wwPDB X-ray Structure Validation Summary Report (i)

May 25, 2020 – 04:50 pm BST

PDB ID	:	1VS0
Title	:	Crystal Structure of the Ligase Domain from M. tuberculosis LigD at 2.4A
Authors	:	Akey, D.; Martins, A.; Aniukwu, J.; Glickman, M.S.; Shuman, S.; Berger, J.M.; TB Structural Genomics Consortium (TBSGC)
Deposited on	:	2006-01-27
Resolution	:	2.40 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 (i) symbol.

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

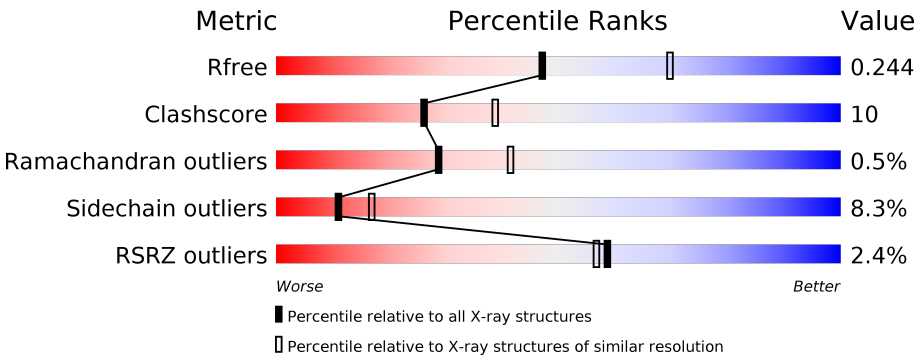
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (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 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 <=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	310	3% 79% 15% • •
1	B	310	2% 72% 22% 5% •

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
3	CL	A	9005	-	-	X	-
3	CL	A	9007	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5287 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 Putative DNA ligase-like protein Rv0938/MT0965.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S	Se			
1	A	299	2409	1507	452	442	1	3	4	26	4	0
1	B	305	2462	1536	460	457	1	3	5	46	7	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	450	GLY	-	CLONING ARTIFACT	UNP P71571
A	451	ALA	-	CLONING ARTIFACT	UNP P71571
A	461	MSE	MET	MODIFIED RESIDUE	UNP P71571
A	481	APK	LYS	MODIFIED RESIDUE	UNP P71571
A	545	MSE	MET	MODIFIED RESIDUE	UNP P71571
A	665	MSE	MET	MODIFIED RESIDUE	UNP P71571
A	694	MSE	MET	MODIFIED RESIDUE	UNP P71571
B	450	GLY	-	CLONING ARTIFACT	UNP P71571
B	451	ALA	-	CLONING ARTIFACT	UNP P71571
B	461	MSE	MET	MODIFIED RESIDUE	UNP P71571
B	481	APK	LYS	MODIFIED RESIDUE	UNP P71571
B	545	MSE	MET	MODIFIED RESIDUE	UNP P71571
B	665	MSE	MET	MODIFIED RESIDUE	UNP P71571
B	694	MSE	MET	MODIFIED RESIDUE	UNP P71571

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
2	B	2	2	2	0	0
2	A	2	2	2	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total Cl 2 2	0	0
3	A	2	Total Cl 2 2	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 5 is water.

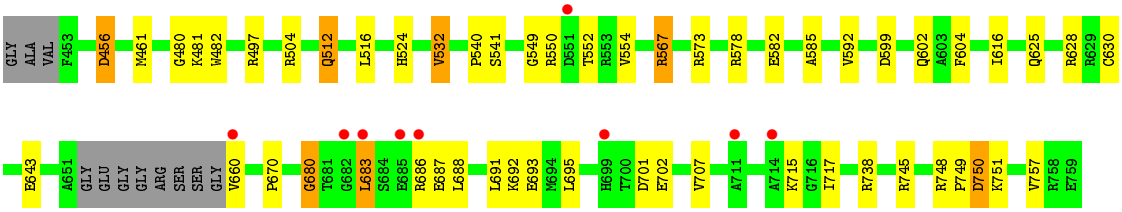
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	223	Total O 223 223	0	0
5	B	184	Total O 184 184	0	0

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.

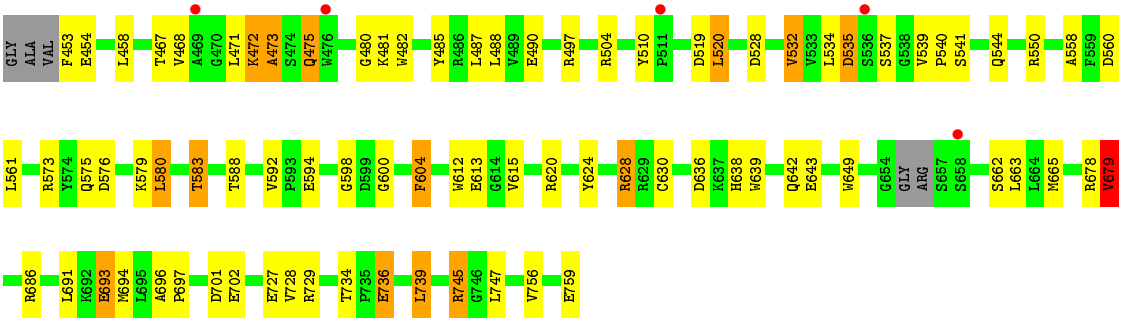
- Molecule 1: Putative DNA ligase-like protein Rv0938/MT0965

Chain A:



- Molecule 1: Putative DNA ligase-like protein Rv0938/MT0965

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	57.10Å 57.10Å 368.96Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.40 28.55 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (50.00-2.40) 99.2 (28.55-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	19.74 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, R_{free}	0.192 , 0.248 0.186 , 0.244	Depositor DCC
R_{free} test set	1453 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	36.3	Xtriage
Anisotropy	0.325	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 39.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.056 for -h,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5287	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

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: APK, ZN, MG, 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	0.72	2/2428 (0.1%)	0.81	2/3278 (0.1%)
1	B	1.06	6/2483 (0.2%)	0.95	8/3350 (0.2%)
All	All	0.91	8/4911 (0.2%)	0.88	10/6628 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	504	ARG	CD-NE	-31.17	0.93	1.46
1	B	472	LYS	CD-CE	-17.76	1.06	1.51
1	B	693	GLU	CG-CD	-12.24	1.33	1.51
1	B	686	ARG	CD-NE	10.50	1.64	1.46
1	A	550	ARG	CB-CG	9.69	1.78	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	504	ARG	CG-CD-NE	19.33	152.40	111.80
1	B	472	LYS	CD-CE-NZ	14.06	144.04	111.70
1	B	472	LYS	CG-CD-CE	12.16	148.39	111.90
1	B	504	ARG	CD-NE-CZ	9.76	137.26	123.60
1	B	679	VAL	CB-CA-C	-6.42	99.20	111.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	480	GLY	Mainchain

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	2409	0	2360	38	2
1	B	2462	0	2399	56	1
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	2	0	0	3	1
3	B	2	0	0	1	1
4	A	1	0	0	0	0
5	A	223	0	0	13	1
5	B	184	0	0	10	2
All	All	5287	0	4759	96	5

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 10.

The worst 5 of 96 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:481:APK:HC	1:A:482:TRP:N	0.98	1.30
1:A:481:APK:HC	1:A:482:TRP:CA	1.81	1.10
1:B:480:GLY:C	1:B:481:APK:H2	1.63	0.93
1:A:582:GLU:OE2	5:A:9022:HOH:O	1.88	0.92
1:B:532:VAL:HG22	1:B:540:PRO:HB3	1.54	0.90

All (5) 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)
1:A:456:ASP:OD2	1:B:701:ASP:OD2[2_674]	1.94	0.26
3:B:9008:CL:CL	5:B:9178:HOH:O[4_456]	1.99	0.21
1:A:456:ASP:OD2	1:A:750:ASP:OD2[6_655]	2.06	0.14
5:B:9037:HOH:O	5:B:9124:HOH:O[4_566]	2.16	0.04
3:A:9007:CL:CL	5:A:9220:HOH:O[6_665]	2.17	0.03

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	298/310 (96%)	292 (98%)	5 (2%)	1 (0%)	41	55
1	B	307/310 (99%)	300 (98%)	5 (2%)	2 (1%)	22	32
All	All	605/620 (98%)	592 (98%)	10 (2%)	3 (0%)	29	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	535	ASP
1	B	473	ALA
1	A	680	GLY

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	244/241 (101%)	225 (92%)	19 (8%)	12	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	250/241 (104%)	229 (92%)	21 (8%)	11 16
All	All	494/482 (102%)	454 (92%)	40 (8%)	11 18

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	757	VAL
1	B	532	VAL
1	B	736	GLU
1	B	519	ASP
1	B	534	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	544	GLN
1	B	741	GLN
1	B	642	GLN
1	A	610	HIS
1	B	638	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are 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	APK	B	481	1,2	29,33,33	1.26	5 (17%)	28,47,47	2.31	6 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	APK	A	481	1,2	29,33,33	1.53	5 (17%)	28,47,47	2.39	5 (17%)

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	APK	B	481	1,2	-	1/15/37/37	0/3/3/3
1	APK	A	481	1,2	-	1/15/37/37	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	481	APK	O4'-C1'	3.55	1.46	1.41
1	A	481	APK	P-O2P	-3.49	1.47	1.56
1	A	481	APK	P-NZ	3.39	1.65	1.61
1	B	481	APK	P-O2P	-3.06	1.48	1.56
1	B	481	APK	P-NZ	-2.86	1.58	1.61

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	481	APK	P-NZ-CE	-9.15	111.58	124.67
1	B	481	APK	P-NZ-CE	-6.68	115.12	124.67
1	B	481	APK	O2P-P-O1P	5.51	121.48	109.92
1	B	481	APK	N3-C2-N1	-5.22	120.52	128.68
1	A	481	APK	N3-C2-N1	-4.33	121.91	128.68

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	481	APK	O4'-C4'-C5'-O5'
1	B	481	APK	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	481	APK	6	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	481	APK	7	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 9 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	2
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	480:GLY	C	481:APK	N	1.81
1	A	481:APK	C	482:TRP	N	1.75
1	B	481:APK	C	482:TRP	N	1.71

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	294/310 (94%)	-0.25	9 (3%)	49	47	15, 28, 54, 78	6 (2%)
1	B	300/310 (96%)	-0.20	5 (1%)	70	68	21, 33, 49, 65	12 (4%)
All	All	594/620 (95%)	-0.23	14 (2%)	59	57	15, 31, 52, 78	18 (3%)

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	685	GLU	4.1
1	A	682	GLY	3.9
1	B	476	TRP	3.7
1	A	699	HIS	3.3
1	A	686	ARG	3.0

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. 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
1	APK	B	481	31/31	0.97	0.20	24,32,36,38	0
1	APK	A	481	31/31	0.98	0.17	13,24,29,31	0

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(Å^2)	Q<0.9
3	CL	B	9006	1/1	0.94	0.06	54,54,54,54	0
2	ZN	B	9001	1/1	0.95	0.04	34,34,34,34	0
3	CL	A	9005	1/1	0.96	0.05	38,38,38,38	0
4	MG	A	9009	1/1	0.96	0.06	23,23,23,23	0
2	ZN	A	9004	1/1	0.99	0.02	21,21,21,21	0
3	CL	A	9007	1/1	0.99	0.03	24,24,24,24	0
2	ZN	A	9002	1/1	0.99	0.04	21,21,21,21	0
3	CL	B	9008	1/1	0.99	0.02	26,26,26,26	0
2	ZN	B	9003	1/1	1.00	0.01	23,23,23,23	0

6.5 Other polymers (i)

There are no such residues in this entry.