

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

#### Nov 20, 2023 – 03:41 PM JST

:	7CU8
:	Crystal structure of the soluble domain of TiME protein from Mycobacterium
	tuberculosis
:	Gong, W.; Cai, X.; Liu, L.; Wen, C.
:	2020-08-21
:	3.30 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:

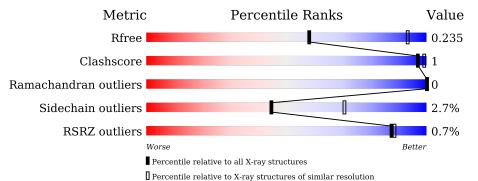
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 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 3.30 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 chain	
1	А	202	% 90%	•• 7%
1	В	202	89%	•• 7%
1	С	202	90%	•• 7%
1	D	202	% <b>9</b> 0%	•• 5%
1	Е	202	91%	• 6%
1	F	202	89%	• 7%



Mol	Chain	Length	Quality of chain		
1	G	202	% 90%	• 7%	

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
2	SO4	D	301	-	-	-	Х



# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 9902 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	А	188	Total	С	Ν	Ο	S	0	0	0	
1	Л	100	1403	873	249	275	6	0	0	0	
1	В	188	Total	С	Ν	Ο	$\mathbf{S}$	0	0	0	
	D	100	1403	873	249	275	6	0	0	0	
1	С	188	Total	С	Ν	Ο	$\mathbf{S}$	0	0	0	
1	U	100	1403	873	249	275	6	0	0	0	
1	D	191	Total	С	Ν	Ο	$\mathbf{S}$	0	0	0	
1	D	191	1420	884	252	278	6	0	0	0	
1	Е	190	Total	С	Ν	Ο	$\mathbf{S}$	0	0	0	
	Ľ	190	1412	878	251	277	6	0	0	0	
1	F	188	Total	С	Ν	Ο	S	0	0	0	
	I.	100	1403	873	249	275	6	0	0	U	
1	G	188	Total	С	Ν	Ο	S	0	0	0	
	G	100	1403	873	249	275	6	0	0	U	

• Molecule 1 is a protein called Tube-forming protein in Mycobacterial Envelope (TiME).

There are 91 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference			
А	215	LYS	-	expression tag	UNP I6XI06			
А	216	LEU	-	expression tag	UNP I6XI06			
А	217	ALA	-	expression tag	UNP I6XI06			
А	218	ALA	-	expression tag	UNP I6XI06			
А	219	ALA	-	expression tag	UNP I6XI06			
А	220	LEU	-	expression tag	UNP I6XI06			
А	221	GLU	-	expression tag	UNP I6XI06			
А	222	HIS	-	expression tag	UNP I6XI06			
А	223	HIS	-	expression tag	UNP I6XI06			
А	224	HIS	-	expression tag	UNP I6XI06			
А	225	HIS	-	expression tag	UNP I6XI06			
А	226	HIS	-	expression tag	UNP I6XI06			
А	227	HIS	-	expression tag	UNP I6XI06			
В	215	LYS	-	expression tag	UNP I6XI06			
В	216	LEU	-	expression tag	UNP I6XI06			
				Continued a	on next page			

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D219ALA-expression tagUNP I6XD220LEU-expression tagUNP I6XD221GLU-expression tagUNP I6XD222HIS-expression tagUNP I6XD223HIS-expression tagUNP I6XD224HIS-expression tagUNP I6XD225HIS-expression tagUNP I6X	I06			
D220LEU-expression tagUNP I6XD221GLU-expression tagUNP I6XD222HIS-expression tagUNP I6XD223HIS-expression tagUNP I6XD224HIS-expression tagUNP I6XD225HIS-expression tagUNP I6X	I06			
D221GLU-expression tagUNP I6XD222HIS-expression tagUNP I6XD223HIS-expression tagUNP I6XD224HIS-expression tagUNP I6XD225HIS-expression tagUNP I6X	I06			
D222HIS-expression tagUNP I6XD223HIS-expression tagUNP I6XD224HIS-expression tagUNP I6XD225HIS-expression tagUNP I6X	I06			
D223HIS-expression tagUNP I6XD224HIS-expression tagUNP I6XD225HIS-expression tagUNP I6X	I06			
D224HIS-expression tagUNP I6XD225HIS-expression tagUNP I6X	I06			
D 225 HIS - expression tag UNP I6X	I06			
1 0	I06			
	I06			
D 226 HIS - expression tag UNP I6X	I06			
D 227 HIS - expression tag UNP I6X	I06			
E 215 LYS - expression tag UNP I6X	I06			
E 216 LEU - expression tag UNP I6X	I06			
E 217 ALA - expression tag UNP I6X	I06			
E 218 ALA - expression tag UNP I6X	I06			
E 219 ALA - expression tag UNP I6X	I06			

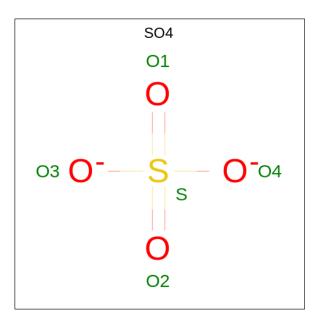


Continued from previous page         Chain       Residue       Modelled       Actual       Comment       Refer												
			Actual		Reference							
E	220	LEU	-	expression tag	UNP I6XI06							
E	221	GLU	-	expression tag	UNP I6XI06							
E	222	HIS	-	expression tag	UNP I6XI06							
E	223	HIS	_	expression tag	UNP I6XI06							
E	224	HIS	-	expression tag	UNP I6XI06							
E	225	HIS	-	expression tag	UNP I6XI06							
E	226	HIS	-	expression tag	UNP I6XI06							
E	227	HIS	-	expression tag	UNP I6XI06							
F	215	LYS	-	expression tag	UNP I6XI06							
F	216	LEU	-	expression tag	UNP I6XI06							
F	217	ALA	-	expression tag	UNP I6XI06							
F	218	ALA	-	expression tag	UNP I6XI06							
F	219	ALA	-	expression tag	UNP I6XI06							
F	220	LEU	-	expression tag	UNP I6XI06							
F	221	GLU	-	expression tag	UNP I6XI06							
F	222	HIS	-	expression tag	UNP I6XI06							
F	223	HIS	-	expression tag	UNP I6XI06							
F	224	HIS	-	expression tag	UNP I6XI06							
F	225	HIS	-	expression tag	UNP I6XI06							
F	226	HIS	-	expression tag	UNP I6XI06							
F	227	HIS	_	expression tag	UNP I6XI06							
G	215	LYS	-	expression tag	UNP I6XI06							
G	216	LEU	_	expression tag	UNP I6XI06							
G	217	ALA	_	expression tag	UNP I6XI06							
G	218	ALA	_	expression tag	UNP I6XI06							
G	219	ALA	-	expression tag	UNP I6XI06							
G	220	LEU	-	expression tag	UNP I6XI06							
G	221	GLU	-	expression tag	UNP I6XI06							
G	222	HIS	-	expression tag	UNP I6XI06							
G	223	HIS	-	expression tag	UNP I6XI06							
G	224	HIS	-	expression tag	UNP I6XI06							
G	225	HIS	-	expression tag	UNP I6XI06							
G	226	HIS	-	expression tag	UNP I6XI06							
G	227	HIS	-	expression tag	UNP I6XI06							

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• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).





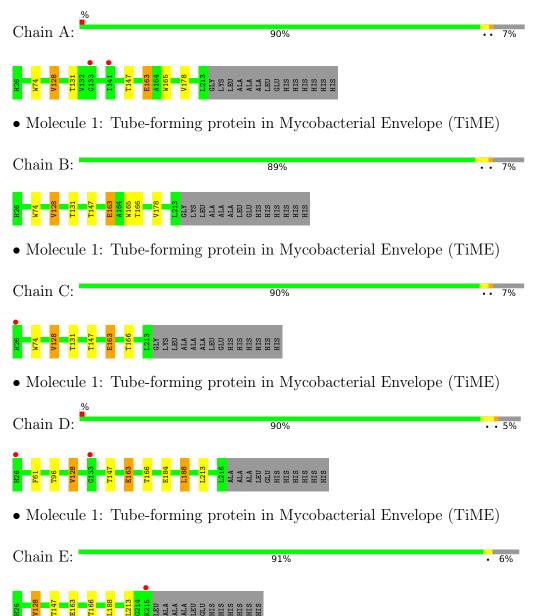
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$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



# 3 Residue-property plots (i)

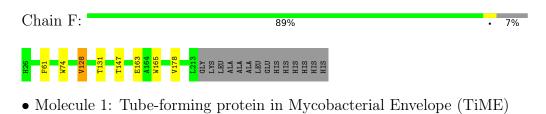
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Tube-forming protein in Mycobacterial Envelope (TiME)



• Molecule 1: Tube-forming protein in Mycobacterial Envelope (TiME)





C	hai	in (	G:	.%	, D		 		 									9	0%	6				·	7%
H26	T98	V128	T139	A140	41	T147	F153	G156	E163 A164	 L213	GLY	LYS	LEU	ALA	ALA	ALA	LEU	GLU	STH	STH	STH	SIH			



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants	198.00Å 198.00Å 364.11Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	49.78 - 3.30	Depositor
Resolution (A)	49.78 - 3.30	EDS
% Data completeness	99.8 (49.78-3.30)	Depositor
(in resolution range)	99.8 (49.78-3.30)	EDS
R <sub>merge</sub>	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$6.73 (at 3.33 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0266	Depositor
D D.	0.223 , $0.235$	Depositor
$R, R_{free}$	0.222 , $0.235$	DCC
$R_{free}$ test set	3242 reflections $(5.07%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	55.7	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.30 , 3.9	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	9902	wwPDB-VP
Average B, all atoms $(Å^2)$	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.06% of the height of the origin peak. No significant pseudotranslation is detected.

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



<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: 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		
WIOI	Ullalli	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.66	0/1435	0.72	0/1962	
1	В	0.66	0/1435	0.72	0/1962	
1	С	0.65	0/1435	0.72	0/1962	
1	D	0.66	0/1452	0.72	0/1985	
1	Ε	0.66	0/1444	0.72	0/1974	
1	F	0.65	0/1435	0.72	0/1962	
1	G	0.66	0/1435	0.72	0/1962	
All	All	0.66	0/10071	0.72	0/13769	

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	А	1403	0	1331	3	0
1	В	1403	0	1331	3	0
1	С	1403	0	1331	2	0
1	D	1420	0	1347	2	0
1	Е	1412	0	1336	2	0
1	F	1403	0	1331	3	0



Mol	Chain	-	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1403	0	1331	2	0
2	А	10	0	0	0	0
2	В	5	0	0	0	0
2	С	10	0	0	0	0
2	D	5	0	0	0	0
2	Е	10	0	0	0	0
2	F	5	0	0	0	0
2	G	10	0	0	0	0
All	All	9902	0	9338	17	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 1.

The worst 5 of 17 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:F:128:VAL:HG12	1:F:163:GLU:HG3	1.84	0.60
1:E:128:VAL:HG12	1:E:163:GLU:HG3	1.84	0.58
1:D:128:VAL:HG12	1:D:163:GLU:HG3	1.85	0.57
1:A:128:VAL:HG12	1:A:163:GLU:HG3	1.89	0.55
1:C:128:VAL:HG12	1:C:163:GLU:HG3	1.90	0.54

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	Favoured Allowed		Percentiles		
1	А	186/202~(92%)	180 (97%)	6 (3%)	0	100 100		
1	В	186/202~(92%)	178 (96%)	8 (4%)	0	100 100		
1	С	186/202~(92%)	178 (96%)	8 (4%)	0	100 100		



Mol	Chain	Analysed	Favoured Allowed		Outliers	Percentiles		
1	D	189/202~(94%)	183~(97%)	6 (3%)	0	100	100	
1	Ε	188/202~(93%)	182 (97%)	6 (3%)	0	100	100	
1	F	186/202~(92%)	180 (97%)	6 (3%)	0	100	100	
1	G	186/202~(92%)	178~(96%)	8 (4%)	0	100	100	
All	All	1307/1414~(92%)	1259 (96%)	48 (4%)	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	Perce	ntiles
1	А	147/157~(94%)	144~(98%)	3~(2%)	55	76
1	В	147/157~(94%)	143~(97%)	4 (3%)	44	71
1	С	147/157~(94%)	143~(97%)	4 (3%)	44	71
1	D	148/157~(94%)	140~(95%)	8 (5%)	22	53
1	Ε	147/157~(94%)	144 (98%)	3(2%)	55	76
1	F	147/157~(94%)	144 (98%)	3(2%)	55	76
1	G	147/157~(94%)	144 (98%)	3 (2%)	55	76
All	All	1030/1099~(94%)	1002~(97%)	28 (3%)	44	71

5 of 28 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	D	147	THR
1	G	147	THR
1	D	184	GLU
1	F	147	THR
1	D	166	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:



Mol	Chain	Res	Type
1	В	97	GLN
1	D	97	GLN
1	Е	97	GLN
1	Е	137	GLN
1	F	97	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 monosaccharides in this entry.

#### 5.6 Ligand geometry (i)

11 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	Turne	Chain	Res	Link	B	ond leng	$\operatorname{gths}$	В	ond ang	gles
10101	Type	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
2	SO4	В	301	-	4,4,4	0.38	0	$6,\!6,\!6$	0.04	0
2	SO4	С	301	-	4,4,4	0.39	0	$6,\!6,\!6$	0.05	0
2	SO4	G	301	-	4,4,4	0.38	0	$6,\!6,\!6$	0.04	0
2	SO4	D	301	-	4,4,4	0.38	0	$6,\!6,\!6$	0.05	0
2	SO4	Е	302	-	4,4,4	0.39	0	$6,\!6,\!6$	0.05	0
2	SO4	А	302	-	4,4,4	0.39	0	$6,\!6,\!6$	0.05	0
2	SO4	Е	301	-	4,4,4	0.38	0	$6,\!6,\!6$	0.05	0
2	SO4	А	301	-	4,4,4	0.39	0	$6,\!6,\!6$	0.05	0
2	SO4	F	301	-	4,4,4	0.38	0	$6,\!6,\!6$	0.05	0
2	SO4	С	302	-	4,4,4	0.40	0	$6,\!6,\!6$	0.05	0



Mol	Type	Chain	Dec	Link	B	ond leng	$\operatorname{gths}$	В	ond ang	gles
IVIOI	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	SO4	G	302	-	4,4,4	0.39	0	$6,\!6,\!6$	0.06	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.

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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q < 0.9
1	А	188/202~(93%)	0.12	2 (1%) 80 81	42, 55, 82, 93	0
1	В	188/202~(93%)	-0.06	0 100 100	39, 55, 69, 96	0
1	С	188/202~(93%)	-0.04	1 (0%) 91 91	44, 54, 67, 101	0
1	D	191/202 (94%)	0.12	2 (1%) 82 82	46, 58, 74, 105	0
1	Е	190/202~(94%)	0.08	1 (0%) 91 91	44, 56, 75, 92	0
1	F	188/202~(93%)	0.05	0 100 100	42, 57, 74, 84	0
1	G	188/202~(93%)	0.15	3 (1%) 72 70	49, 68, 95, 102	0
All	All	1321/1414 (93%)	0.06	9 (0%) 87 88	39, 57, 80, 105	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	133	GLY	3.1
1	С	26	HIS	3.0
1	G	139	THR	3.0
1	Е	215	LYS	2.9
1	G	141	ILE	2.6

## 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	$\mathbf{RSR}$	B-factors(Å <sup>2</sup> )	$Q{<}0.9$
2	SO4	D	301	5/5	0.70	0.46	$124,\!124,\!125,\!126$	0
2	SO4	С	301	5/5	0.77	0.32	109,109,109,110	0
2	SO4	F	301	5/5	0.77	0.32	116,117,118,118	0
2	SO4	В	301	5/5	0.84	0.33	113,113,114,114	0
2	SO4	G	301	5/5	0.84	0.26	$116,\!117,\!117,\!117$	0
2	SO4	Е	301	5/5	0.89	0.38	111,112,112,113	0
2	SO4	G	302	5/5	0.89	0.42	114,115,115,116	0
2	SO4	А	301	5/5	0.90	0.24	109,110,110,110	0
2	SO4	Е	302	5/5	0.92	0.42	112,113,113,116	0
2	SO4	А	302	5/5	0.93	0.29	$105,\!105,\!106,\!108$	0
2	SO4	С	302	5/5	0.94	0.42	$105,\!105,\!106,\!108$	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

