



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 29, 2017 – 01:03 PM EST

PDB ID : 5WS2
Title : Crystal structure of mpy-RNase J (mutant S247A), an archaeal RNase J from Methanlobus psychrophilus R15, complex with RNA
Authors : Li, D.F.; Feng, N.
Deposited on : unknown
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

<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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

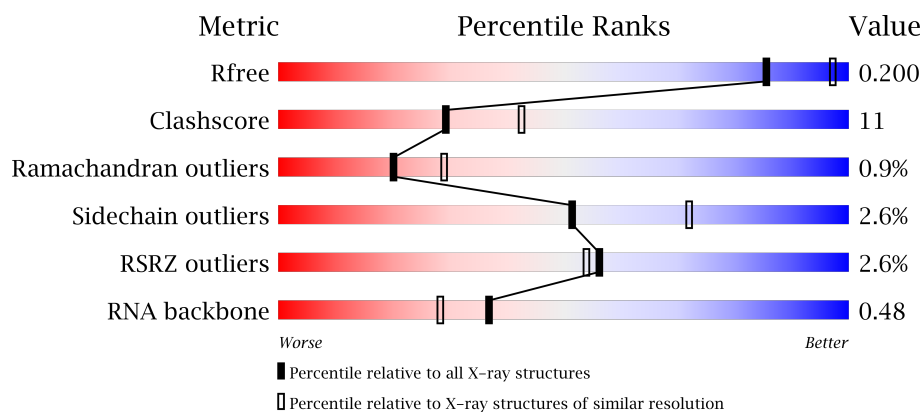
1 Overall quality at a glance

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}	100719	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)
RNA backbone	2435	1034 (2.86-1.94)

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	A	470	<div> <div>3%</div> <div> <div></div> <div>77%</div> <div>19%</div> <div>..</div> </div> </div>
1	B	470	<div> <div>3%</div> <div> <div></div> <div>77%</div> <div>19%</div> <div>..</div> </div> </div>
2	C	5	<div> <div>60%</div> <div>20%</div> <div>20%</div> </div>
2	D	5	<div> <div>40%</div> <div>20%</div> <div>20%</div> <div>20%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7790 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 Ribonuclease J.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	463	Total	C	N	O	S	0	0	0
			3605	2265	636	684	20			
1	B	463	Total	C	N	O	S	0	0	0
			3602	2263	635	683	21			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	initiating methionine	UNP K4MAF9
A	-20	GLY	-	expression tag	UNP K4MAF9
A	-19	SER	-	expression tag	UNP K4MAF9
A	-18	SER	-	expression tag	UNP K4MAF9
A	-17	HIS	-	expression tag	UNP K4MAF9
A	-16	HIS	-	expression tag	UNP K4MAF9
A	-15	HIS	-	expression tag	UNP K4MAF9
A	-14	HIS	-	expression tag	UNP K4MAF9
A	-13	HIS	-	expression tag	UNP K4MAF9
A	-12	HIS	-	expression tag	UNP K4MAF9
A	-11	SER	-	expression tag	UNP K4MAF9
A	-10	SER	-	expression tag	UNP K4MAF9
A	-9	GLY	-	expression tag	UNP K4MAF9
A	-8	LEU	-	expression tag	UNP K4MAF9
A	-7	VAL	-	expression tag	UNP K4MAF9
A	-6	PRO	-	expression tag	UNP K4MAF9
A	-5	ARG	-	expression tag	UNP K4MAF9
A	-4	GLY	-	expression tag	UNP K4MAF9
A	-3	SER	-	expression tag	UNP K4MAF9
A	-2	HIS	-	expression tag	UNP K4MAF9
A	-1	MET	-	expression tag	UNP K4MAF9
A	0	ALA	-	expression tag	UNP K4MAF9
A	1	SER	-	expression tag	UNP K4MAF9
A	247	ALA	SER	engineered mutation	UNP K4MAF9
B	-21	MET	-	initiating methionine	UNP K4MAF9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	GLY	-	expression tag	UNP K4MAF9
B	-19	SER	-	expression tag	UNP K4MAF9
B	-18	SER	-	expression tag	UNP K4MAF9
B	-17	HIS	-	expression tag	UNP K4MAF9
B	-16	HIS	-	expression tag	UNP K4MAF9
B	-15	HIS	-	expression tag	UNP K4MAF9
B	-14	HIS	-	expression tag	UNP K4MAF9
B	-13	HIS	-	expression tag	UNP K4MAF9
B	-12	HIS	-	expression tag	UNP K4MAF9
B	-11	SER	-	expression tag	UNP K4MAF9
B	-10	SER	-	expression tag	UNP K4MAF9
B	-9	GLY	-	expression tag	UNP K4MAF9
B	-8	LEU	-	expression tag	UNP K4MAF9
B	-7	VAL	-	expression tag	UNP K4MAF9
B	-6	PRO	-	expression tag	UNP K4MAF9
B	-5	ARG	-	expression tag	UNP K4MAF9
B	-4	GLY	-	expression tag	UNP K4MAF9
B	-3	SER	-	expression tag	UNP K4MAF9
B	-2	HIS	-	expression tag	UNP K4MAF9
B	-1	MET	-	expression tag	UNP K4MAF9
B	0	ALA	-	expression tag	UNP K4MAF9
B	1	SER	-	expression tag	UNP K4MAF9
B	247	ALA	SER	engineered mutation	UNP K4MAF9

- Molecule 2 is a RNA chain called RNA (5'-R(P*AP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	5	Total	C	N	O	P	0	0	0
			111	50	25	31	5			
2	D	5	Total	C	N	O	P	0	0	0
			111	50	25	31	5			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	158	Total	O	0	0
			158	158		
5	B	141	Total	O	0	0
			141	141		
5	C	5	Total	O	0	0
			5	5		

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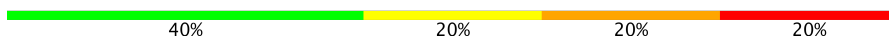
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	8	Total	O	0	0
			8	8		



- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*A)-3')

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	168.61Å 168.61Å 165.87Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.67 – 2.40 48.67 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.67-2.40) 93.5 (48.67-2.40)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.09 (at 2.39Å)	Xtriage
Refinement program	PHENIX (1.10 _2155: ???)	Depositor
R, R_{free}	0.173 , 0.208 0.166 , 0.200	Depositor DCC
R_{free} test set	1873 reflections (3.65%)	DCC
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 37.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7790	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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, 0.333 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: ZN, SO4

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	0.42	0/3673	0.69	3/4972 (0.1%)
1	B	0.42	0/3669	0.73	8/4966 (0.2%)
2	C	1.30	1/125 (0.8%)	1.18	0/191
2	D	1.17	1/125 (0.8%)	1.18	0/191
All	All	0.47	2/7592 (0.0%)	0.73	11/10320 (0.1%)

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
1	B	0	2
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	A	OP3-P	-10.69	1.48	1.61
2	D	1	A	OP3-P	-9.60	1.49	1.61

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	121	LYS	CA-CB-CG	-7.89	96.04	113.40
1	B	46	VAL	CG1-CB-CG2	-7.68	98.61	110.90
1	A	60	GLY	N-CA-C	6.32	128.91	113.10
1	A	251	ARG	NE-CZ-NH2	-6.23	117.19	120.30
1	B	60	GLY	N-CA-C	6.02	128.15	113.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	124	VAL	Peptide
1	B	124	VAL	Peptide
1	B	125	LYS	Peptide

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	3605	0	3593	86	1
1	B	3602	0	3597	74	1
2	C	111	0	56	4	0
2	D	111	0	56	3	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	15	0	0	1	0
4	B	25	0	0	1	0
4	C	5	0	0	0	0
5	A	158	0	0	5	0
5	B	141	0	0	6	0
5	C	5	0	0	0	0
5	D	8	0	0	0	0
All	All	7790	0	7302	160	1

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 11.

The worst 5 of 160 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:19:MET:HE3	1:A:65:ASP:HB3	1.48	0.95
1:A:208:THR:HA	1:A:415:MET:CE	2.04	0.86
1:B:19:MET:HE3	1:B:65:ASP:HB3	1.61	0.82
1:A:208:THR:HA	1:A:415:MET:HE3	1.62	0.82
1:B:339:THR:HG22	1:B:341:PHE:H	1.45	0.81

All (1) 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:-19:SER:N	1:B:404:GLU:OE2[9_865]	2.19	0.01

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	459/470 (98%)	446 (97%)	9 (2%)	4 (1%)	20	29
1	B	461/470 (98%)	443 (96%)	14 (3%)	4 (1%)	20	29
All	All	920/940 (98%)	889 (97%)	23 (2%)	8 (1%)	20	29

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	125	LYS
1	A	61	ALA
1	A	25	ASN
1	B	61	ALA
1	B	25	ASN

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	388/393 (99%)	377 (97%)	11 (3%)	49	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	387/393 (98%)	378 (98%)	9 (2%)	56	75
All	All	775/786 (99%)	755 (97%)	20 (3%)	51	72

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	358	ASN
1	A	391	ARG
1	B	156	ASP
1	A	300	ASP
1	A	339	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	394	HIS
1	A	405	HIS
1	B	223	HIS
1	A	364	ASN
1	B	257	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	5/5 (100%)	1 (20%)	1 (20%)
2	D	5/5 (100%)	2 (40%)	1 (20%)
All	All	10/10 (100%)	3 (30%)	2 (20%)

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	2	A
2	D	2	A
2	D	3	A

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	C	1	A

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Mol	Chain	Res	Type
2	D	1	A

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 13 ligands modelled in this entry, 4 are 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	$\# Z > 2$
4	SO4	A	503	-	4,4,4	0.26	0	6,6,6	0.30	0
4	SO4	A	504	-	4,4,4	0.23	0	6,6,6	0.29	0
4	SO4	A	505	-	4,4,4	0.23	0	6,6,6	0.13	0
4	SO4	B	503	-	4,4,4	0.30	0	6,6,6	0.24	0
4	SO4	B	504	-	4,4,4	0.21	0	6,6,6	0.18	0
4	SO4	B	505	-	4,4,4	0.22	0	6,6,6	0.13	0
4	SO4	B	506	-	4,4,4	0.17	0	6,6,6	0.19	0
4	SO4	B	507	-	4,4,4	0.23	0	6,6,6	0.27	0
4	SO4	C	101	-	4,4,4	0.19	0	6,6,6	0.17	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
4	SO4	A	503	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SO4	A	504	-	-	0/0/0/0	0/0/0/0
4	SO4	A	505	-	-	0/0/0/0	0/0/0/0
4	SO4	B	503	-	-	0/0/0/0	0/0/0/0
4	SO4	B	504	-	-	0/0/0/0	0/0/0/0
4	SO4	B	505	-	-	0/0/0/0	0/0/0/0
4	SO4	B	506	-	-	0/0/0/0	0/0/0/0
4	SO4	B	507	-	-	0/0/0/0	0/0/0/0
4	SO4	C	101	-	-	0/0/0/0	0/0/0/0

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	504	SO4	1	0
4	B	507	SO4	1	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	463/470 (98%)	-0.16	12 (2%) 56 54	26, 39, 64, 102	0
1	B	463/470 (98%)	-0.12	12 (2%) 56 54	27, 41, 66, 104	0
2	C	5/5 (100%)	1.02	0 100 100	55, 60, 64, 66	0
2	D	5/5 (100%)	0.96	0 100 100	59, 62, 67, 69	0
All	All	936/950 (98%)	-0.13	24 (2%) 56 54	26, 40, 66, 104	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	124	VAL	4.6
1	A	-7	VAL	4.5
1	B	46	VAL	4.4
1	A	-6	PRO	4.1
1	A	45	ASP	3.6

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(\AA^2)	Q<0.9
4	SO4	B	507	5/5	0.84	0.30	1.45	86,93,96,97	0
4	SO4	B	505	5/5	0.94	0.16	0.90	64,70,74,81	0
4	SO4	B	504	5/5	0.91	0.20	0.78	76,78,82,86	0
4	SO4	C	101	5/5	0.95	0.17	0.22	80,88,89,89	0
4	SO4	A	505	5/5	0.95	0.15	0.19	79,79,85,86	0
3	ZN	B	501	1/1	0.99	0.14	-0.22	31,31,31,31	1
3	ZN	A	502	1/1	0.99	0.15	-0.29	22,22,22,22	1
3	ZN	B	502	1/1	0.99	0.12	-0.69	24,24,24,24	1
3	ZN	A	501	1/1	0.98	0.13	-1.02	30,30,30,30	1
4	SO4	A	504	5/5	0.93	0.20	-	79,79,82,83	0
4	SO4	A	503	5/5	0.83	0.25	-	68,76,85,85	0
4	SO4	B	503	5/5	0.82	0.27	-	73,80,89,90	0
4	SO4	B	506	5/5	0.92	0.28	-	84,86,87,88	0

6.5 Other polymers [i](#)

There are no such residues in this entry.