WORLDWIDE wwPDB

PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Feb 26, 2014 – 10:14 PM GMT

PDB ID : 1VAF
Title : Inducible nitric oxide synthase oxygenase domain complexed with the inhibitor AR-R17477
Authors : Fedorov, R.; Vasan, R.; Ghosh, D.K.; Schlichting, I.
Deposited on : 2004-02-16
Resolution : 2.90 Å(reported)

> This is a wwPDB validation summary report for a publicly released PDB entry.
> We welcome your comments at validation@mail.wwpdb.org
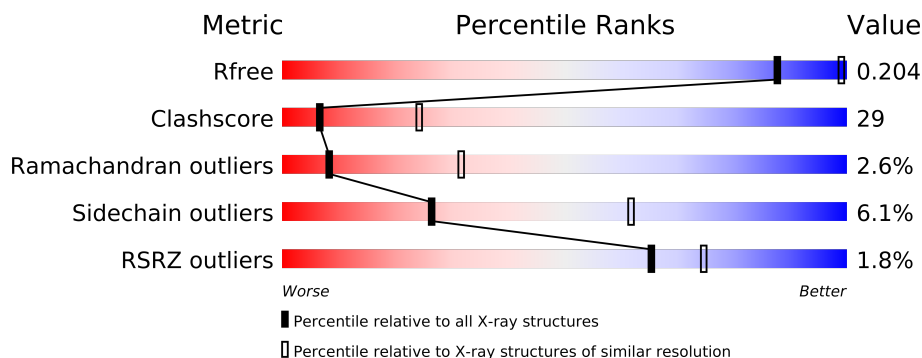> A user guide is available at http://wwpdb.org/ValidationPDFNotes.html

1 Overall quality at a glance ⓘ

The reported resolution of this entry is 2.90 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	Percentile Ranks	Value
Rfree		0.204
Clashscore		29
Ramachandran outliers		2.6%
Sidechain outliers		6.1%
RSRZ outliers		1.8%

Worse → Better

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1053 (2.90-2.90)
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (2.90-2.90)

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. 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	419	
1	B	419	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
5	ARR	A	902[A]	-	X
5	ARR	A	902[B]	-	X
5	ARR	B	903[A]	-	X
5	ARR	B	903[B]	-	X

2 Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 7233 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 Nitric oxide synthase, inducible.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	419	Total	C	N	O	S	0	0	0
			3415	2189	588	617	21			
1	B	419	Total	C	N	O	S	0	0	0
			3415	2189	588	617	21			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).
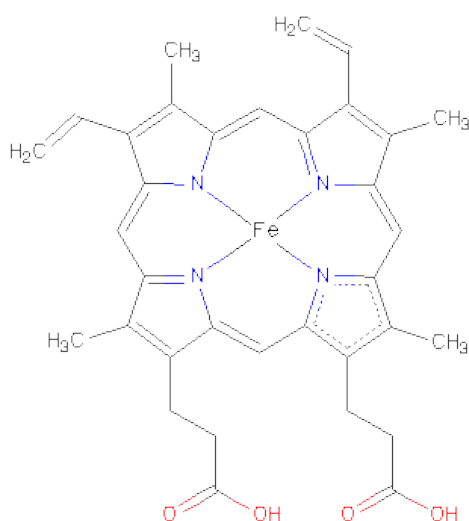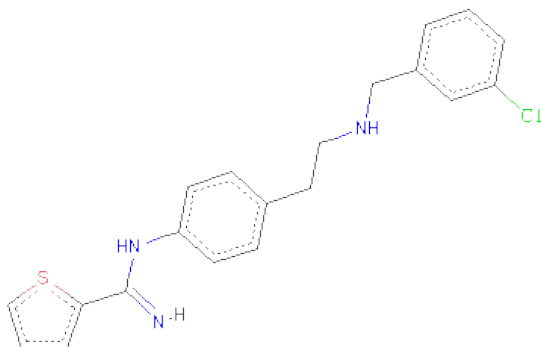
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 4 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula: $C_9H_{15}N_5O_3$).
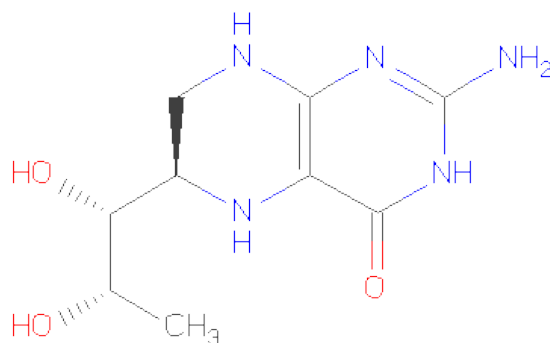
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			17	9	5	3		
4	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 5 is N-(4-{2-[(3-CHLOROBENZYL)AMINO]ETHYL}PHENYL)THIOPHENE-2-CARBOXIMIDAMIDE (three-letter code: ARR) (formula: $C_{20}H_{20}ClN_3S$).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Cl	N	S	0	1
			50	40	2	6	2		
5	B	1	Total	C	Cl	N	S	0	1
			50	40	2	6	2		

• Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	89	Total	O	0	0
			89	89		
6	B	92	Total	O	0	0
			92	92		

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: Nitric oxide synthase, inducible

Chain A:

- Molecule 1: Nitric oxide synthase, inducible

Chain B:

S480 P481 F482 Y483 Y484 I487 E488 P489 W490 H493 I494 W495
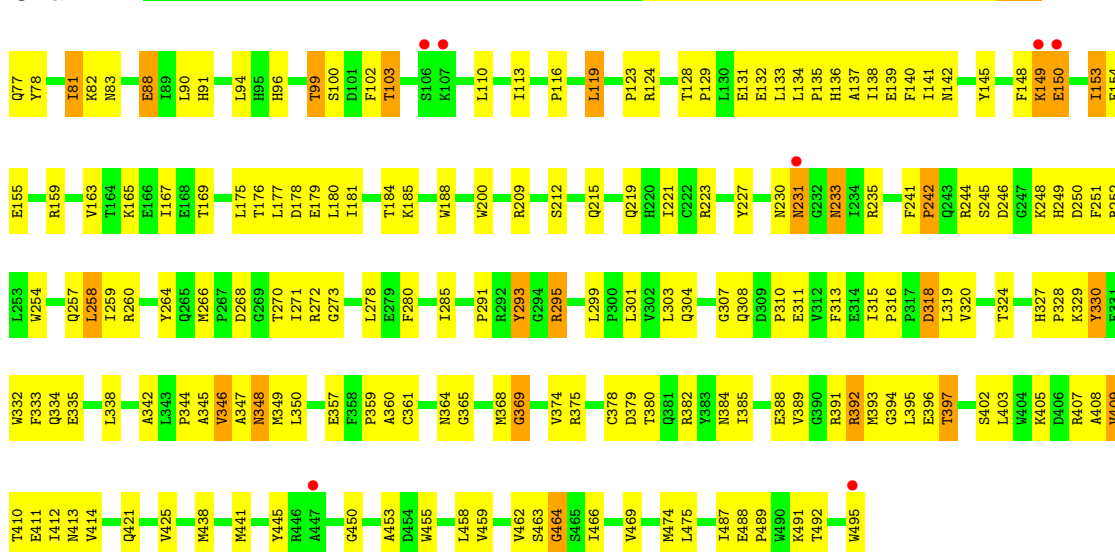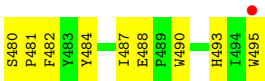
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α, β, γ	216.34Å 216.34Å 117.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.90 19.95 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.90) 98.1 (19.95-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$<I/\sigma(I)>$ [1]	2.83 (at 2.71Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.207 , 0.262 0.213 , 0.204	Depositor DCC
R_{free} test set	1790 reflections (5.30%)	DCC
Wilson B-factor (Å^2)	67.5	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 59.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$<|L|> = 0.49, <L^2> = 0.33$	Xtriage
Outliers	0 of 43964 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7233	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]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: HEM, ARR, ZN, H4B

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	0.43	0/3515	0.66	1/4778 (0.0%)
1	B	0.42	0/3515	0.63	1/4778 (0.0%)
All	All	0.43	0/7030	0.65	2/9556 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	365	GLY	N-CA-C	-6.26	97.44	113.10
1	B	365	GLY	N-CA-C	-5.29	99.87	113.10

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	3415	0	3312	175	0
1	B	3415	0	3312	207	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	43	0	30	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	43	0	30	1	0
4	A	17	0	15	0	0
4	B	17	0	15	0	0
5	A	50	0	38	13	3
5	B	50	0	38	20	0
6	A	89	0	0	4	3
6	B	92	0	0	3	0
All	All	7233	0	6790	406	3

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 29.

The worst 5 of 406 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:254:TRP:HE1	1:B:304:GLN:NE2	1.49	1.09
1:B:153:ILE:H	1:B:153:ILE:HD12	1.20	1.06
1:A:271:ILE:HD13	1:A:278:LEU:HD11	1.37	1.05
1:A:153:ILE:HD12	1:A:153:ILE:H	1.18	1.05
5:B:903[A]:ARR:C10	5:B:903[A]:ARR:H3	1.86	1.05

All (3) 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	Distance(Å)	Clash(Å)
5:A:902[B]:ARR:C17	6:A:1002:HOH:O[10_665]	0.71	1.49
5:A:902[B]:ARR:C18	6:A:1002:HOH:O[10_665]	1.34	0.86
5:A:902[B]:ARR:C16	6:A:1002:HOH:O[10_665]	2.04	0.16

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	417/419 (100%)	359 (86%)	43 (10%)	15 (4%)	5	22
1	B	417/419 (100%)	366 (88%)	44 (11%)	7 (2%)	14	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	834/838 (100%)	725 (87%)	87 (10%)	22 (3%)	8 32

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	99	THR
1	B	99	THR
1	B	330	TYR
1	B	384	ASN
1	A	295	ARG

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	367/367 (100%)	349 (95%)	18 (5%)	35 73
1	B	367/367 (100%)	340 (93%)	27 (7%)	20 50
All	All	734/734 (100%)	689 (94%)	45 (6%)	26 62

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	110	LEU
1	B	149	LYS
1	B	386	LEU
1	B	128	THR
1	B	150	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	421	GLN
1	B	96	HIS
1	B	348	ASN
1	B	83	ASN
1	B	91	HIS

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, 2 are monoatomic - leaving 8 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	HEM	A	900	1	49,50,50	3.19	9 (18%)	46,82,82	1.69	10 (21%)
4	H4B	A	901	-	18,18,18	1.51	4 (22%)	24,26,26	2.38	7 (29%)
5	ARR	A	902[A]	-	27,27,27	4.30	11 (40%)	35,35,35	2.60	2 (5%)
5	ARR	A	902[B]	-	27,27,27	4.30	11 (40%)	35,35,35	2.60	2 (5%)
4	H4B	B	1901	-	18,18,18	1.43	4 (22%)	24,26,26	2.40	7 (29%)
3	HEM	B	900	1	49,50,50	2.43	8 (16%)	46,82,82	1.34	6 (13%)
5	ARR	B	903[A]	-	27,27,27	4.31	10 (37%)	35,35,35	2.60	2 (5%)
5	ARR	B	903[B]	-	27,27,27	4.31	10 (37%)	35,35,35	2.60	2 (5%)

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	HEM	A	900	1	-	0/14/114/114	0/0/8/8
4	H4B	A	901	-	-	0/8/17/17	0/0/2/2
5	ARR	A	902[A]	-	-	0/11/15/15	0/3/3/3
5	ARR	A	902[B]	-	-	0/11/15/15	0/3/3/3
4	H4B	B	1901	-	-	0/8/17/17	0/0/2/2
3	HEM	B	900	1	-	0/14/114/114	0/0/8/8
5	ARR	B	903[A]	-	-	0/11/15/15	0/3/3/3
5	ARR	B	903[B]	-	-	0/11/15/15	0/3/3/3

The worst 5 of 67 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	903[B]	ARR	C4-S	-19.40	1.47	1.72
5	B	903[A]	ARR	C4-S	-19.40	1.47	1.72
5	A	902[B]	ARR	C4-S	-19.36	1.47	1.72
5	A	902[A]	ARR	C4-S	-19.36	1.47	1.72
3	A	900	HEM	C2D-C1D	13.02	1.47	1.44

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	903[B]	ARR	C1-S-C4	14.49	98.29	91.91
5	B	903[A]	ARR	C1-S-C4	14.49	98.29	91.91
5	A	902[B]	ARR	C1-S-C4	14.47	98.28	91.91
5	A	902[A]	ARR	C1-S-C4	14.47	98.28	91.91
4	B	1901	H4B	C4-C4A-C8A	8.01	121.98	114.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers (i)

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 (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	419/419 (100%)	-0.30	7 (1%)	67	76	42, 59, 78, 93	0
1	B	419/419 (100%)	-0.28	8 (1%)	64	72	48, 62, 82, 95	0
All	All	838/838 (100%)	-0.29	15 (1%)	65	74	42, 60, 80, 95	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	106	SER	7.1
1	B	101	ASP	4.2
1	A	106	SER	3.7
1	B	149	LYS	3.3
1	A	150	GLU	3.1

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. 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	RSR	LLDF	B-factors(Å^2)	Q<0.9
5	ARR	B	903[A]	25/25	0.41	10.07	41,56,59,59	25
5	ARR	B	903[B]	25/25	0.41	9.90	40,55,58,59	25
5	ARR	A	902[A]	25/25	0.40	7.76	40,48,58,59	25
5	ARR	A	902[B]	25/25	0.40	7.69	40,48,57,59	25
3	HEM	B	900	43/43	0.16	0.24	48,51,52,53	0
3	HEM	A	900	43/43	0.12	-0.87	42,45,48,50	0
4	H4B	B	1901	17/17	0.12	-1.01	51,52,55,57	0
4	H4B	A	901	17/17	0.11	-1.05	48,49,51,54	0
2	ZN	A	950	1/1	0.04	-2.12	55,55,55,55	1
2	ZN	B	950	1/1	0.04	-11.20	53,53,53,53	1

6.5 Other polymers ⓘ

There are no such residues in this entry.