



# wwPDB X-ray Structure Validation Summary Report

Jun 12, 2014 – 06:41 PM EDT

PDB ID : 2X50  
Title : Crystal structure of Trypanothione reductase from Leishmania infantum in complex with NADPH and silver  
Authors : Baiocco, P.; Ilari, A.; Colotti, G.  
Deposited on : 2010-02-03  
Resolution : 3.30 Å(reported)

This is a wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

---

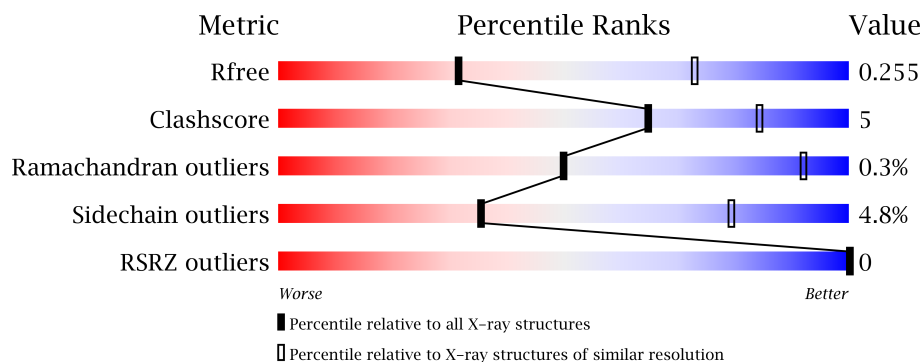
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtriage (Phenix) : dev-1439  
EDS : stable23161  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable23161

# 1 Overall quality at a glance



The reported resolution of this entry is 3.30 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))
$R_{free}$	66092	1341 (3.40-3.20)
Clashscore	79885	1696 (3.40-3.20)
Ramachandran outliers	78287	1664 (3.40-3.20)
Sidechain outliers	78261	1662 (3.40-3.20)
RSRZ outliers	66119	1342 (3.40-3.20)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	510	
1	B	510	

## 2 Entry composition i

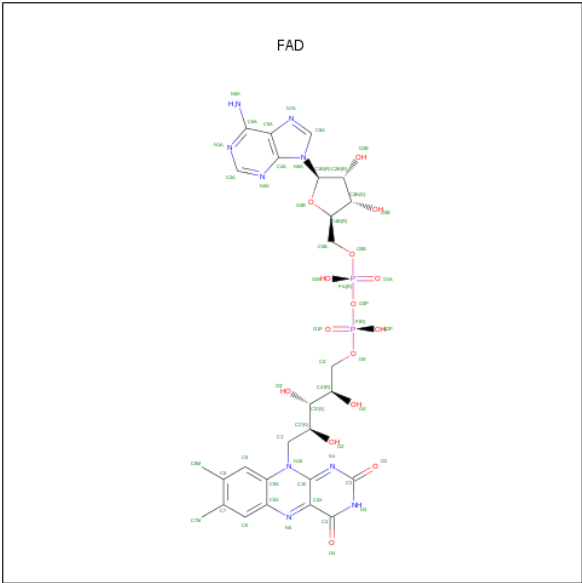
There are 6 unique types of molecules in this entry. The entry contains 7591 atoms, of which 0 are hydrogen and 0 are deuterium.

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 TRYPANOTHIONE REDUCTASE.

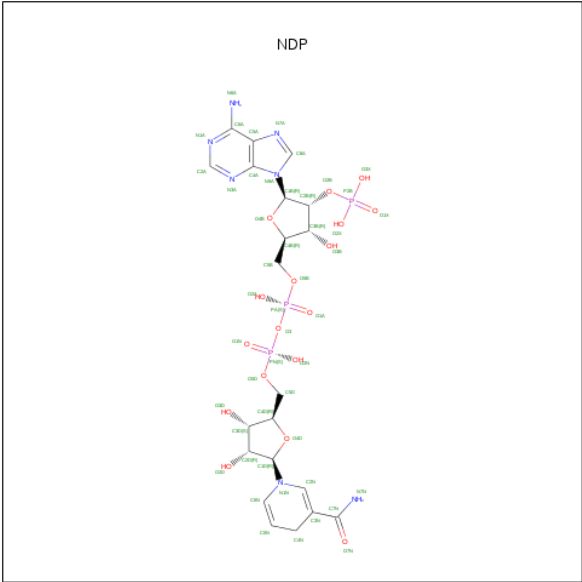
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	485	Total	C	N	O	S	0	0	0
			3672	2308	631	707	26			
1	B	487	Total	C	N	O	S	0	0	0
			3686	2317	633	710	26			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDEPHOSPHATE (three-letter code: NDP) (formula:  $C_{21}H_{30}N_7O_{17}P_3$ ).

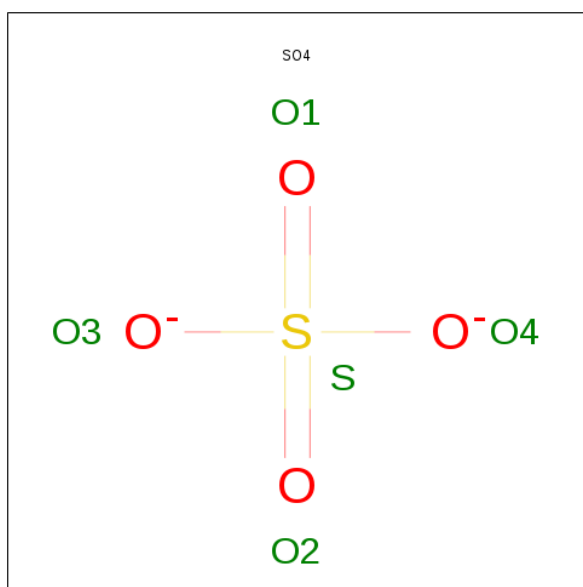


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 4 is SILVER ION (three-letter code: AG) (formula: Ag).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Ag	0	0
			2	2		
4	A	2	Total	Ag	0	0
			2	2		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 6 is water.

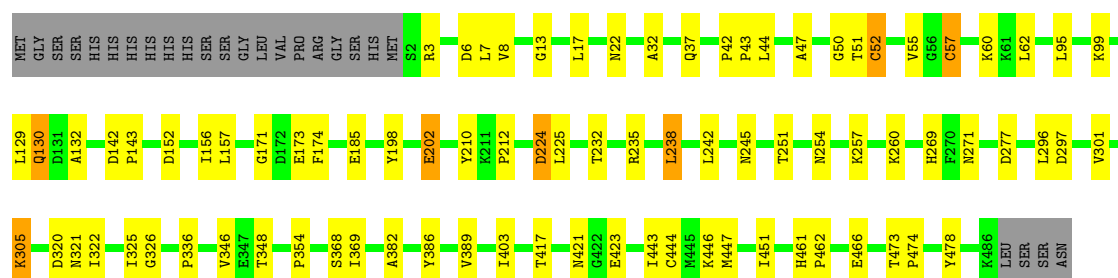
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	9	Total	O	0	0
			9	9		
6	B	8	Total	O	0	0
			8	8		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

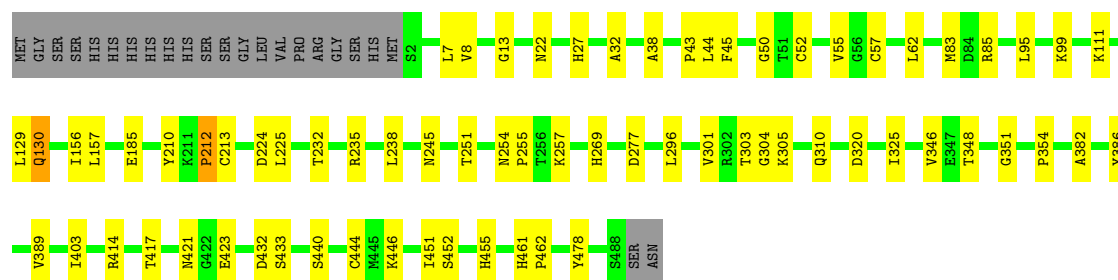
#### • Molecule 1: TRYPANOTHIONE REDUCTASE

Chain A:



#### • Molecule 1: TRYPANOTHIONE REDUCTASE

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.32Å 102.32Å 193.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.30 37.33 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.1 (40.00-3.30) 99.1 (37.33-3.30)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.30 (at 3.32Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.229 , 0.265 0.229 , 0.255	Depositor DCC
$R_{free}$ test set	1508 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	70.1	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 17.5	EDS
Estimated twinning fraction	0.439 for h,-k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 29702 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	7591	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NDP, SO4, AG, FAD

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	0.34	1/3745 (0.0%)	0.48	0/5071
1	B	0.32	0/3759	0.48	0/5090
All	All	0.33	1/7504 (0.0%)	0.48	0/10161

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	202	GLU	CG-CD	5.16	1.59	1.51

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3672	0	3619	42	0
1	B	3686	0	3635	34	0
2	A	53	0	31	2	0
2	B	53	0	31	1	0
3	A	48	0	26	0	0
3	B	48	0	26	0	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	2	0	0	2	0
4	B	2	0	0	1	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
6	A	9	0	0	0	0
6	B	8	0	0	0	0
All	All	7591	0	7368	74	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

The worst 5 of 74 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:444:CYS:SG	4:A:1490:AG:AG	1.89	1.15
1:B:52:CYS:SG	4:B:1490:AG:AG	1.98	1.08
1:A:389:VAL:HG23	1:A:478:TYR:HB2	1.62	0.80
1:B:389:VAL:HG23	1:B:478:TYR:HB2	1.61	0.79
4:A:1490:AG:AG	1:B:444:CYS:HG	1.58	0.70

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	483/510 (95%)	456 (94%)	26 (5%)	1 (0%)	56	94
1	B	485/510 (95%)	454 (94%)	29 (6%)	2 (0%)	43	89
All	All	968/1020 (95%)	910 (94%)	55 (6%)	3 (0%)	50	92

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	212	PRO
1	B	43	PRO

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	212	PRO

### 5.3.2 Protein sidechains ⓘ

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	394/416 (95%)	373 (95%)	21 (5%)	32	76
1	B	396/416 (95%)	379 (96%)	17 (4%)	40	82
All	All	790/832 (95%)	752 (95%)	38 (5%)	35	79

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	320	ASP
1	B	7	LEU
1	B	414	ARG
1	A	446	LYS
1	B	44	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	37	GLN
1	B	130	GLN
1	B	266	ASN
1	A	340	ASN
1	B	252	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 4 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$
2	FAD	A	1487	-	58,58,58	1.08	4 (6%)	85,89,89	1.90	13 (15%)
3	NDP	A	1488	-	52,52,52	1.62	12 (23%)	80,80,80	1.67	8 (10%)
5	SO4	A	1491	-	4,4,4	0.23	0	6,6,6	0.07	0
2	FAD	B	1489	-	58,58,58	1.08	5 (8%)	85,89,89	1.89	12 (14%)
3	NDP	B	1492	-	52,52,52	1.59	11 (21%)	80,80,80	1.66	7 (8%)
5	SO4	B	1493	-	4,4,4	0.21	0	6,6,6	0.09	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
2	FAD	A	1487	-	-	0/34/50/50	0/6/6/6
3	NDP	A	1488	-	-	0/35/77/77	0/5/5/5
5	SO4	A	1491	-	-	0/0/0/0	0/0/0/0
2	FAD	B	1489	-	-	0/34/50/50	0/6/6/6
3	NDP	B	1492	-	-	0/35/77/77	0/5/5/5
5	SO4	B	1493	-	-	0/0/0/0	0/0/0/0

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1488	NDP	C4N-C5N	-4.18	1.40	1.49
3	B	1492	NDP	C4N-C5N	-4.14	1.40	1.49
2	B	1489	FAD	C2A-N3A	3.69	1.38	1.32

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1487	FAD	C2A-N3A	3.68	1.38	1.32
3	A	1488	NDP	P2B-O1X	3.67	1.63	1.51

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1487	FAD	N3A-C2A-N1A	-10.17	119.94	128.89
2	B	1489	FAD	N3A-C2A-N1A	-10.08	120.02	128.89
3	A	1488	NDP	N3A-C2A-N1A	-8.20	121.68	128.89
3	B	1492	NDP	N3A-C2A-N1A	-8.15	121.72	128.89
3	A	1488	NDP	C5A-C4A-N3A	-7.05	119.10	125.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	485/510 (95%)	0.34	0 100 100	48, 67, 88, 95	0
1	B	487/510 (95%)	0.33	0 100 100	48, 67, 88, 96	0
All	All	972/1020 (95%)	0.34	0 100 100	48, 67, 88, 96	0

There are no RSRZ outliers to report.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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, 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	AG	A	1490	1/1	0.25	-0.24	95,95,95,95	0
2	FAD	A	1487	53/53	0.26	-0.37	55,56,56,57	0
2	FAD	B	1489	53/53	0.26	-0.43	55,56,56,57	0
5	SO4	B	1493	5/5	0.24	-0.75	86,86,86,86	0
3	NDP	B	1492	48/48	0.24	-0.93	51,53,54,54	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NDP	A	1488	48/48	0.23	-1.00	51,53,54,54	0
4	AG	A	1489	1/1	0.20	-1.15	83,83,83,83	1
5	SO4	A	1491	5/5	0.19	-1.27	92,92,92,92	0
4	AG	B	1490	1/1	0.18	-1.36	88,88,88,88	1
4	AG	B	1491	1/1	0.19	-1.39	79,79,79,79	1

## 6.5 Other polymers

There are no such residues in this entry.