



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2020 – 09:17 pm BST

PDB ID : 3CK1  
Title : CRYSTAL STRUCTURE OF a putative thioesterase (REUT\_A2179) FROM RALSTONIA EUTROPHA JMP134 AT 1.74 Å RESOLUTION  
Authors : Joint Center for Structural Genomics (JCSG)  
Deposited on : 2008-03-14  
Resolution : 1.74 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](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.

---

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

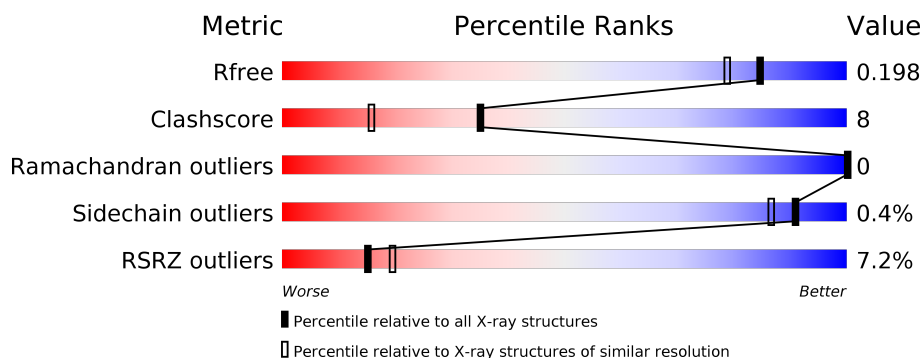
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.74 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	3764 (1.76-1.72)
Clashscore	141614	3923 (1.76-1.72)
Ramachandran outliers	138981	3878 (1.76-1.72)
Sidechain outliers	138945	3878 (1.76-1.72)
RSRZ outliers	127900	3705 (1.76-1.72)

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	150	<div> <div>9%</div> <div> <div></div> <div>84%</div> <div>10%</div> <div>• 5%</div> </div> </div>
1	B	150	<div> <div>5%</div> <div> <div></div> <div>81%</div> <div>15%</div> <div>5%</div> </div> </div>

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	GOL	B	158	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2828 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 thioesterase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	143	Total	C	N	O	S	Se	0	18	0
			1252	795	221	227	4	5			
1	B	143	Total	C	N	O	S	Se	0	14	0
			1234	783	215	225	4	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	LEADER SEQUENCE	UNP Q46Z90
B	0	GLY	-	LEADER SEQUENCE	UNP Q46Z90

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	6	Total	Cl	0	3
			9	9		
2	A	4	Total	Cl	0	0
			4	4		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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


- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	144	Total	O	0	0
			144	144		
4	B	147	Total	O	0	2
			149	149		

### 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 thioesterase

Chain A: 



#### • Molecule 1: Putative thioesterase

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.07Å 77.07Å 242.86Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.30 – 1.74 29.24 – 1.74	Depositor EDS
% Data completeness (in resolution range)	99.9 (29.30-1.74) 100.0 (29.24-1.74)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 1.74Å)	Xtriage
Refinement program	REFMAC 5.4.0069, PHENIX	Depositor
R, $R_{free}$	0.174 , 0.196 0.178 , 0.198	Depositor DCC
$R_{free}$ test set	2264 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.1	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 48.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2828	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.65% 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: GOL, 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	0.86	3/1274 (0.2%)	0.94	4/1724 (0.2%)
1	B	0.78	0/1256	0.92	2/1697 (0.1%)
All	All	0.82	3/2530 (0.1%)	0.93	6/3421 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	0	GLY	N-CA	10.27	1.61	1.46
1	A	1	MSE	N-CA	6.20	1.58	1.46
1	A	0	GLY	CA-C	5.25	1.60	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	MSE	CB-CA-C	-8.04	94.31	110.40
1	A	48	ASP	CB-CG-OD1	6.82	124.44	118.30
1	B	17	ASP	CB-CG-OD1	6.46	124.11	118.30
1	A	130[A]	ARG	NE-CZ-NH2	-6.15	117.22	120.30
1	A	130[B]	ARG	NE-CZ-NH2	-6.15	117.22	120.30
1	B	17	ASP	CB-CG-OD2	-5.73	113.15	118.30

There are no chirality outliers.

There are no planarity outliers.

### 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	1252	0	1209	16	0
1	B	1234	0	1192	24	0
2	A	4	0	0	0	0
2	B	9	0	0	2	0
3	A	18	0	24	0	0
3	B	18	0	24	3	0
4	A	144	0	0	1	0
4	B	149	0	0	6	0
All	All	2828	0	2449	41	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 8.

All (41) 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:63[B]:LEU:HD21	1:B:65[B]:CYS:SG	1.66	1.35
1:B:63[B]:LEU:CD2	1:B:65[B]:CYS:SG	2.24	1.23
1:A:106[B]:LEU:CD2	1:A:108[B]:VAL:HG23	1.81	1.09
1:A:106[B]:LEU:HD21	1:A:108[B]:VAL:CG2	1.83	1.07
1:A:106[B]:LEU:HD21	1:A:108[B]:VAL:HG23	1.07	1.04
1:B:86:LEU:HD13	1:B:133[B]:MSE:HE2	1.45	0.97
1:B:63[B]:LEU:HD23	1:B:65[B]:CYS:SG	2.12	0.86
1:B:63[B]:LEU:HD21	1:B:65[B]:CYS:HG	1.47	0.79
1:B:86:LEU:HD13	1:B:133[B]:MSE:CE	2.14	0.77
1:B:127:ASP:O	1:B:131:GLN:HG3	1.85	0.77
1:B:101:ASP:N	2:B:153[B]:CL:CL	2.57	0.75
1:A:19[B]:ALA:HB2	4:B:264:HOH:O	1.89	0.72
1:B:91:PHE:CB	1:B:133[B]:MSE:HE1	2.21	0.71
1:B:86:LEU:CD1	1:B:133[B]:MSE:HE2	2.22	0.69
1:A:127:ASP:O	1:A:131:GLN:HG3	1.94	0.68
1:B:88:GLN:N	2:B:155[B]:CL:CL	2.64	0.67
1:A:19[B]:ALA:CB	4:B:264:HOH:O	2.43	0.66
1:A:106[A]:LEU:HD12	1:A:106[A]:LEU:C	2.18	0.63
1:B:80:GLU:HG3	1:B:98[A]:MSE:HE1	1.84	0.59
1:A:106[A]:LEU:HD12	1:A:106[A]:LEU:O	2.02	0.59
1:B:86:LEU:CD1	1:B:133[B]:MSE:CE	2.81	0.59
1:A:18[B]:ALA:N	4:A:284:HOH:O	2.35	0.57
1:A:63[A]:LEU:HD23	1:A:63[A]:LEU:C	2.25	0.57
1:A:17[B]:ASP:HB3	1:A:23:PHE:HB2	1.88	0.56

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63[B]:LEU:HD23	1:B:63[B]:LEU:C	2.26	0.56
1:B:67:PHE:HB3	3:B:158:GOL:H12	1.88	0.56
1:B:106:LEU:HD13	1:B:108[B]:VAL:HG23	1.88	0.55
1:B:41[B]:GLN:NE2	4:B:290:HOH:O	2.27	0.54
1:B:91:PHE:HB2	1:B:133[B]:MSE:HE1	1.87	0.54
1:B:131:GLN:NE2	4:B:271:HOH:O	2.44	0.50
1:A:64:HIS:HE1	1:B:62[B]:ASP:OD1	1.96	0.48
1:B:106:LEU:C	1:B:106:LEU:HD12	2.35	0.47
1:A:28:PHE:CE1	1:A:63[A]:LEU:HD11	2.51	0.46
3:B:158:GOL:H11	4:B:187:HOH:O	2.16	0.45
1:A:127:ASP:OD1	1:A:130[A]:ARG:NH2	2.50	0.45
1:A:106[A]:LEU:CD1	1:A:106[A]:LEU:C	2.85	0.45
3:B:158:GOL:C1	4:B:187:HOH:O	2.64	0.45
1:B:116[A]:ASP:O	1:B:120:ILE:HA	2.18	0.44
1:B:35[B]:ILE:HD11	1:B:110:GLN:OE1	2.17	0.44
1:A:116[A]:ASP:O	1:A:120:ILE:HA	2.17	0.42
1:B:127:ASP:HB2	1:B:128:PRO:HD3	2.03	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	Percentiles	
1	A	159/150 (106%)	153 (96%)	6 (4%)	0	100	100
1	B	155/150 (103%)	150 (97%)	5 (3%)	0	100	100
All	All	314/300 (105%)	303 (96%)	11 (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	130/119 (109%)	128 (98%)	2 (2%)	65	47
1	B	131/119 (110%)	131 (100%)	0	100	100
All	All	261/238 (110%)	259 (99%)	2 (1%)	91	72

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106[A]	LEU
1	A	106[B]	LEU

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 19 ligands modelled in this entry, 13 are monoatomic - leaving 6 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
3	GOL	B	158	-	5,5,5	0.46	0	5,5,5	0.64	0
3	GOL	B	157	-	5,5,5	0.33	0	5,5,5	0.33	0
3	GOL	A	154	-	5,5,5	0.81	0	5,5,5	0.76	0
3	GOL	B	156	-	5,5,5	0.43	0	5,5,5	0.72	0
3	GOL	A	155	-	5,5,5	0.46	0	5,5,5	0.77	0
3	GOL	A	156	-	5,5,5	0.33	0	5,5,5	0.22	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	GOL	B	158	-	-	2/4/4/4	-
3	GOL	B	157	-	-	2/4/4/4	-
3	GOL	A	154	-	-	2/4/4/4	-
3	GOL	B	156	-	-	3/4/4/4	-
3	GOL	A	155	-	-	3/4/4/4	-
3	GOL	A	156	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	158	GOL	C1-C2-C3-O3
3	B	156	GOL	O1-C1-C2-C3
3	B	157	GOL	C1-C2-C3-O3
3	A	156	GOL	C1-C2-C3-O3
3	A	156	GOL	O2-C2-C3-O3
3	A	154	GOL	O1-C1-C2-C3
3	B	158	GOL	O2-C2-C3-O3
3	B	157	GOL	O2-C2-C3-O3
3	A	154	GOL	O1-C1-C2-O2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
3	B	156	GOL	O1-C1-C2-O2
3	A	155	GOL	O1-C1-C2-O2
3	A	155	GOL	O1-C1-C2-C3
3	B	156	GOL	O2-C2-C3-O3
3	A	155	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	158	GOL	3	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

### 6.1 Protein, DNA and RNA chains

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	138/150 (92%)	0.31	13 (9%) <b>8</b> <b>10</b>	17, 20, 37, 57	0
1	B	138/150 (92%)	0.27	7 (5%) <b>28</b> <b>33</b>	17, 21, 34, 56	0
All	All	276/300 (92%)	0.29	20 (7%) <b>15</b> <b>19</b>	17, 21, 35, 57	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	120	ILE	7.0
1	A	142	ALA	6.0
1	B	119	LYS	5.4
1	B	142	ALA	5.2
1	A	18[A]	ALA	4.3
1	A	2	THR	3.8
1	A	120	ILE	3.8
1	B	118	ASP	3.6
1	A	118	ASP	3.3
1	A	20[A]	GLY	3.2
1	A	140	THR	3.2
1	A	19[A]	ALA	3.0
1	A	0	GLY	3.0
1	A	139	GLU	2.7
1	B	19	ALA	2.6
1	A	53	ALA	2.4
1	B	116[A]	ASP	2.2
1	B	53	ALA	2.2
1	A	119	LYS	2.2
1	A	138	ASP	2.1

## 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
3	GOL	B	157	6/6	0.57	0.40	63,65,68,69	0
3	GOL	B	158	6/6	0.73	0.45	33,52,64,68	0
3	GOL	A	156	6/6	0.79	0.18	62,64,65,67	0
2	CL	B	154	1/1	0.81	0.28	58,58,58,58	0
3	GOL	B	156	6/6	0.89	0.12	26,34,39,51	0
3	GOL	A	154	6/6	0.92	0.37	27,38,47,54	0
3	GOL	A	155	6/6	0.92	0.13	26,44,49,55	0
2	CL	B	155[B]	1/1	0.96	0.27	39,39,39,39	1
2	CL	B	155[A]	1/1	0.96	0.27	24,24,24,24	1
2	CL	B	150	1/1	0.96	0.12	26,26,26,26	0
2	CL	B	151	1/1	0.96	0.22	51,51,51,51	0
2	CL	A	152	1/1	0.98	0.11	34,34,34,34	0
2	CL	B	152[B]	1/1	0.99	0.16	27,27,27,27	1
2	CL	A	153	1/1	0.99	0.07	27,27,27,27	0
2	CL	B	153[B]	1/1	0.99	0.11	24,24,24,24	1
2	CL	B	153[A]	1/1	0.99	0.11	12,12,12,12	1
2	CL	A	151	1/1	0.99	0.06	20,20,20,20	0
2	CL	A	150	1/1	0.99	0.14	27,27,27,27	0
2	CL	B	152[A]	1/1	0.99	0.16	19,19,19,19	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.