



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:39 AM GMT

PDB ID : 3MKY  
Title : Structure of SopB(155-323)-18mer DNA complex, I23 form  
Authors : Schumacher, M.A.; Piro, K.; Xu, W.  
Deposited on : 2010-04-15  
Resolution : 2.86 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

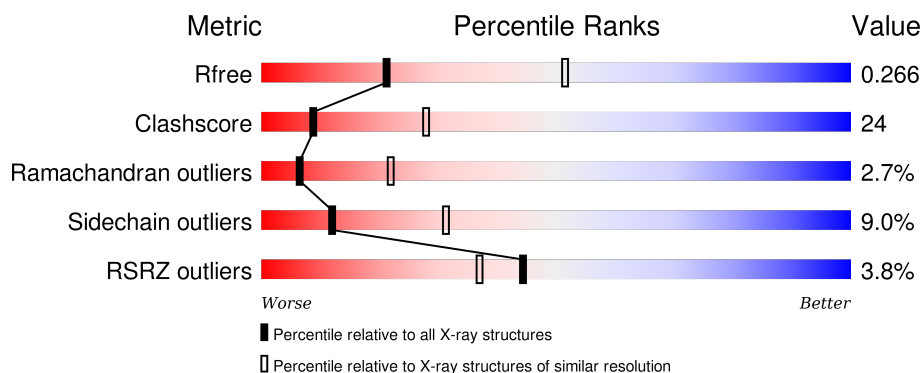
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.86 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))
$R_{free}$	91344	2228 (2.90-2.82)
Clashscore	102246	2499 (2.90-2.82)
Ramachandran outliers	100387	2439 (2.90-2.82)
Sidechain outliers	100360	2442 (2.90-2.82)
RSRZ outliers	91569	2236 (2.90-2.82)

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. 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  $\leq 5\%$ . 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	T	18	
1	U	18	
2	B	189	
2	P	189	

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
3	SO4	B	835	-	-	-	X
3	SO4	P	344	-	-	-	X
3	SO4	P	845	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2531 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 DNA chain called DNA (5'-D(\*CP\*TP\*GP\*GP\*GP\*AP\*CP\*CP\*AP\*TP\*GP\*GP\*TP\*CP\*CP\*CP\*AP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	U	18	Total	C	N	O	P	0	0	0
			366	174	69	106	17			
1	T	18	Total	C	N	O	P	0	0	0
			366	174	69	106	17			

- Molecule 2 is a protein called Protein sopB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	115	Total	C	N	O	S	0	0	0
			877	546	157	173	1			
2	P	114	Total	C	N	O	S	0	0	0
			872	543	156	172	1			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	135	MET	-	EXPRESSION TAG	UNP P62558
B	136	GLY	-	EXPRESSION TAG	UNP P62558
B	137	SER	-	EXPRESSION TAG	UNP P62558
B	138	SER	-	EXPRESSION TAG	UNP P62558
B	139	HIS	-	EXPRESSION TAG	UNP P62558
B	140	HIS	-	EXPRESSION TAG	UNP P62558
B	141	HIS	-	EXPRESSION TAG	UNP P62558
B	142	HIS	-	EXPRESSION TAG	UNP P62558
B	143	HIS	-	EXPRESSION TAG	UNP P62558
B	144	HIS	-	EXPRESSION TAG	UNP P62558
B	145	SER	-	EXPRESSION TAG	UNP P62558
B	146	SER	-	EXPRESSION TAG	UNP P62558
B	147	GLY	-	EXPRESSION TAG	UNP P62558
B	148	LEU	-	EXPRESSION TAG	UNP P62558
B	149	VAL	-	EXPRESSION TAG	UNP P62558

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	150	PRO	-	EXPRESSION TAG	UNP P62558
B	151	ARG	-	EXPRESSION TAG	UNP P62558
B	152	GLY	-	EXPRESSION TAG	UNP P62558
B	153	SER	-	EXPRESSION TAG	UNP P62558
B	154	HIS	-	EXPRESSION TAG	UNP P62558
B	255	ASP	GLU	CONFLICT	UNP P62558
P	135	MET	-	EXPRESSION TAG	UNP P62558
P	136	GLY	-	EXPRESSION TAG	UNP P62558
P	137	SER	-	EXPRESSION TAG	UNP P62558
P	138	SER	-	EXPRESSION TAG	UNP P62558
P	139	HIS	-	EXPRESSION TAG	UNP P62558
P	140	HIS	-	EXPRESSION TAG	UNP P62558
P	141	HIS	-	EXPRESSION TAG	UNP P62558
P	142	HIS	-	EXPRESSION TAG	UNP P62558
P	143	HIS	-	EXPRESSION TAG	UNP P62558
P	144	HIS	-	EXPRESSION TAG	UNP P62558
P	145	SER	-	EXPRESSION TAG	UNP P62558
P	146	SER	-	EXPRESSION TAG	UNP P62558
P	147	GLY	-	EXPRESSION TAG	UNP P62558
P	148	LEU	-	EXPRESSION TAG	UNP P62558
P	149	VAL	-	EXPRESSION TAG	UNP P62558
P	150	PRO	-	EXPRESSION TAG	UNP P62558
P	151	ARG	-	EXPRESSION TAG	UNP P62558
P	152	GLY	-	EXPRESSION TAG	UNP P62558
P	153	SER	-	EXPRESSION TAG	UNP P62558
P	154	HIS	-	EXPRESSION TAG	UNP P62558
P	255	ASP	GLU	CONFLICT	UNP P62558

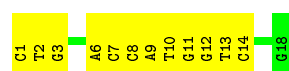
- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



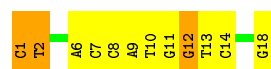
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total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



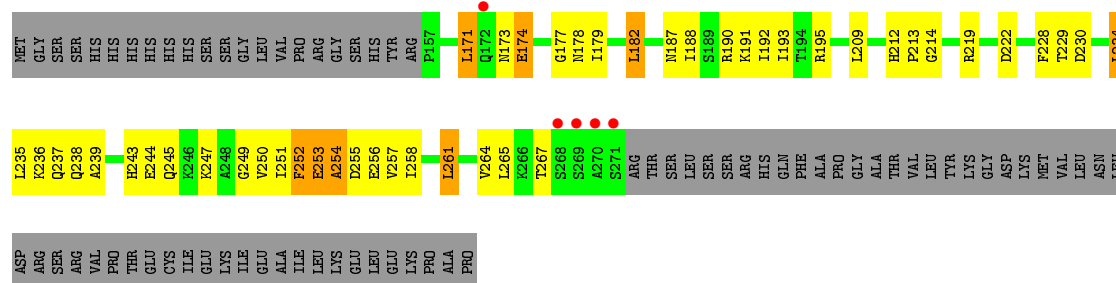
- Molecule 1: DNA (5'-D(\*CP\*TP\*GP\*GP\*GP\*AP\*CP\*CP\*AP\*TP\*GP\*GP\*TP\*CP\*CP\*CP\*AP\*G)-3')



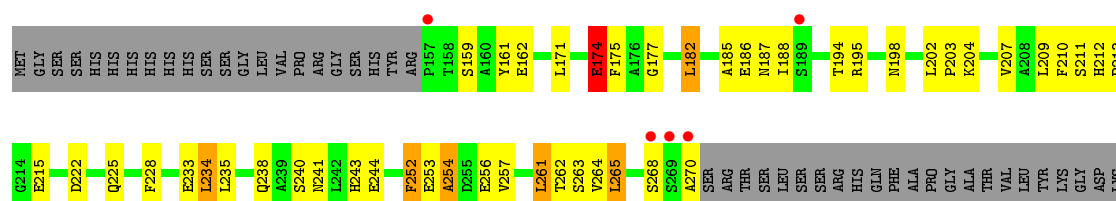
- Molecule 1: DNA (5'-D(\*CP\*TP\*GP\*GP\*GP\*AP\*CP\*CP\*AP\*TP\*GP\*GP\*TP\*CP\*CP\*CP\*AP\*G)-3')



- Molecule 2: Protein sopB



- Molecule 2: Protein sopB



MET
VAL
LEU
ASN
LEU
ASP
ARG
SER
ARG
VAL
PRO
THR
GLU
CYS
ILE
GLU
LYS
ILE
ILE
GLU
ALA
ILE
LEU
LYS
GLU
LEU
GLU
LYS
PRO
ALA
PRO



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	200.78Å 200.78Å 200.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	63.49 – 2.86 63.49 – 2.86	Depositor EDS
% Data completeness (in resolution range)	98.0 (63.49-2.86) 98.1 (63.49-2.86)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.86 (at 2.86Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.242 , 0.266 0.242 , 0.266	Depositor DCC
$R_{free}$ test set	3067 reflections (10.03%)	DCC
Wilson B-factor (Å <sup>2</sup> )	72.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 81.7	EDS
Estimated twinning fraction	0.030 for -l,-k,-h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 30569 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	2531	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.37% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 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

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	T	0.55	0/410	0.81	0/631
1	U	0.51	0/410	0.80	0/631
2	B	0.34	0/887	0.58	0/1194
2	P	0.34	0/882	0.62	0/1187
All	All	0.41	0/2589	0.68	0/3643

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	T	0	4
1	U	0	1
All	All	0	5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	T	1	DC	Sidechain
1	T	12	DG	Sidechain
1	T	18	DG	Sidechain
1	T	2	DT	Sidechain
1	U	12	DG	Sidechain

## 5.2 Too-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 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	T	366	0	203	27	0
1	U	366	0	203	17	0
2	B	877	0	892	40	0
2	P	872	0	890	38	0
3	B	20	0	0	0	0
3	P	30	0	0	2	0
All	All	2531	0	2188	110	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 24.

The worst 5 of 110 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:T:6:DA:H2''	1:T:7:DC:H5''	1.41	0.98
1:T:11:DG:H2''	1:T:12:DG:H5'	1.51	0.91
1:T:11:DG:H2''	1:T:12:DG:C5'	2.01	0.90
1:T:6:DA:C2'	1:T:7:DC:H5''	2.05	0.85
1:T:6:DA:H2''	1:T:7:DC:C5'	2.11	0.80

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
2	B	113/189 (60%)	98 (87%)	12 (11%)	3 (3%)	6 22

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	P	112/189 (59%)	97 (87%)	12 (11%)	3 (3%)	6	22
All	All	225/378 (60%)	195 (87%)	24 (11%)	6 (3%)	6	22

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	254	ALA
2	P	254	ALA
2	P	268	SER
2	B	174	GLU
2	P	174	GLU

### 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	
2	B	94/160 (59%)	86 (92%)	8 (8%)	13	34
2	P	94/160 (59%)	85 (90%)	9 (10%)	10	28
All	All	188/320 (59%)	171 (91%)	17 (9%)	12	31

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	261	LEU
2	P	174	GLU
2	P	235	LEU
2	B	253	GLU
2	P	252	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	225	GLN
2	P	225	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
2	P	187	ASN
2	B	187	ASN
2	B	238	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](#)

10 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	SO4	B	324	-	4,4,4	0.32	0	6,6,6	0.10	0
3	SO4	B	835	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	B	836	-	4,4,4	0.21	0	6,6,6	0.14	0
3	SO4	B	936	-	4,4,4	0.28	0	6,6,6	0.11	0
3	SO4	P	344	-	4,4,4	0.23	0	6,6,6	0.10	0
3	SO4	P	844	-	4,4,4	0.30	0	6,6,6	0.07	0
3	SO4	P	845	-	4,4,4	0.23	0	6,6,6	0.17	0
3	SO4	P	846	-	4,4,4	0.20	0	6,6,6	0.24	0
3	SO4	P	849	-	4,4,4	0.29	0	6,6,6	0.11	0
3	SO4	P	945	-	4,4,4	0.27	0	6,6,6	0.11	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
3	SO4	B	324	-	-	0/0/0/0	0/0/0/0
3	SO4	B	835	-	-	0/0/0/0	0/0/0/0
3	SO4	B	836	-	-	0/0/0/0	0/0/0/0
3	SO4	B	936	-	-	0/0/0/0	0/0/0/0
3	SO4	P	344	-	-	0/0/0/0	0/0/0/0
3	SO4	P	844	-	-	0/0/0/0	0/0/0/0
3	SO4	P	845	-	-	0/0/0/0	0/0/0/0
3	SO4	P	846	-	-	0/0/0/0	0/0/0/0
3	SO4	P	849	-	-	0/0/0/0	0/0/0/0
3	SO4	P	945	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	P	344	SO4	1	0
3	P	844	SO4	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<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	T	18/18 (100%)	0.43	0 100 100	38, 49, 57, 59	0
1	U	18/18 (100%)	0.47	0 100 100	41, 53, 58, 58	0
2	B	115/189 (60%)	0.51	5 (4%) 39 32	45, 72, 99, 126	0
2	P	114/189 (60%)	0.41	5 (4%) 38 31	47, 71, 93, 112	0
All	All	265/414 (64%)	0.46	10 (3%) 44 37	38, 69, 96, 126	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	270	ALA	7.6
2	P	270	ALA	5.5
2	B	268	SER	4.7
2	P	269	SER	4.6
2	B	269	SER	4.4

### 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, 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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SO4	B	835	5/5	0.96	0.39	6.35	98,100,101,101	0
3	SO4	P	344	5/5	0.83	0.44	4.70	131,131,132,133	0
3	SO4	P	845	5/5	0.96	0.39	3.70	90,91,93,96	0
3	SO4	B	324	5/5	0.92	0.24	0.22	112,112,114,117	0
3	SO4	P	844	5/5	0.86	0.24	-0.12	121,121,122,123	0
3	SO4	B	936	5/5	0.96	0.17	-1.41	75,78,79,80	0
3	SO4	B	836	5/5	0.98	0.17	-1.66	71,72,73,74	0
3	SO4	P	846	5/5	0.96	0.16	-2.65	73,73,74,76	0
3	SO4	P	849	5/5	0.89	0.11	-	129,130,130,131	0
3	SO4	P	945	5/5	0.96	0.16	-	83,85,87,88	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.