

wwPDB X-ray Structure Validation Summary Report (i)

Dec 8, 2022 – 06:16 pm GMT

PDB ID	:	7ZHT
Title	:	Leishmania donovani Glucose 6-Phosphate Dehydrogenase apo form
Authors	:	Fritz-Wolf, K.; Berneburg, I.
Deposited on	:	2022-04-07
Resolution	:	2.80 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.3
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569(2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 of 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 ch	ain	
1	А	562	4% 61%	27%	• • 6%
1	В	562	6%	28%	• 7%
1	С	562	5%	31% •	• 14%
1	D	562	3% 54%	27% •	• 14%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard



residues	s in	protein,	DNA,	RNA	chains	that	are	outliers	for	geometric	or	electron	-density-fi	t crite-
ria:														
Mal	т.			Dec	China	1:+	C	aamatm		Clasher	T.I	laatnan	donaitu	

Mol	Type	Chain	\mathbf{Res}	Chirality	Geometry	Clashes	Electron density
2	EDO	А	602	-	-	-	Х
2	EDO	В	1001	-	-	-	Х
2	EDO	С	601	_	-	-	Х



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 16104 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	Δ	520	Total	С	Ν	Ο	\mathbf{S}	0	0	0
	A	530	4208	2676	724	792	16	0	0	0
1	B	525	Total	С	Ν	0	S	0	0	0
1	D	525	4158	2647	713	782	16	0	0	U
1	C	492	Total	С	Ν	0	S	0	0	0
1	C	400	3823	2432	656	718	17	0	0	0
1	П	485	Total	С	Ν	0	S	0	0	0
1	D	485	3838	2442	658	721	17	0	0	0

• Molecule 1 is a protein called Glucose-6-phosphate 1-dehydrogenase.

• Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
2	С	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
2	С	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	С	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	D	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 4 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	3	Total O 3 3	0	0
4	В	14	Total O 14 14	0	0
4	С	4	Total O 4 4	0	0
4	D	5	$\begin{array}{cc} \text{Total} & \text{O} \\ 5 & 5 \end{array}$	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Glucose-6-phosphate 1-dehydrogenase

• Molecule 1: Glucose-6-phosphate 1-dehydrogenase













4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants	117.69Å 65.82 Å 189.22 Å	Deperitor
a, b, c, α , β , γ	90.00° 92.35° 90.00°	Depositor
$\mathbf{P}_{\text{oscolution}}(\hat{\mathbf{A}})$	39.20 - 2.80	Depositor
Resolution (A)	39.20 - 2.80	EDS
% Data completeness	98.1 (39.20-2.80)	Depositor
(in resolution range)	98.5(39.20-2.80)	EDS
R_{merge}	0.10	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.25 (at 2.81 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.19.2_4158, PHENIX 1.19.2_4158	Depositor
D D.	0.244 , 0.304	Depositor
Π, Π_{free}	0.244 , 0.305	DCC
R_{free} test set	7073 reflections (10.00%)	wwPDB-VP
Wilson B-factor $(Å^2)$	72.7	Xtriage
Anisotropy	0.227	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16104	wwPDB-VP
Average B, all atoms $(Å^2)$	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 29.63 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4996e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical 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.



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: SO4, EDO

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).

Mal	Chain	Bo	ond lengths	B	ond angles
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.46	5/4296~(0.1%)	0.90	20/5810~(0.3%)
1	В	0.32	0/4244	0.69	6/5740~(0.1%)
1	С	0.54	5/3905~(0.1%)	1.03	40/5281~(0.8%)
1	D	0.50	6/3919~(0.2%)	0.94	32/5299~(0.6%)
All	All	0.46	16/16364~(0.1%)	0.89	98/22130~(0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	А	0	17
1	С	0	6
1	D	1	7
All	All	1	30

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\operatorname{Ideal}(\operatorname{\AA})$
1	А	124	GLU	CG-CD	9.12	1.65	1.51
1	D	169	GLU	CB-CG	7.56	1.66	1.52
1	D	462	GLN	CB-CG	-7.49	1.32	1.52
1	D	376	GLU	CG-CD	-7.19	1.41	1.51
1	С	326	ARG	CZ-NH2	6.96	1.42	1.33

The worst 5 of 98 bond angle outliers are listed below:

WIOI	Unain	Res	Type	Atoms	Z	Observed(^o)	Ideal(°)
1	А	376	GLU	CG-CD-OE1	17.41	153.12	118.30



• • • • • •	- $ -$									
Mol	Chain	\mathbf{Res}	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$			
1	D	534	ARG	CB-CG-CD	-16.60	68.43	111.60			
1	А	376	GLU	CG-CD-OE2	-16.47	85.36	118.30			
1	С	411	LYS	CD-CE-NZ	13.17	141.98	111.70			
1	А	376	GLU	OE1-CD-OE2	-13.08	107.61	123.30			

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All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	D	289	THR	CB

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	124	GLU	Peptide
1	А	134	SER	Peptide
1	А	20	ILE	Peptide
1	А	67	GLN	Sidechain,Peptide
1	А	69	SER	Mainchain

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	А	4208	0	4181	142	2
1	В	4158	0	4135	117	0
1	С	3823	0	3791	166	1
1	D	3838	0	3814	148	0
2	А	8	0	11	2	0
2	В	12	0	18	0	0
2	С	12	0	18	0	0
2	D	4	0	6	0	0
3	А	5	0	0	1	0
3	В	5	0	0	0	0
3	С	5	0	0	0	0
4	А	3	0	0	3	0
4	В	14	0	0	2	0
4	С	4	0	0	0	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	5	0	0	0	0
All	All	16104	0	15974	544	2

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 17.

The worst 5 of 544 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:C:120:LYS:HD3	1:C:124:GLU:OE1	1.32	1.23
1:D:112:ARG:NH1	1:D:113:THR:HG23	1.57	1.18
1:D:112:ARG:HH12	1:D:113:THR:CG2	1.57	1.17
1:D:112:ARG:NH1	1:D:113:THR:CG2	2.09	1.14
1:D:112:ARG:HH12	1:D:113:THR:HG22	1.13	1.04

All (2) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:ARG:NH1	$1:C:159:ASP:OD1[2_646]$	1.93	0.27
1:A:175:LYS:NZ	$1:A:526:PRO:O[1_545]$	2.16	0.04

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	ntiles
1	А	526/562~(94%)	488 (93%)	34 (6%)	4 (1%)	19	49
1	В	519/562~(92%)	493 (95%)	26~(5%)	0	100	100
1	С	479/562~(85%)	451 (94%)	27 (6%)	1 (0%)	47	78
1	D	481/562~(86%)	457 (95%)	24 (5%)	0	100	100



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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	2005/2248~(89%)	1889 (94%)	111 (6%)	5~(0%)	47 78

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	133	LEU
1	А	376	GLU
1	С	443	GLU
1	А	33	PRO
1	А	34	ASP

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	А	454/482~(94%)	427 (94%)	27~(6%)	19 49
1	В	449/482~(93%)	431 (96%)	18 (4%)	31 65
1	С	412/482~(86%)	380 (92%)	32 (8%)	12 35
1	D	414/482~(86%)	381 (92%)	33~(8%)	12 34
All	All	1729/1928~(90%)	1619 (94%)	110 (6%)	17 45

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	200	SER
1	С	470	LEU
1	D	552	LYS
1	D	438	ARG
1	С	271	SER

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such side chains are listed below:



Mol	Chain	Res	Type
1	В	410	GLN
1	D	440	GLN
1	С	67	GLN
1	D	489	ASN
1	D	259	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

12 ligands 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).

Mal	Turne	Chain	Dec	Tiple	B	ond leng	gths	E	ond ang	gles					
INIOI	туре	Unain	ries	nes	nes	ries	rtes	TIES		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	EDO	С	602	-	3,3,3	0.47	0	$2,\!2,\!2$	0.32	0					
2	EDO	А	602	-	3,3,3	0.47	0	2,2,2	0.33	0					
2	EDO	В	1003	-	3,3,3	0.47	0	$2,\!2,\!2$	0.31	0					
3	SO4	С	604	-	4,4,4	0.17	0	$6,\!6,\!6$	0.16	0					
3	SO4	А	603	-	4,4,4	0.15	0	$6,\!6,\!6$	0.05	0					
3	SO4	В	1004	-	4,4,4	0.15	0	$6,\!6,\!6$	0.05	0					
2	EDO	В	1001	-	3,3,3	0.47	0	2,2,2	0.28	0					
2	EDO	А	601	1	3,3,3	0.49	0	$2,\!2,\!2$	0.22	0					
2	EDO	D	601	-	3,3,3	0.46	0	$2,\!2,\!2$	0.37	0					
2	EDO	В	1002	-	3,3,3	0.48	0	$2,\!2,\!2$	0.39	0					



Mal Trma C		Chain	Chain Bag		nin Dec		Dec Link		Bond lengths			Bond angles		
	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2				
2	EDO	С	601	-	$3,\!3,\!3$	0.51	0	$2,\!2,\!2$	0.22	0				
2	EDO	С	603	-	3,3,3	0.48	0	$2,\!2,\!2$	0.32	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	EDO	С	602	-	-	1/1/1/1	-
2	EDO	А	602	-	-	0/1/1/1	-
2	EDO	В	1003	-	-	1/1/1/1	-
2	EDO	В	1001	-	-	0/1/1/1	-
2	EDO	А	601	1	-	1/1/1/1	-
2	EDO	D	601	-	-	0/1/1/1	-
2	EDO	В	1002	-	-	1/1/1/1	-
2	EDO	С	601	-	-	0/1/1/1	-
2	EDO	С	603	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	С	602	EDO	O1-C1-C2-O2
2	А	601	EDO	O1-C1-C2-O2
2	В	1003	EDO	O1-C1-C2-O2
2	С	603	EDO	O1-C1-C2-O2
2	В	1002	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	602	EDO	1	0
3	А	603	SO4	1	0
2	А	601	EDO	1	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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	530/562~(94%)	0.12	20 (3%) 40 30	49, 80, 140, 204	0
1	В	525/562~(93%)	0.15	31 (5%) 22 14	48, 81, 140, 199	0
1	С	483/562~(85%)	0.24	29 (6%) 21 14	51, 88, 149, 199	0
1	D	485/562~(86%)	0.16	15 (3%) 49 39	60, 87, 132, 179	0
All	All	2023/2248 (89%)	0.16	95 (4%) 31 22	48, 85, 140, 204	0

The worst 5 of 95 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	138	CYS	7.4
1	В	11	ASP	6.7
1	D	134	SER	6.1
1	В	456	LEU	5.5
1	D	291	GLY	4.7

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 monosaccharides 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	$B-factors(A^2)$	Q<0.9
2	EDO	С	601	4/4	0.50	0.57	113,117,119,128	0
2	EDO	А	602	4/4	0.56	0.46	65,77,78,83	0
2	EDO	С	603	4/4	0.56	0.27	83,109,111,114	0
2	EDO	В	1001	4/4	0.80	0.40	64,72,80,91	0
2	EDO	В	1003	4/4	0.84	0.38	69,73,73,75	0
2	EDO	В	1002	4/4	0.85	0.41	50,59,67,71	0
2	EDO	А	601	4/4	0.87	0.21	79,96,97,107	0
3	SO4	С	604	5/5	0.91	0.14	97,108,124,130	0
2	EDO	С	602	4/4	0.92	0.22	89,90,102,110	0
3	SO4	А	603	5/5	0.94	0.11	$109,\!111,\!130,\!142$	0
2	EDO	D	601	4/4	0.94	0.37	81,87,88,107	0
3	SO4	B	1004	$\overline{5/5}$	0.95	0.09	115,119,122,140	0

6.5 Other polymers (i)

There are no such residues in this entry.

