

wwPDB X-ray Structure Validation Summary Report (i)

May 21, 2020 – 03:23 am BST

PDB ID : 4AY8

Title: SeMet-derivative of a methyltransferase from M. mazei

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P.; Faust, A.

 $Deposited \ on \quad : \quad 2012\text{-}06\text{-}18$

Resolution : 2.10 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

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) 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

 $\begin{array}{cccc} & CCP4 & : & 7.0.044 \; (Gargrove) \\ Ideal \; geometry \; (proteins) & : & Engh \; \& \; Huber \; (2001) \end{array}$

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

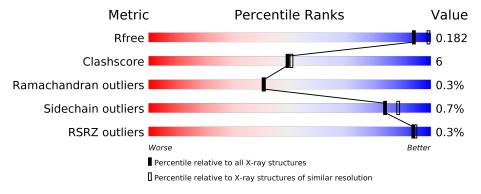
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 2.10 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
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 >=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 <=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	348	86%	11%	.
1	В	348	88%	10%	

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
5	GOL	В	700	-	-	X	-



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 5455 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.

 \bullet Molecule 1 is a protein called METHYLCOBALAMIN\: COENZYME M METHYLTRANSFERASE.

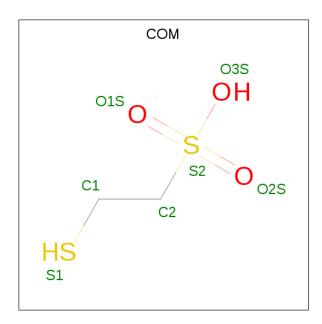
Mol	Chain	Residues	Atoms			ZeroOcc	$\mathbf{AltConf}$	Trace		
1	A	340	Total 2525	C 1602				0	0	0
1	В	340	Total 2525	C 1602		O 485		0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP Q8PXZ6
A	-4	HIS	-	expression tag	UNP Q8PXZ6
A	-3	HIS	-	expression tag	UNP Q8PXZ6
A	-2	HIS	_	expression tag	UNP Q8PXZ6
A	-1	HIS	_	expression tag	UNP Q8PXZ6
A	0	HIS	_	expression tag	UNP Q8PXZ6
В	-5	HIS	_	expression tag	UNP Q8PXZ6
В	-4	HIS	_	expression tag	UNP Q8PXZ6
В	-3	HIS	_	expression tag	UNP Q8PXZ6
В	-2	HIS	_	expression tag	UNP Q8PXZ6
В	-1	HIS	_	expression tag	UNP Q8PXZ6
В	0	HIS	_	expression tag	UNP Q8PXZ6

• Molecule 2 is 1-THIOETHANESULFONIC ACID (three-letter code: COM) (formula: C₂H₆O₃S₂).





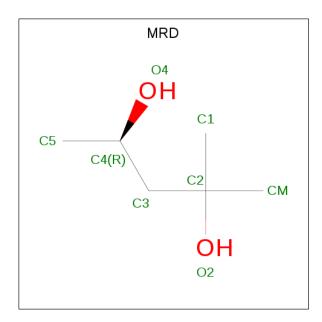
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
9	Δ	1	Total	С	О	S	0	0	
	Λ	1	7	2	3	2	0	U	
2	D	1	Total	С	О	S	0	0	
	D	1	7	2	3	2	0	U	

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total Zn 1 1	0	0
3	A	1	Total Zn 1 1	0	0

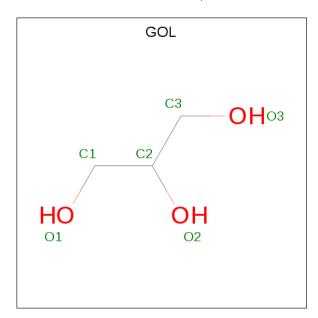
• Molecule 4 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: $C_6H_{14}O_2$).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total C 8 6	O 2	0	0

• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	1	Total C O 6 3 3	0	0
5	В	1	Total C O 6 3 3	0	0

• Molecule 6 is water.



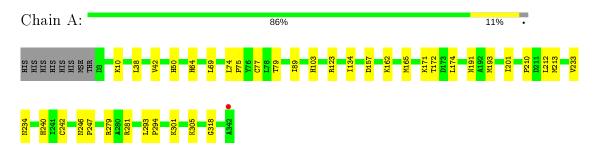
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	191	Total O 191 191	0	0
6	В	178	Total O 178 178	0	0



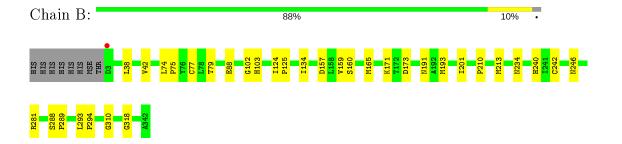
3 Residue-property plots (i)

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: METHYLCOBALAMIN\: COENZYME M METHYLTRANSFERASE



• Molecule 1: METHYLCOBALAMIN\: COENZYME M METHYLTRANSFERASE





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 32	Depositor	
Cell constants	$125.21 ext{Å}$ $125.21 ext{Å}$ $38.88 ext{Å}$	Danasitan	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	33.03 - 2.10	Depositor	
rtesoration (A)	33.03 - 2.10	EDS	
% Data completeness	99.9 (33.03-2.10)	Depositor	
(in resolution range)	99.9 (33.03-2.10)	EDS	
R_{merge}	0.07	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	$3.71~({\rm at}~2.10{\rm \AA})$	Xtriage	
Refinement program	REFMAC 5.5.0109	Depositor	
R, R_{free}	0.146 , 0.177	Depositor	
	0.151 , 0.182	DCC	
R_{free} test set	1994 reflections (5.02%)	wwPDB-VP	
Wilson B-factor (Å ²)	11.7	Xtriage	
Anisotropy	0.050	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	$0.35\;,23.0$	EDS	
L-test for twinning ²	$< L >=0.49, < L^2>=0.33$	Xtriage	
	0.487 for -h,-k,l		
Estimated twinning fraction	0.025 for h,-h-k,-l	Xtriage	
	0.025 for -k,-h,-l		
F_o, F_c correlation	0.96	EDS	
Total number of atoms	5455	wwPDB-VP	
Average B, all atoms (\mathring{A}^2)	10.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.99% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $< L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MRD, GOL, ZN, COM, CSD

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		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.45	0/2549	0.60	1/3445 (0.0%)	
1	В	0.44	0/2549	0.55	0/3445	
All	All	0.44	0/5098	0.57	1/6890 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}(^{o})$
1	A	279	ARG	NE-CZ-NH2	-6.32	117.14	120.30

There are no chirality outliers.

There are no planarity outliers.

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	2525	0	2598	29	0
1	В	2525	0	2598	28	0
2	A	7	0	4	0	0
2	В	7	0	5	0	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
4	A	8	0	14	5	0
5	В	12	0	16	6	0

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Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
6	A	191	0	0	4	1
6	В	178	0	0	1	1
All	All	5455	0	5235	61	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 6.

The worst 5 of 61 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} ext{Interatomic} \ ext{distance} & (ext{Å}) \end{aligned}$	Clash overlap (Å)
1:B:165:MSE:HG2	1:B:213:MSE:CE	1.61	1.29
4:A:800:MRD:H5C3	4:A:800:MRD:CM	1.62	1.27
1:B:165:MSE:CG	1:B:213:MSE:HE1	1.76	1.14
4:A:800:MRD:HMC1	4:A:800:MRD:C5	1.80	1.07
4:A:800:MRD:HMC1	4:A:800:MRD:H5C3	1.05	1.02

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	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
6:A:2130:HOH:O	6:B:2173:HOH:O[2_674]	1.87	0.33

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	337/348 (97%)	326 (97%)	10 (3%)	1 (0%)	41 41
1	В	337/348 (97%)	328 (97%)	8 (2%)	1 (0%)	41 41
All	All	674/696 (97%)	654 (97%)	18 (3%)	2 (0%)	41 41

All (2) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	75	PRO
1	В	75	PRO

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	$276/272\ (102\%)$	274 (99%)	2 (1%)	84 88		
1	В	$276/272 \; (102\%)$	274 (99%)	2 (1%)	84 88		
All	All	$552/544 \; (102\%)$	548 (99%)	4 (1%)	84 88		

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	242	CYS
1	A	281	ARG
1	В	242	CYS
1	В	281	ARG

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	A	220	GLN
1	A	234	ASN
1	В	191	ASN
1	A	191	ASN
1	В	103	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.



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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Dag	T ! 1.	Bond lengths			Bond angles		
MIOI	Type	Chain	m Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2									
1	CSD	В	77	1	3,7,8	1.30	0	1,8,10	1.68	0									
1	CSD	A	77	1	3,7,8	1.33	1 (33%)	1,8,10	2.20	1 (100%)									

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	${f Res}$	Link	Chirals	Torsions	Rings
1	CSD	В	77	1	-	1/2/6/8	-
1	CSD	A	77	1	-	1/2/6/8	-

All (1) bond length outliers are listed below:

Mol	Chain	${f Res}$	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(\mathbf{\AA})$	$\operatorname{Ideal}(ext{\AA})$
1	A	77	CSD	CB-SG	-2.03	1.67	1.79

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	77	CSD	OD1-SG-CB	2.20	109.73	105.54

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	В	77	CSD	CA-CB-SG-OD1
1	A	77	CSD	CA-CB-SG-OD1

There are no ring outliers.



2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	В	77	CSD	1	0
1	A	77	CSD	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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).

Mal	Т	Chain	Des	Res Link Bond lengths			gths	Е	ond ang	gles
Mol	Type	Chain	nes	Link	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
5	GOL	В	701	-	5,5,5	0.38	0	5,5,5	0.13	0
4	MRD	A	800	_	7,7,7	0.35	0	9,10,10	0.27	0
2	COM	A	500	3	6,6,6	2.75	1 (16%)	7,8,8	2.30	2 (28%)
2	COM	В	500	3	6,6,6	2.77	1 (16%)	7,8,8	2.73	2 (28%)
5	GOL	В	700	-	5,5,5	0.39	0	5,5,5	0.34	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
5	GOL	В	701	-	-	3/4/4/4	_
4	MRD	A	800	-	-	5/5/5/5	-
2	COM	A	500	3	-	0/4/4/4	-
2	COM	В	500	3	-	0/4/4/4	_
5	GOL	В	700	-	-	4/4/4/4	-

All (2) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(ext{\AA})$
2	В	500	COM	C2-S2	-6.67	1.68	1.77
2	A	500	COM	C2-S2	-6.54	1.68	1.77

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
2	В	500	COM	O2S-S2-C2	5.66	113.73	106.92
2	A	500	COM	O3S-S2-C2	4.89	113.67	105.77
2	В	500	COM	O1S-S2-C2	3.81	111.50	106.92
2	A	500	COM	O1S-S2-C2	2.83	110.33	106.92

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	В	701	GOL	O1-C1-C2-C3
4	A	800	MRD	O2-C2-C3-C4
4	A	800	MRD	CM-C2-C3-C4
4	A	800	MRD	C2-C3-C4-O4
5	В	700	GOL	C1-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	800	MRD	5	0
5	В	700	GOL	6	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^{th} 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 $>$	#RS	\mathbf{RZ}	>2	$OWAB(Å^2)$	Q < 0.9
1	A	328/348 (94%)	-0.95	1 (0%)	94	94	3, 8, 18, 36	0
1	В	$328/348 \ (94\%)$	-0.95	1 (0%)	94	94	3, 8, 18, 36	0
All	All	656/696 (94%)	-0.95	2 (0%)	94	94	3, 8, 18, 36	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	342	ALA	3.6
1	В	3	ASP	2.3

6.2 Non-standard residues in protein, DNA, RNA chains (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^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	CSD	В	77	8/9	0.96	0.09	6,8,18,19	0
1	CSD	A	77	8/9	0.97	0.08	6,9,17,17	0

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^{th} 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	${f B\text{-factors}}({f \AA}^2)$	Q < 0.9
5	GOL	В	701	6/6	0.62	0.14	51,51,51,51	0
5	GOL	В	700	6/6	0.82	0.13	33,36,37,39	0
4	MRD	A	800	8/8	0.83	0.18	30,32,33,34	0
2	COM	A	500	7/7	0.98	0.07	13,14,15,16	0
3	ZN	A	600	1/1	0.99	0.05	16,16,16,16	0
2	COM	В	500	7/7	0.99	0.06	13,14,16,16	0
3	ZN	В	600	1/1	0.99	0.05	16,16,16,16	0

6.5 Other polymers (i)

There are no such residues in this entry.

