



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 06:46 am BST

PDB ID : 3I63  
Title : Peroxide Bound Toluene 4-Monooxygenase  
Authors : Bailey, L.J.; Fox, B.G.  
Deposited on : 2009-07-06  
Resolution : 2.09 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](mailto: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.

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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

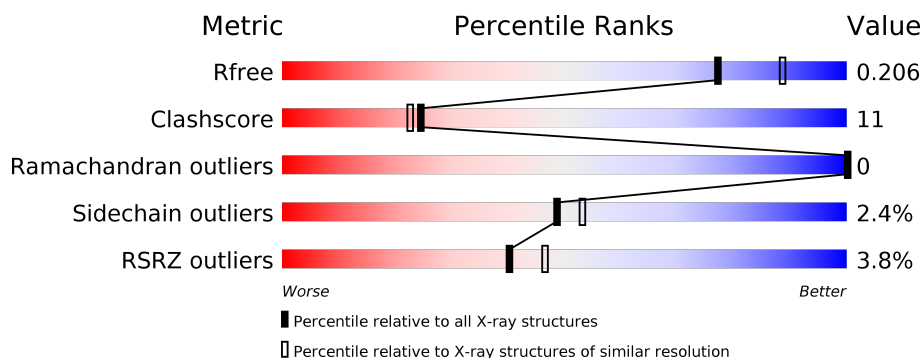
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.09 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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  $\geq 3$ , 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	500	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>18%</div> <div>••</div> </div> </div>
2	B	327	<div> <div>%</div> <div> <div></div> <div>79%</div> <div>12%</div> <div>• 7%</div> </div> </div>
3	C	84	<div> <div>17%</div> <div> <div></div> <div>65%</div> <div>31%</div> <div>••</div> </div> </div>
4	E	103	<div> <div>8%</div> <div> <div></div> <div>76%</div> <div>19%</div> <div>••</div> </div> </div>

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 8720 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 Toluene-4-monooxygenase system protein A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	491	Total	C	N	O	S	0	10	0
			4100	2635	688	753	24			

- Molecule 2 is a protein called Toluene-4-monooxygenase system protein E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	303	Total	C	N	O	S	0	5	0
			2549	1611	445	478	15			

- Molecule 3 is a protein called Toluene-4-monooxygenase system protein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	82	Total	C	N	O	S	0	0	0
			650	411	117	118	4			

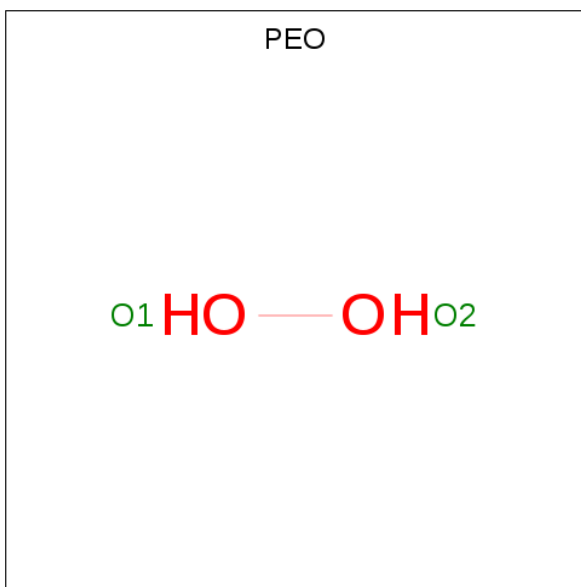
- Molecule 4 is a protein called Toluene-4-monooxygenase system protein D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	101	Total	C	N	O	S	0	0	0
			801	500	139	160	2			

- Molecule 5 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Fe	0	0
			2	2		

- Molecule 6 is HYDROGEN PEROXIDE (three-letter code: PEO) (formula: H<sub>2</sub>O<sub>2</sub>).



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

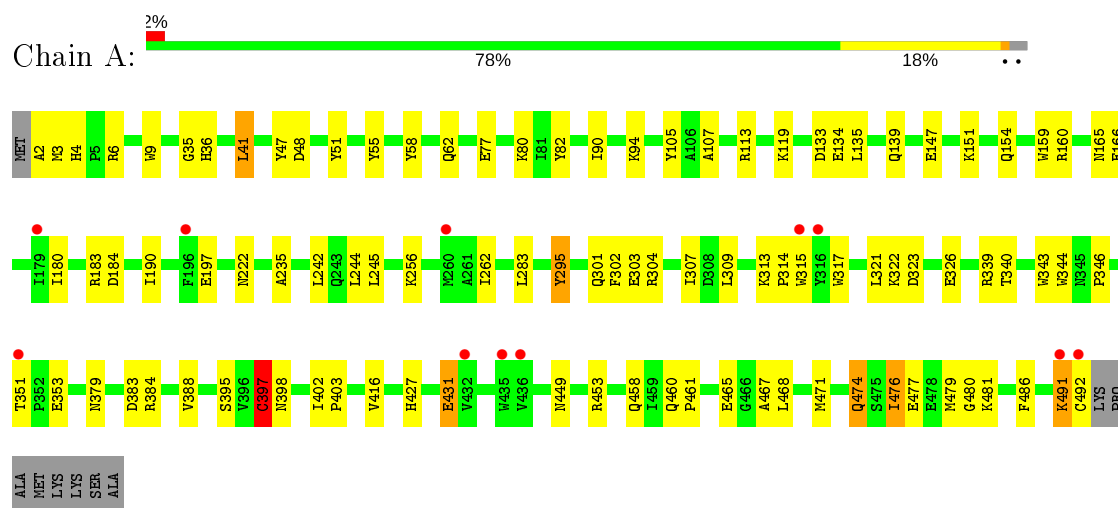
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	295	Total	O	0	0
			295	295		
7	B	202	Total	O	0	0
			202	202		
7	C	25	Total	O	0	0
			25	25		
7	E	92	Total	O	0	0
			92	92		

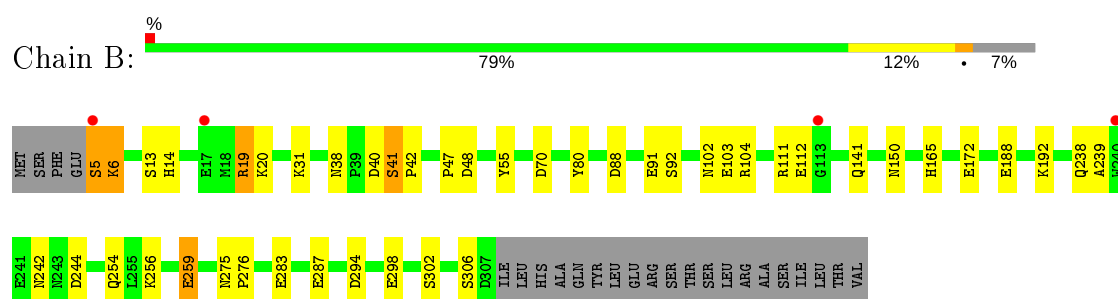
### 3 Residue-property plots [i](#)

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.

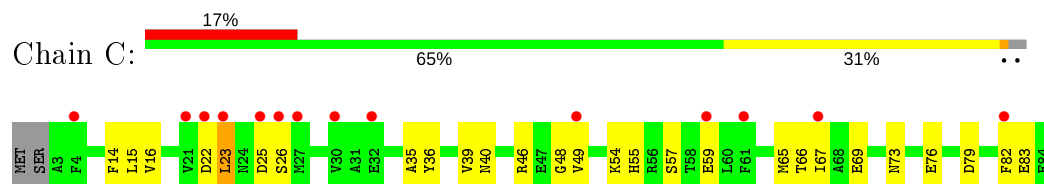
#### • Molecule 1: Toluene-4-monooxygenase system protein A



#### • Molecule 2: Toluene-4-monooxygenase system protein E



#### • Molecule 3: Toluene-4-monooxygenase system protein B



#### • Molecule 4: Toluene-4-monooxygenase system protein D





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.79Å 116.93Å 181.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.40 – 2.09 49.40 – 2.09	Depositor EDS
% Data completeness (in resolution range)	99.3 (49.40-2.09) 99.2 (49.40-2.09)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.34 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, $R_{free}$	0.156 , 0.201 0.169 , 0.206	Depositor DCC
$R_{free}$ test set	3143 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.4	Xtriage
Anisotropy	0.143	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 50.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8720	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PEO, FE

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	1.14	9/4244 (0.2%)	0.94	5/5763 (0.1%)
2	B	1.04	2/2628 (0.1%)	0.88	2/3573 (0.1%)
3	C	0.87	0/662	0.80	0/897
4	E	1.16	2/811 (0.2%)	1.07	4/1097 (0.4%)
All	All	1.10	13/8345 (0.2%)	0.92	11/11330 (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
4	E	0	1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	397	CYS	CB-SG	-13.09	1.59	1.82
1	A	486	PHE	CG-CD2	6.99	1.49	1.38
2	B	259	GLU	CG-CD	6.56	1.61	1.51
1	A	486	PHE	CE1-CZ	6.14	1.49	1.37
4	E	78	GLU	CG-CD	6.08	1.61	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	61	ARG	NE-CZ-NH1	7.05	123.82	120.30
4	E	4	LEU	CA-CB-CG	6.64	130.58	115.30
1	A	431	GLU	CA-CB-CG	6.12	126.87	113.40
2	B	40[A]	ASP	CB-CG-OD1	5.91	123.62	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	40[B]	ASP	CB-CG-OD1	5.91	123.62	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	E	37	GLY	Peptide

## 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	4100	0	3878	107	1
2	B	2549	0	2417	38	1
3	C	650	0	644	26	0
4	E	801	0	789	28	0
5	A	2	0	0	0	0
6	A	4	0	0	1	0
7	A	295	0	0	12	1
7	B	202	0	0	7	0
7	C	25	0	0	1	0
7	E	92	0	0	2	0
All	All	8720	0	7728	173	2

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 173 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:303[A]:GLU:HG3	1:A:317:TRP:CZ2	1.73	1.20
6:A:6079:PEO:O2	6:A:6079:PEO:O1	1.54	1.20
4:E:3:THR:CG2	4:E:4:LEU:H	1.56	1.19
4:E:3:THR:HG23	4:E:4:LEU:N	1.63	1.09
1:A:480:GLY:O	1:A:481:LYS:HE2	1.53	1.08

All (2) 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)
2:B:5:SER:CB	2:B:259:GLU:OE2[8_555]	2.04	0.16
1:A:431:GLU:OE1	7:A:696:HOH:O[3_554]	2.09	0.11

## 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	499/500 (100%)	475 (95%)	24 (5%)	0	100	100
2	B	306/327 (94%)	297 (97%)	9 (3%)	0	100	100
3	C	80/84 (95%)	74 (92%)	6 (8%)	0	100	100
4	E	99/103 (96%)	97 (98%)	2 (2%)	0	100	100
All	All	984/1014 (97%)	943 (96%)	41 (4%)	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	426/423 (101%)	417 (98%)	9 (2%)	53	59
2	B	278/296 (94%)	271 (98%)	7 (2%)	47	52
3	C	71/75 (95%)	69 (97%)	2 (3%)	43	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	E	85/87 (98%)	83 (98%)	2 (2%)	49	53
All	All	860/881 (98%)	840 (98%)	20 (2%)	49	55

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

Mol	Chain	Res	Type
2	B	5	SER
2	B	6	LYS
3	C	23	LEU
1	A	476	ILE
1	A	491	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	77	GLN
2	B	141	GLN
4	E	67	GLN
2	B	84	ASN
2	B	95	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z  > 2$
6	PEO	A	6079	5	1,1,1	1.17	0	-		
6	PEO	A	503	-	1,1,1	0.76	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	6079	PEO	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	491/500 (98%)	0.12	11 (2%) 62 66	6, 17, 25, 33	0
2	B	303/327 (92%)	0.04	4 (1%) 77 80	11, 18, 29, 41	0
3	C	82/84 (97%)	1.18	14 (17%) 1 1	2, 19, 25, 29	0
4	E	101/103 (98%)	0.04	8 (7%) 12 16	10, 17, 27, 29	0
All	All	977/1014 (96%)	0.18	37 (3%) 40 46	2, 17, 27, 41	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	492	CYS	5.7
4	E	3	THR	5.5
3	C	67	ILE	4.8
3	C	82	PHE	4.6
3	C	49	VAL	4.4

### 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
6	PEO	A	503	2/2	0.85	0.68	46,46,46,48	0
6	PEO	A	6079	2/2	0.95	0.45	15,15,15,21	2
5	FE	A	501	1/1	0.99	0.11	21,21,21,21	0
5	FE	A	502	1/1	0.99	0.13	20,20,20,20	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.