

# Full wwPDB X-ray Structure Validation Report (i)

May 23, 2020 – 12:16 am BST

PDB ID : 2WNH

Title : Crystal Structure Analysis of Klebsiella sp ASR1 Phytase

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Deposited on : 2009-07-09

Resolution : 1.68 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
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

CCP4 : 7.0.044 (Gargrove) roteins) : Engh & Huber (2001)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

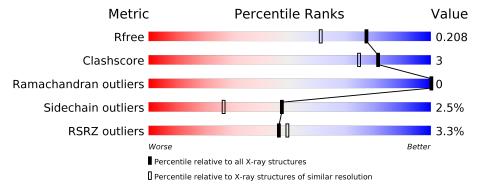
Validation Pipeline (wwPDB-VP) : 2.11

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.68 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	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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	418	91%	5%	5%		
1	В	418	90%	5%			



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7047 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 3-PHYTASE.

$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	399	Total 3137	C 1963	N 579	O 582	S 13	0	12	1
1	В	400	Total 3123	C 1956	N	O 577	S 14	0	7	1

There are 57 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q84CN9
A	2	ASP	-	expression tag	UNP Q84CN9
A	3	ILE	-	expression tag	UNP Q84CN9
A	4	GLY	=	expression tag	UNP Q84CN9
A	5	ILE	=	expression tag	UNP Q84CN9
A	6	ASN	=	expression tag	UNP Q84CN9
A	7	SER	=	expression tag	UNP Q84CN9
A	8	ASP	_	expression tag	UNP Q84CN9
A	9	PRO	=	expression tag	UNP Q84CN9
A	10	PRO	_	expression tag	UNP Q84CN9
A	11	PRO	=	expression tag	UNP Q84CN9
A	12	ARG	=	expression tag	UNP Q84CN9
A	123	ALA	VAL	engineered mutation	UNP Q84CN9
A	279	SER	ASN	engineered mutation	UNP Q84CN9
A	397	ALA	THR	engineered mutation	UNP Q84CN9
A	406	LYS	=	expression tag	UNP Q84CN9
A	407	LEU	=	expression tag	UNP Q84CN9
A	408	ALA	=	expression tag	UNP Q84CN9
A	409	ALA	=	expression tag	UNP Q84CN9
A	410	ALA	=	expression tag	UNP Q84CN9
A	411	LEU	-	expression tag	UNP Q84CN9
A	412	GLU	=	expression tag	UNP Q84CN9
A	413	HIS	-	expression tag	UNP Q84CN9
A	414	HIS	-	expression tag	UNP Q84CN9
A	415	HIS	-	expression tag	UNP Q84CN9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	416	HIS	_	expression tag	UNP Q84CN9
A	417	HIS	_	expression tag	UNP Q84CN9
A	418	HIS	_	expression tag	UNP Q84CN9
A	279	SER	ASN	conflict	UNP Q84CN9
В	1	MET	-	expression tag	UNP Q84CN9
В	2	ASP	-	expression tag	UNP Q84CN9
В	3	ILE	-	expression tag	UNP Q84CN9
В	4	GLY	-	expression tag	UNP Q84CN9
В	5	ILE	-	expression tag	UNP Q84CN9
В	6	ASN	-	expression tag	UNP Q84CN9
В	7	SER	-	expression tag	UNP Q84CN9
В	8	ASP	-	expression tag	UNP Q84CN9
В	9	PRO	-	expression tag	UNP Q84CN9
В	10	PRO	-	expression tag	UNP Q84CN9
В	11	PRO	-	expression tag	UNP Q84CN9
В	12	ARG	-	expression tag	UNP Q84CN9
В	123	ALA	VAL	engineered mutation	UNP Q84CN9
В	279	SER	ASN	engineered mutation	UNP Q84CN9
В	397	ALA	THR	engineered mutation	UNP Q84CN9
В	406	LYS	_	expression tag	UNP Q84CN9
В	407	LEU	-	expression tag	UNP Q84CN9
В	408	ALA	_	expression tag	UNP Q84CN9
В	409	ALA	_	expression tag	UNP Q84CN9
В	410	ALA	_	expression tag	UNP Q84CN9
В	411	LEU	_	expression tag	UNP Q84CN9
В	412	GLU	_	expression tag	UNP Q84CN9
В	413	HIS	-	expression tag	UNP Q84CN9
В	414	HIS	-	expression tag	UNP Q84CN9
В	415	HIS	-	expression tag	UNP Q84CN9
В	416	HIS	-	expression tag	UNP Q84CN9
В	417	HIS	-	expression tag	UNP Q84CN9
В	418	HIS	-	expression tag	UNP Q84CN9

• Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

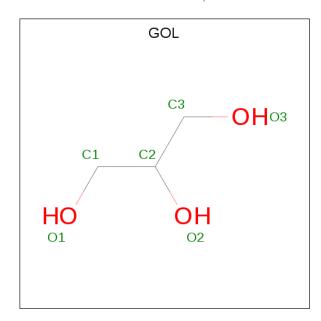
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	2	Total Na 2 2	0	0
2	A	1	Total Na 1 1	0	0

• Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0

• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



N	/Iol	Chain	Residues	Atoms	ZeroOcc	AltConf
	4	A	1	Total C O 6 3 3	0	0
	4	В	1	Total C O 6 3 3	0	0

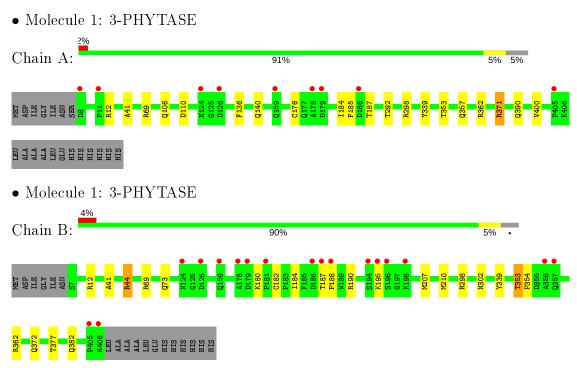
• Molecule 5 is water.

$\mathbf{M}$	[ol	Chain	Residues	Atoms	ZeroOcc	AltConf
	5	A	395	Total O 395 395	0	0
ţ	5	В	376	Total O 376 376	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.





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	133.68Å 133.68Å 111.24Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	94.49 - 1.68	Depositor
Resolution (A)	19.55 - 1.68	EDS
% Data completeness	99.2 (94.49-1.68)	Depositor
(in resolution range)	99.3 (19.55-1.68)	EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.45 (at 1.68Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
D D.	0.181 , 0.207	Depositor
$R, R_{free}$	0.181 , 0.208	DCC
$R_{free}$ test set	5643 reflections $(4.98%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.8	Xtriage
Anisotropy	0.001	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.38 , 48.2	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7047	wwPDB-VP
Average B, all atoms $(Å^2)$	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.58% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: GOL, MG, NA

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	0.58	0/3257	0.64	0/4437	
1	В	0.55	0/3221	0.65	0/4385	
All	All	0.57	0/6478	0.65	0/8822	

There are no bond length outliers.

There are no bond angle outliers.

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	3137	0	3113	17	0
1	В	3123	0	3102	15	0
2	A	1	0	0	0	0
2	В	2	0	0	0	0
3	A	1	0	0	0	0
4	A	6	0	8	0	0
4	В	6	0	8	0	0
5	A	395	0	0	0	0
5	В	376	0	0	1	0
All	All	7047	0	6231	32	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 3.

All (32) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{ll}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{array}$	Clash overlap (Å)
1:B:44:ARG:HH11	1:B:44:ARG:HG3	1.16	1.08
1:A:69[A]:ARG:NH2	1:A:353[A]:THR:HG21	1.67	1.07
1:A:69[A]:ARG:NH2	1:A:353[A]:THR:CG2	2.24	1.01
1:A:69[A]:ARG:HH21	1:A:353[A]:THR:HG21	1.40	0.86
1:A:69[A]:ARG:HH22	1:A:353[A]:THR:CG2	1.87	0.85
1:B:207:MET:HA	1:B:210:MET:HE3	1.67	0.77
1:A:69[A]:ARG:NH2	1:A:353[A]:THR:HG22	2.05	0.72
1:B:44:ARG:NH1	1:B:44:ARG:HG3	1.94	0.70
1:A:69[A]:ARG:HH22	1:A:353[A]:THR:HG21	1.52	0.61
1:A:69[B]:ARG:HH11	1:A:69[B]:ARG:HG3	1.67	0.60
1:B:69[B]:ARG:HH11	1:B:69[B]:ARG:HG3	1.66	0.60
1:B:372:GLN:NE2	1:B:377:THR:OG1	2.35	0.59
1:A:69[A]:ARG:HH21	1:A:353[A]:THR:CG2	2.05	0.57
1:A:69[A]:ARG:HH22	1:A:353[A]:THR:HG22	1.64	0.56
1:B:69[A]:ARG:HH21	1:B:353:THR:HG21	1.71	0.55
1:B:207:MET:HA	1:B:210:MET:CE	2.40	0.51
1:B:353:THR:HG22	1:B:354:PRO:HD2	1.94	0.50
1:A:12:ARG:HH21	1:A:371[B]:ARG:NE	2.10	0.50
1:B:41:ALA:HB1	1:B:184:ILE:HB	1.94	0.49
1:B:73:GLN:HG2	5:B:2085:HOH:O	2.13	0.49
1:A:41:ALA:HB1	1:A:184:ILE:HB	1.96	0.48
1:A:12:ARG:HH21	1:A:371[B]:ARG:CZ	2.27	0.47
1:B:69[A]:ARG:NH2	1:B:353:THR:HG21	2.31	0.45
1:A:339:TYR:CD2	1:A:362:ARG:HD2	2.52	0.45
1:B:188:PRO:HD2	1:B:190:ARG:NH2	2.31	0.45
1:B:339:TYR:CD2	1:B:362:ARG:HD3	2.52	0.45
1:A:136:PHE:O	1:A:140:GLN:HG3	2.18	0.44
1:B:69[B]:ARG:CG	1:B:69[B]:ARG:HH11	2.31	0.44
1:A:106:GLN:O	1:A:110:ASP:HB2	2.19	0.43
1:B:12:ARG:HA	1:B:12:ARG:HD2	1.83	0.42
1:A:176:CYS:SG	1:A:185:PHE:CE2	3.13	0.42
1:A:12:ARG:HE	1:A:371[B]:ARG:NH2	2.18	0.41

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	Perce	$\mathbf{ntiles}$
1	A	$409/418 \; (98\%)$	405 (99%)	4 (1%)	0	100	100
1	В	$405/418 \; (97\%)$	398 (98%)	7 (2%)	0	100	100
All	All	814/836 (97%)	803 (99%)	11 (1%)	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	Percentile	$\mathbf{s}$
1	A	335/339~(99%)	326 (97%)	9 (3%)	44 24	
1	В	330/339~(97%)	320 (97%)	10 (3%)	41 20	
All	All	665/678 (98%)	646 (97%)	19 (3%)	47 21	

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	187	THR
1	A	292[A]	THR
1	A	292[B]	THR
1	A	298	ARG
1	A	357	GLN
1	A	371[A]	ARG
1	A	371[B]	ARG
1	A	390	GLN

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Mol	Chain	Res	Type
1	A	400	VAL
1	В	44	ARG
1	В	180	LYS
1	В	182	CYS
1	В	187	THR
1	В	195	LYS
1	В	298	ARG
1	В	302	ASN
1	В	353	THR
1	В	382[A]	GLN
1	В	382[B]	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	GLN
1	A	234	GLN
1	A	253	ASN
1	A	281	ASN
1	A	390	GLN
1	В	66	ASN
1	В	106	GLN
1	В	159	GLN
1	В	169	GLN
1	В	173	GLN
1	В	234	GLN
1	В	248	ASN
1	В	302	ASN
1	В	372	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 6 ligands modelled in this entry, 4 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	Tuna	Chain	Res	Link	$\mathbf{B}$	ond leng	${ m gths}$	В	ond ang	gles
MIGI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
4	GOL	A	1409	_	5,5,5	0.41	0	5, 5, 5	0.45	0
4	GOL	В	1409	-	5,5,5	0.44	0	5,5,5	1.04	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
4	GOL	A	1409	_	-	1/4/4/4	_
4	GOL	В	1409	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	${ m Res}$	$\mathbf{Type}$	${f Atoms}$
4	В	1409	GOL	O1-C1-C2-C3
4	A	1409	GOL	O1-C1-C2-C3
4	В	1409	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.



# 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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q < 0.9
1	A	399/418 (95%)	-0.21	9 (2%) 60 64	13, 20, 35, 54	0
1	В	400/418 (95%)	-0.13	17 (4%) 35 37	13, 21, 38, 55	1 (0%)
All	All	799/836 (95%)	-0.17	26 (3%) 46 49	13, 21, 36, 55	1 (0%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	11	PRO	7.4
1	В	178	ALA	5.7
1	В	179	ASP	5.2
1	A	186	ASP	4.4
1	A	178	ALA	4.3
1	В	195	LYS	4.0
1	В	124	ASN	4.0
1	A	179	ASP	3.9
1	В	405	PRO	3.7
1	В	186	ASP	3.5
1	В	181	PRO	3.4
1	В	187	THR	3.3
1	A	124	ASN	3.2
1	A	405	PRO	3.2
1	В	356	ALA	3.1
1	A	126	ASP	3.1
1	A	8	ASP	2.9
1	В	126	ASP	2.9
1	В	188	PRO	2.8
1	В	406	LYS	2.7
1	В	196	SER	2.7
1	В	357	GLN	2.6
1	В	198	LYS	2.5
1	В	194	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	В	159	GLN	2.4
1	A	159	GLN	2.2

## 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,  $95^{th}$  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
4	GOL	В	1409	6/6	0.92	0.09	23,27,29,29	0
2	NA	В	1407	1/1	0.96	0.27	45,45,45,45	0
4	GOL	A	1409	6/6	0.97	0.06	18,19,19,21	0
2	NA	A	1407	1/1	0.98	0.14	32,32,32,32	0
2	NA	В	1408	1/1	0.99	0.07	13,13,13,13	1
3	MG	A	1408	1/1	1.00	0.07	19,19,19,19	1

## 6.5 Other polymers (i)

There are no such residues in this entry.

