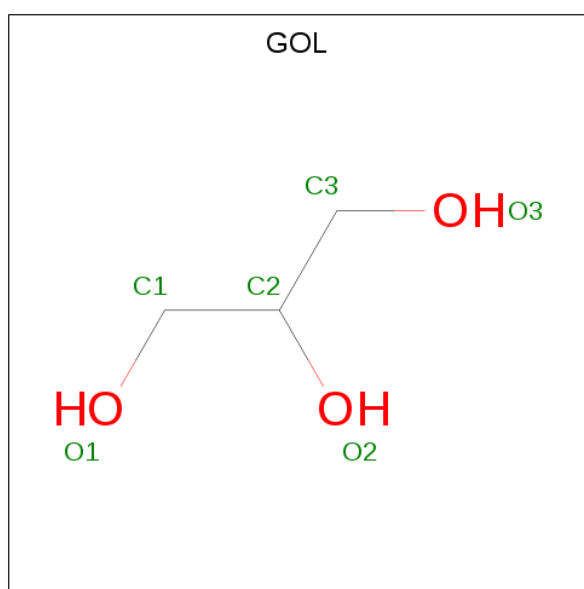
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	B	1	15	10	1	4	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
4	A	1	1	1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	6	3	3	0	0
5	A	1	6	3	3	0	0
5	B	1	6	3	3	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

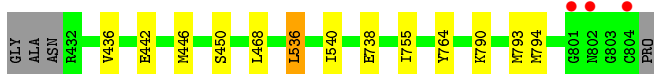
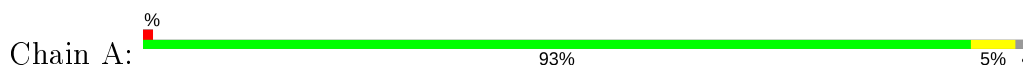
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	285	Total	O	0	0
			285	285		
7	B	297	Total	O	0	0
			297	297		

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: Glutamate receptor ionotropic, kainate 1, Glutamate receptor ionotropic, kainate 1



- Molecule 1: Glutamate receptor ionotropic, kainate 1, Glutamate receptor ionotropic, kainate 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.01Å 71.01Å 234.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.43 – 1.90 29.43 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.43-1.90) 99.8 (29.43-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.96 (at 1.91Å)	Xtrriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.155 , 0.195 0.155 , 0.195	Depositor DCC
R_{free} test set	2452 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	18.2	Xtrriage
Anisotropy	0.642	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4788	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.93% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, KAI, SO4, 2J9, 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	0.34	0/2104	0.49	0/2836
1	B	0.34	0/2130	0.53	0/2871
All	All	0.34	0/4234	0.51	0/5707

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 [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	2048	0	2080	8	0
1	B	2067	0	2104	7	0
2	A	32	0	22	0	0
3	A	15	0	13	0	0
3	B	15	0	13	0	0
4	A	1	0	0	0	0
5	A	12	0	16	0	0
5	B	6	0	8	2	0
6	A	5	0	0	0	0
6	B	5	0	0	0	0
7	A	285	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	297	0	0	3	0
All	All	4788	0	4256	16	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 16 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:459:ARG:HH12	5:B:902:GOL:H31	1.66	0.61
1:A:790:LYS:NZ	1:A:794:MET:HG3	2.22	0.55
1:A:790:LYS:HZ2	1:A:794:MET:HG3	1.73	0.53
1:A:540:ILE:HB	1:A:755:ILE:HB	1.96	0.48
1:A:442:GLU:HG2	1:A:446:MET:SD	2.54	0.47

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	257/257 (100%)	254 (99%)	3 (1%)	0	100	100
1	B	260/257 (101%)	254 (98%)	6 (2%)	0	100	100
All	All	517/514 (101%)	508 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	227/223 (102%)	225 (99%)	2 (1%)	78	79
1	B	230/223 (103%)	226 (98%)	4 (2%)	60	57
All	All	457/446 (102%)	451 (99%)	6 (1%)	67	68

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	494	ASP
1	B	713	GLN
1	B	536	LEU
1	A	536	LEU
1	B	678	THR

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](#)

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 for Mogul analysis.

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
2	2J9	A	901	-	17,18,18	2.24	5 (29%)	23,28,28	5.20	4 (17%)
6	SO4	A	907	-	4,4,4	0.14	0	6,6,6	0.07	0
5	GOL	A	905	-	5,5,5	0.37	0	5,5,5	0.56	0
5	GOL	A	906	-	5,5,5	0.39	0	5,5,5	0.28	0
5	GOL	B	902	-	5,5,5	0.32	0	5,5,5	0.38	0
3	KAI	A	903	-	6,15,15	0.69	0	8,21,21	0.65	0
3	KAI	B	901	-	6,15,15	0.59	0	8,21,21	0.63	0
6	SO4	B	903	-	4,4,4	0.14	0	6,6,6	0.11	0
2	2J9	A	902	-	17,18,18	2.36	6 (35%)	23,28,28	4.98	5 (21%)

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
2	2J9	A	901	-	-	0/4/22/22	0/3/3/3
5	GOL	A	905	-	-	2/4/4/4	-
5	GOL	A	906	-	-	4/4/4/4	-
5	GOL	B	902	-	-	4/4/4/4	-
3	KAI	A	903	-	-	0/6/25/25	0/1/1/1
3	KAI	B	901	-	-	0/6/25/25	0/1/1/1
2	2J9	A	902	-	-	0/4/22/22	0/3/3/3

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	902	2J9	SAP-NAJ	5.27	1.70	1.63
2	A	901	2J9	SAP-NAJ	4.94	1.69	1.63
2	A	902	2J9	OAA-SAP	4.29	1.48	1.43
2	A	901	2J9	OAA-SAP	4.27	1.48	1.43
2	A	901	2J9	OAB-SAP	3.99	1.48	1.43

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	2J9	CAI-NAO-CAL	24.23	121.09	110.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	902	2J9	CAI-NAO-CAL	22.97	120.53	110.25
2	A	902	2J9	CAM-SAP-NAJ	-3.24	99.80	102.37
2	A	901	2J9	CAF-CAM-SAP	-3.21	117.19	119.82
2	A	902	2J9	CAK-CAF-CAM	2.78	118.76	116.86

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	905	GOL	O1-C1-C2-C3
5	A	906	GOL	O1-C1-C2-C3
5	B	902	GOL	O1-C1-C2-C3
5	B	902	GOL	C1-C2-C3-O3
5	A	906	GOL	C1-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	902	GOL	2	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, 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	253/257 (98%)	-0.23	3 (1%) 79 81	9, 19, 38, 68	0
1	B	254/257 (98%)	-0.22	8 (3%) 49 51	9, 19, 42, 72	0
All	All	507/514 (98%)	-0.23	11 (2%) 62 64	9, 19, 40, 72	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	804	CYS	4.1
1	B	804	CYS	3.2
1	B	802	ASN	3.1
1	B	494	ASP	3.0
1	A	801	GLY	2.9

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, 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(\AA^2)	Q<0.9
6	SO4	B	903	5/5	0.76	0.19	75,79,81,85	0
5	GOL	A	906	6/6	0.83	0.24	34,45,55,58	0
5	GOL	B	902	6/6	0.87	0.18	31,39,46,53	0
5	GOL	A	905	6/6	0.93	0.18	17,36,42,43	0
6	SO4	A	907	5/5	0.94	0.14	69,70,77,77	0
3	KAI	A	903	15/15	0.97	0.10	8,12,18,20	0
3	KAI	B	901	15/15	0.98	0.08	8,13,19,23	0
2	2J9	A	901	16/16	0.99	0.12	7,9,14,14	0
4	CL	A	904	1/1	0.99	0.05	26,26,26,26	0
2	2J9	A	902	16/16	0.99	0.10	8,11,14,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.