

Full wwPDB X-ray Structure Validation Report (i)

Apr 21, 2024 – 12:04 am BST

PDB ID : 10KO

Title: Crystal structure of Pseudomonas Aeruginosa Lectin 1 complexed with galac-

tose at 1.6 A resolution

Authors: Cioci, G.; Mitchell, E.; Gautier, C.; Wimmerova, M.; Perez, S.; Gilboa-Garber,

N.; Imberty, A.

Deposited on : 2003-07-28

Resolution : 1.60 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

Mol Probity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.36.2

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

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

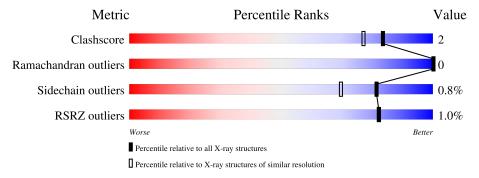
Validation Pipeline (wwPDB-VP) : 2.36.2

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 1.60 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	Similar resolution
Wiedlie	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 <=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	121	95%	5%
1	В	121	93%	7% •
1	С	121	95%	•••
1	D	121	96%	•



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 4272 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 PA-I GALACTOPHILIC LECTIN.

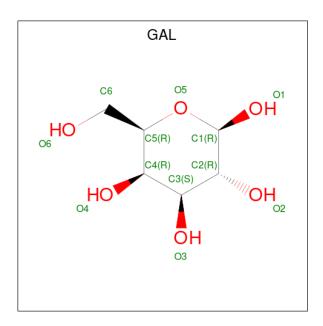
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	121	Total	С	N	О	S	0	3	0
1	A	121	922	578	160	181	3	0	3	U
1	В	121	Total	С	N	О	S	0	4	0
1	Б	121	929	582	161	183	3	0	4	U
1	С	121	Total	С	N	О	S	0	4	0
1		121	927	583	160	181	3	0	4	U
1	1 D	121	Total	С	N	О	S	0	0	0
1		121	901	567	156	175	3	0	U	U

• Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	В	1	Total Ca 1 1	0	0
2	С	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0

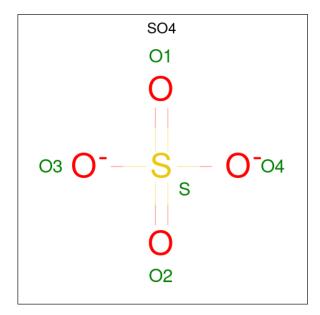
• Molecule 3 is beta-D-galactopyranose (three-letter code: GAL) (formula: C₆H₁₂O₆).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	Λ	1	Total C O	0	0
3	A	1	12 6 6	U	U
3	В	1	Total C O	0	1
3	Б	1	12 6 6	U	
3	С	1	Total C O	0	1
3	3	1	12 6 6	U	1
3	D	1	Total C O	0	1
3	D	1	12 6 6	U	1

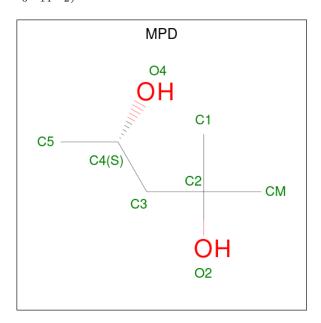
 \bullet Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: $\mathrm{O_4S}).$





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

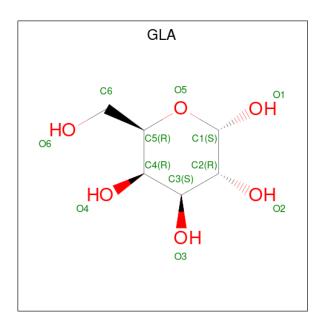
 \bullet Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 8 6 2	0	0

• Molecule 6 is alpha-D-galactopyranose (three-letter code: GLA) (formula: $C_6H_{12}O_6$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	В	1	Total C O 12 6 6	0	1
6	С	1	Total C O 12 6 6	0	1
6	D	1	Total C O 12 6 6	0	1

• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	137	Total O 137 137	0	0
7	В	104	Total O 104 104	0	0
7	С	120	Total O 120 120	0	0
7	D	121	Total O 121 121	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: PA-I GALACTOPHILIC LECTIN

Chain A:

95%

• Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain B:

93%

7%

• Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain C:

95%

• Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain C:

95%

• Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain C:

95%

• Molecule 1: PA-I GALACTOPHILIC LECTIN

Chain D:

96%

• Molecule 1: PA-I GALACTOPHILIC LECTIN



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	49.06Å 53.27Å 160.68Å	Donogitor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	18.60 - 1.60	Depositor
resolution (A)	18.59 - 1.60	EDS
% Data completeness	94.9 (18.60-1.60)	Depositor
(in resolution range)	95.0 (18.59-1.60)	EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.91 (at 1.60Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.154 , 0.187	Depositor
It, It free	0.169 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	11.2	Xtriage
Anisotropy	0.500	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34, 45.3	EDS
L-test for twinning ²	$ < L >=0.45, < L^2>=0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4272	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.54% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities 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: SO4, GLA, CA, GAL, MPD

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	
MIOI	Mol Chain		RMSZ $ $ $\# Z > 5$		# Z > 5
1	A	0.76	0/945	0.83	$2/1287 \ (0.2\%)$
1	В	0.77	0/952	0.80	0/1301
1	С	2.36	2/950~(0.2%)	0.80	0/1295
1	D	0.82	0/924	0.84	$1/1262 \ (0.1\%)$
All	All	1.36	$2/3771 \ (0.1\%)$	0.82	3/5145 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	${f Z}$	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
1	С	121[A]	SER	C-OXT	48.53	2.15	1.23
1	С	121[B]	SER	C-OXT	48.53	2.15	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
1	A	59	ASP	CB-CG-OD2	7.29	124.86	118.30
1	D	100	ASP	CB-CG-OD2	5.31	123.08	118.30
1	A	119	ASP	CB-CG-OD2	5.12	122.91	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	922	0	878	6	0
1	В	929	0	882	8	0
1	С	927	0	886	7	0
1	D	901	0	861	3	0
2	A	1	0	0	0	0
2	В	1	0	0	0	0
2	С	1	0	0	0	0
2	D	1	0	0	0	0
3	A	12	0	10	0	0
3	В	12	0	10	0	0
3	С	12	0	10	0	0
3	D	12	0	10	0	0
4	A	10	0	0	0	0
4	В	5	0	0	0	0
5	A	8	0	14	0	0
6	В	12	0	10	0	0
6	С	12	0	9	0	0
6	D	12	0	9	0	0
7	A	137	0	0	0	0
7	В	104	0	0	3	0
7	С	120	0	0	0	0
7	D	121	0	0	1	0
All	All	4272	0	3589	18	0

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is 2.

All (18) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:120[B]:GLN:HE22	1:C:120:GLN:H	1.38	0.72
1:B:95[A]:THR:HG23	7:B:2080:HOH:O	1.99	0.63
1:B:15:VAL:HA	1:B:95[A]:THR:HG22	1.81	0.62
1:A:120[A]:GLN:HE22	1:C:120:GLN:H	1.50	0.60
1:B:63:GLY:HA2	1:B:98:TYR:CZ	2.38	0.58
1:B:95[A]:THR:HG21	7:B:2081:HOH:O	2.03	0.57
1:B:10:ASN:HD22	1:B:10:ASN:C	2.10	0.54
1:A:120[A]:GLN:HG3	1:D:118:LYS:O	2.13	0.49
1:A:63:GLY:HA2	1:A:98:TYR:CZ	2.48	0.48
1:A:120[B]:GLN:NE2	1:C:120:GLN:H	2.09	0.46
1:B:119:ASP:HA	1:C:120:GLN:HG3	1.98	0.46
1:D:63:GLY:HA2	1:D:98:TYR:CZ	2.51	0.45

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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance} ({ m \AA})$	overlap (Å)
1:C:63:GLY:HA2	1:C:98:TYR:CZ	2.52	0.44
1:C:41:LYS:NZ	1:C:109:SER:OG	2.51	0.43
1:D:19:ILE:HD12	7:D:2041:HOH:O	2.18	0.43
1:A:120[A]:GLN:NE2	1:C:120:GLN:H	2.13	0.43
1:B:28:ILE:HD12	1:B:81:LEU:HD12	2.01	0.42
1:B:91:GLN:NE2	7:B:2077:HOH:O	2.55	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	Percentile	es
1	A	121/121 (100%)	118 (98%)	3 (2%)	0	100 100)
1	В	123/121 (102%)	119 (97%)	4 (3%)	0	100 100)
1	С	122/121 (101%)	119 (98%)	3 (2%)	0	100 100)
1	D	119/121 (98%)	117 (98%)	2 (2%)	0	100 100)
All	All	485/484 (100%)	473 (98%)	12 (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	97/94 (103%)	96 (99%)	1 (1%)	76	61	
1	В	98/94 (104%)	97 (99%)	1 (1%)	76	61	
1	С	98/94 (104%)	96 (98%)	2 (2%)	55	31	
1	D	94/94 (100%)	94 (100%)	0	100	100	
All	All	387/376 (103%)	383 (99%)	4 (1%)	81	61	

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

Mol	Chain	Res	Type
1	A	48	ARG
1	В	10	ASN
1	С	121[A]	SER
1	С	121[B]	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	ASN
1	В	10	ASN
1	В	91	GLN
1	С	53	GLN
1	С	91	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 15 ligands modelled in this entry, 4 are monoatomic - leaving 11 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	Trunc	Chain	Res	Link	Во	ond leng	ths	Bond angles		
MIOI	Type	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	A	903	-	4,4,4	0.19	0	6,6,6	0.39	0
3	GAL	D	902[B]	-	12,12,12	0.90	0	17,17,17	0.82	1 (5%)
3	GAL	A	901	2	12,12,12	0.63	0	17,17,17	1.11	2 (11%)
6	GLA	В	901[A]	-	12,12,12	0.76	0	17,17,17	0.74	0
6	GLA	D	901[A]	_	12,12,12	1.05	1 (8%)	17,17,17	0.79	1 (5%)
3	GAL	С	902[B]	-	12,12,12	0.61	0	17,17,17	0.93	0
6	GLA	С	901[A]	_	12,12,12	0.68	0	17,17,17	0.94	0
3	GAL	В	902[B]	-	12,12,12	0.62	0	17,17,17	0.72	0
4	SO4	В	904	-	4,4,4	0.20	0	6,6,6	0.42	0
4	SO4	A	902	-	4,4,4	0.40	0	6,6,6	0.24	0
5	MPD	A	905	-	7,7,7	0.75	0	9,10,10	0.65	0

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	GAL	D	902[B]	-	-	0/2/22/22	0/1/1/1
3	GAL	A	901	2	-	0/2/22/22	0/1/1/1
6	GLA	В	901[A]	-	-	0/2/22/22	0/1/1/1
6	GLA	D	901[A]	-	-	0/2/22/22	0/1/1/1
3	GAL	С	902[B]	-	-	0/2/22/22	0/1/1/1
6	GLA	С	901[A]	-	-	0/2/22/22	0/1/1/1
3	GAL	В	902[B]	-	-	0/2/22/22	0/1/1/1
5	MPD	A	905	-	-	0/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(Å)	$Ideal(\AA)$
6	D	901[A]	GLA	O1-C1	-2.06	1.33	1.39

All (4) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
3	D	902[B]	GAL	C4-C3-C2	-2.21	106.96	110.82
6	D	901[A]	GLA	C4-C3-C2	-2.21	106.96	110.82
3	A	901	GAL	O5-C1-C2	-2.11	106.52	110.28
3	A	901	GAL	O2-C2-C1	2.08	113.98	109.16

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 (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.

Mol	Chain	Analysed	$\langle { m RSRZ} \rangle$	# RSRZ > 2	$OWAB(A^2)$	Q < 0.9
1	A	121/121 (100%)	-0.28	1 (0%) 86 86	6, 11, 19, 23	0
1	В	121/121 (100%)	-0.00	3 (2%) 57 55	8, 13, 23, 34	0
1	С	121/121 (100%)	-0.16	1 (0%) 86 86	6, 12, 20, 28	0
1	D	121/121 (100%)	-0.31	0 100 100	6, 10, 17, 20	0
All	All	484/484 (100%)	-0.19	5 (1%) 82 82	6, 11, 20, 34	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	В	87	PRO	3.5	
1	В	89	ASN	3.5	
1	С	88	ASN	3.0	
1	В	71[A]	ASN	2.5	
1	A	121[A]	SER	2.3	

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 monosaccharides 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
5	MPD	A	905	8/8	0.86	0.12	17,19,20,23	0
4	SO4	A	902	5/5	0.87	0.18	32,34,37,41	0
4	SO4	A	903	5/5	0.91	0.20	38,39,40,40	0
3	GAL	A	901	12/12	0.93	0.10	9,14,19,25	0
3	GAL	С	902[B]	12/12	0.95	0.08	8,11,15,17	12
6	GLA	С	901[A]	12/12	0.95	0.09	8,11,15,19	12
6	GLA	В	901[A]	12/12	0.96	0.08	11,16,18,21	12
3	GAL	В	902[B]	12/12	0.97	0.08	11,16,18,22	12
3	GAL	D	902[B]	12/12	0.97	0.07	9,10,14,15	12
4	SO4	В	904	5/5	0.97	0.15	35,36,38,38	0
6	GLA	D	901[A]	12/12	0.97	0.07	9,10,14,17	12
2	CA	В	900	1/1	0.99	0.05	9,9,9,9	0
2	CA	D	900	1/1	1.00	0.04	8,8,8,8	0
2	CA	A	900	1/1	1.00	0.04	8,8,8,8	0
2	CA	С	900	1/1	1.00	0.05	7,7,7,7	0

6.5 Other polymers (i)

There are no such residues in this entry.

