

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

#### Sep 19, 2023 – 04:50 AM EDT

PDB ID : 5CTU

> Title Crystal structure of the ATP binding domain of S. aureus GyrB complexed

> > with a fragment

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Deposited on 2015-07-24

Resolution 1.45 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

> 1.8.5 (274361), CSD as 541 be (2020)Mogul

Xtriage (Phenix) 1.13

EDS 2.35.1

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)

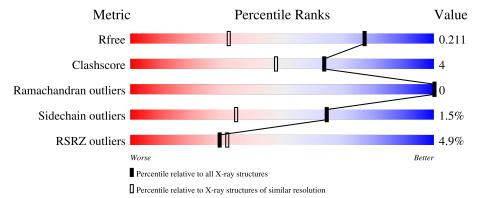
Validation Pipeline (wwPDB-VP) 2.35.1

### 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 1.45 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{\rm A})}) \end{array}$
$R_{free}$	130704	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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	A	212	81%	8%	•	9%		
1	В	212	83%	6%		9%		



## 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3678 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 DNA gyrase subunit B.

$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	192	Total 1572	C 989	N 272	O 309	S 2	0	5	0
1	R	192	Total			O	S	0	5	0
1	Ъ	132	1571	986	277	307	1			U

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P0A0K8
A	1	SER	-	expression tag	UNP P0A0K8
A	?	-	VAL	deletion	UNP P0A0K8
A	?	-	LEU	deletion	UNP P0A0K8
A	?	-	HIS	deletion	UNP P0A0K8
A	?	-	ALA	deletion	UNP P0A0K8
A	?	-	GLY	deletion	UNP P0A0K8
A	?	-	GLY	deletion	UNP P0A0K8
A	?	-	LYS	deletion	UNP P0A0K8
A	?	-	PHE	deletion	UNP P0A0K8
A	?	-	GLY	deletion	UNP P0A0K8
A	?	-	GLY	deletion	UNP P0A0K8
A	?	-	GLY	deletion	UNP P0A0K8
A	?	-	GLY	deletion	UNP P0A0K8
A	?	-	TYR	deletion	UNP P0A0K8
A	?	-	LYS	deletion	UNP P0A0K8
A	?	-	VAL	deletion	UNP P0A0K8
A	?	-	SER	deletion	UNP P0A0K8
A	?	-	GLY	deletion	UNP P0A0K8
A	?	-	GLY	deletion	UNP P0A0K8
A	?	-	LEU	deletion	UNP P0A0K8
A	?	-	HIS	deletion	UNP P0A0K8
A	?	-	GLY	deletion	UNP P0A0K8
A	?	-	VAL	deletion	UNP P0A0K8
A	?	-	GLY	deletion	UNP P0A0K8

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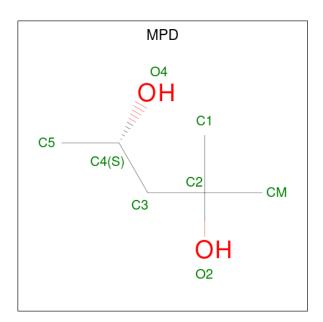


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Chain	Residue	Modelled	Actual	Comment	Reference
В	0	GLY	-	expression tag	UNP P0A0K8
В	1	SER	-	expression tag	UNP P0A0K8
В	?	-	VAL	deletion	UNP P0A0K8
В	?	-	LEU	deletion	UNP P0A0K8
В	?	-	HIS	deletion	UNP P0A0K8
В	?	-	ALA	deletion	UNP P0A0K8
В	?	-	GLY	deletion	UNP P0A0K8
В	?	-	GLY	deletion	UNP P0A0K8
В	?	-	LYS	deletion	UNP P0A0K8
В	?	-	PHE	deletion	UNP P0A0K8
В	?	-	GLY	deletion	UNP P0A0K8
В	?	-	GLY	deletion	UNP P0A0K8
В	?	-	GLY	deletion	UNP P0A0K8
В	?	-	GLY	deletion	UNP P0A0K8
В	?	-	TYR	deletion	UNP P0A0K8
В	?	-	LYS	deletion	UNP P0A0K8
В	?	-	VAL	deletion	UNP P0A0K8
В	?	-	SER	deletion	UNP P0A0K8
В	?	-	GLY	deletion	UNP P0A0K8
В	?	-	GLY	deletion	UNP P0A0K8
В	?	-	LEU	deletion	UNP P0A0K8
В	?	-	HIS	deletion	UNP P0A0K8
В	?	-	GLY	deletion	UNP P0A0K8
В	?	-	VAL	deletion	UNP P0A0K8
В	?	-	GLY	deletion	UNP P0A0K8

• Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula:  $C_6H_{14}O_2$ ).





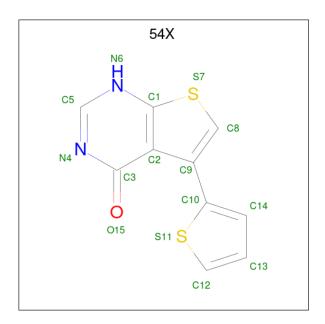
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 8 6 2	0	0
2	В	1	Total C O 8 6 2	0	0
2	В	1	Total C O 8 6 2	0	0

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

• Molecule 4 is 5-(thiophen-2-yl)thieno[2,3-d]pyrimidin-4(1H)-one (three-letter code: 54X) (formula:  $C_{10}H_6N_2OS_2$ ).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
1	Λ	1	Total	С	N	О	S	0	0	
4	A	1	15	10	2	1	2	U	U	
1	D	1	Total	С	N	О	S	0	0	
4	D	1	15	10	2	1	2	U	0	

• Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	1	Total M 1 1	g 0	0

• Molecule 6 is water.

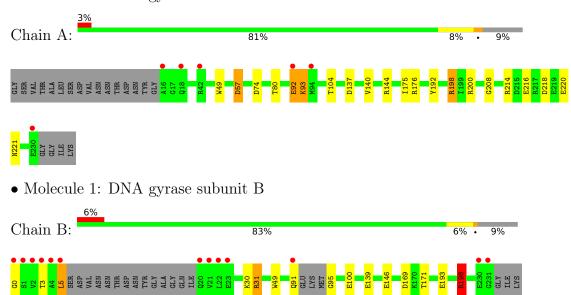
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	235	Total O 235 235	0	0
6	В	244	Total O 244 244	0	0



# 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: DNA gyrase subunit B





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	142.66Å 55.65Å 51.14Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 101.01° 90.00°	Depositor
Resolution (Å)	25.86 - 1.45	Depositor
Resolution (A)	25.10 - 1.45	EDS
% Data completeness	99.3 (25.86-1.45)	Depositor
(in resolution range)	99.3 (25.10-1.45)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.14	Depositor
$< I/\sigma(I) > 1$	1.98 (at 1.45Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
D D	0.176 , 0.204	Depositor
$R, R_{free}$	0.182 , 0.211	DCC
$R_{free}$ test set	3472 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	8.2	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.42, 52.3	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3678	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.50% 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: 54X, MPD, MG, CL

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		nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	1.13	$2/1612 \ (0.1\%)$	1.16	$10/2182 \ (0.5\%)$	
1	В	1.08	2/1609 (0.1%)	1.27	9/2175 (0.4%)	
All	All	1.11	4/3221 (0.1%)	1.21	19/4357 (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	A	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
1	В	100	GLU	CD-OE2	-5.43	1.19	1.25
1	В	139	GLU	CD-OE2	5.26	1.31	1.25
1	A	192	TYR	CG-CD2	-5.16	1.32	1.39
1	A	216	GLU	CD-OE2	-5.02	1.20	1.25

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	${f Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	В	198[A]	ARG	NE-CZ-NH2	15.73	128.17	120.30
1	В	198[B]	ARG	NE-CZ-NH2	15.73	128.17	120.30
1	В	198[A]	ARG	NE-CZ-NH1	-15.43	112.58	120.30
1	В	198[B]	ARG	NE-CZ-NH1	-15.43	112.58	120.30
1	A	144	ARG	NE-CZ-NH1	7.72	124.16	120.30

There are no chirality outliers.



All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	104	THR	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	A	1572	0	1561	11	1
1	В	1571	0	1564	16	1
2	A	8	0	14	2	0
2	В	16	0	28	0	0
3	A	1	0	0	0	0
4	A	15	0	6	1	0
4	В	15	0	5	4	0
5	В	1	0	0	0	0
6	A	235	0	0	6	0
6	В	244	0	0	8	0
All	All	3678	0	3178	27	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 4.

The worst 5 of 27 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} &  ext{Interatomic} \ &  ext{distance} \ &  ext{(Å)} \end{aligned}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:B:0:GLY:N	6:B:403:HOH:O	1.98	0.95
1:B:0:GLY:O	6:B:406:HOH:O	1.88	0.91
1:B:95:GLY:N	6:B:410:HOH:O	2.18	0.75
1:A:93:LYS:HE2	1:B:31[A]:ARG:HE	1.52	0.74
1:B:193:GLU:OE1	6:B:409:HOH:O	2.09	0.71

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-1 Atom-2		Clash overlap (Å)
1:A:74[B]:ASP:OD1	1:B:146:GLU:OE2[2_566]	2.11	0.09

#### 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	Chain Analysed Favoured Allowed		Outliers	Perce	ntiles	
1	A	$195/212 \ (92\%)$	189 (97%)	6 (3%)	0	100	100
1	В	191/212 (90%)	188 (98%)	3 (2%)	0	100	100
All	All	386/424 (91%)	377 (98%)	9 (2%)	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	Analysed Rotameric Outliers		Percentiles		
1	A	173/183 (94%)	171 (99%)	2 (1%)	71 43		
1	В	172/183 (94%)	167 (97%)	5 (3%)	42 10		
All	All	345/366~(94%)	338 (98%)	7 (2%)	65 22		

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	31[A]	ARG
1	В	31[B]	ARG
1	В	198[B]	ARG

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Mol	Chain	Res	Type
1	В	198[A]	ARG
1	В	5	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 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)

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).

Mol Type C		Chain	Clasia Dan	Dag	Dog	Res	Link	B	ond leng	$\operatorname{gths}$	В	ond ang	les
MIOI	$\operatorname{Mol} \mid \operatorname{Type} \mid \operatorname{Chain} \mid \operatorname{Res}$	nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2				
2	MPD	A	301	-	7,7,7	0.83	0	9,10,10	0.57	0			
4	54X	В	303	1	17,17,17	2.69	10 (58%)	11,24,24	3.85	6 (54%)			
2	MPD	В	302	-	7,7,7	0.78	0	9,10,10	1.79	2 (22%)			
4	54X	A	303	-	17,17,17	2.79	5 (29%)	11,24,24	5.46	4 (36%)			
2	MPD	В	301	-	7,7,7	0.64	0	9,10,10	1.51	1 (11%)			

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.

I	Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
	2	MPD	A	301	-	-	2/5/5/5	-
	4	54X	В	303	1	-	0/0/4/4	0/3/3/3
	2	MPD	В	302	-	-	0/5/5/5	-
	4	54X	A	303	_	-	0/0/4/4	0/3/3/3
	2	MPD	В	301	-	-	5/5/5/5	-

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
4	A	303	54X	C9-C2	8.55	1.51	1.41
4	A	303	54X	C8-C9	5.59	1.40	1.37
4	В	303	54X	C9-C2	5.36	1.47	1.41
4	В	303	54X	C8-C9	4.91	1.40	1.37
4	В	303	54X	C2-C3	-3.59	1.42	1.47

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
4	A	303	54X	C8-C9-C2	14.89	115.79	111.69
4	В	303	54X	O15-C3-N4	7.91	130.70	120.52
4	A	303	54X	C9-C8-S7	-7.50	110.43	112.53
4	В	303	54X	C9-C8-S7	-6.78	110.64	112.53
4	A	303	54X	C13-C12-S11	-5.72	108.34	112.98

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	301	MPD	C1-C2-C3-C4
2	В	301	MPD	O2-C2-C3-C4
2	В	301	MPD	C2-C3-C4-C5
2	A	301	MPD	C1-C2-C3-C4
2	В	301	MPD	CM-C2-C3-C4

There are no ring outliers.

3 monomers are involved in 7 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	MPD	2	0
4	В	303	54X	4	0
4	A	303	54X	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	<rsrz></rsrz>	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	$192/212 \ (90\%)$	0.11	6 (3%) 49 52	3, 8, 22, 51	0
1	В	192/212 (90%)	0.45	13 (6%) 17 19	3, 8, 25, 48	6 (3%)
All	All	384/424 (90%)	0.28	19 (4%) 29 32	3, 8, 25, 51	6 (1%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	5	LEU	9.4
1	В	21	VAL	6.8
1	В	1	SER	5.6
1	В	4	ALA	4.9
1	В	2	VAL	4.8

### 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	MPD	A	301	8/8	0.58	0.19	27,32,37,39	0
2	MPD	В	301	8/8	0.71	0.18	24,28,30,31	0
2	MPD	В	302	8/8	0.74	0.17	16,21,23,27	0
4	54X	В	303	15/15	0.79	0.21	12,15,18,20	15
4	54X	A	303	15/15	0.83	0.17	15,18,23,27	15
5	MG	В	304	1/1	0.97	0.18	26,26,26,26	0
3	CL	A	302	1/1	0.99	0.05	19,19,19,19	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

