



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 9I1Y / pdb\_00009i1y  
Title : WxLIP from Enterococcus faecium  
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Deposited on : 2025-01-17  
Resolution : 1.95 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

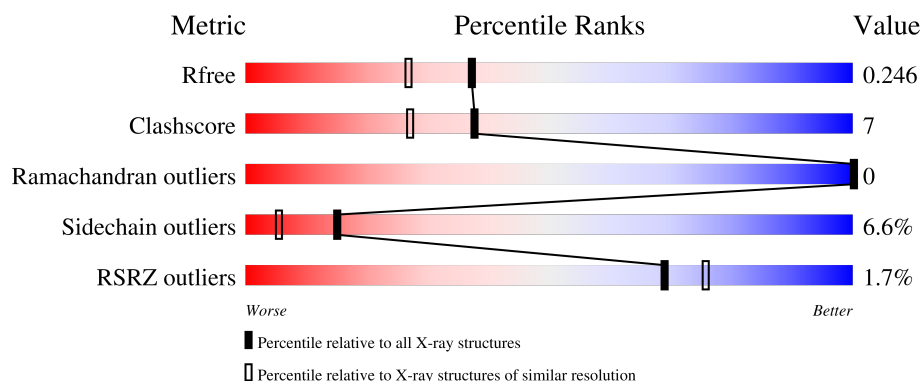
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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))
$R_{free}$	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	A	290	
1	B	290	

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	EDO	A	305	-	-	X	-
2	EDO	B	303	-	X	-	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8614 atoms, of which 4215 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 EfmWxLIP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	H	N	O	44	0	0
			4192	1331	2094	352	415			
1	B	263	Total	C	H	N	O	44	0	0
			4150	1318	2073	348	411			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	135	LYS	THR	conflict	UNP A0A6N3AEW7
A	278	LYS	-	expression tag	UNP A0A6N3AEW7
A	279	LEU	-	expression tag	UNP A0A6N3AEW7
A	280	ALA	-	expression tag	UNP A0A6N3AEW7
A	281	ALA	-	expression tag	UNP A0A6N3AEW7
A	282	ALA	-	expression tag	UNP A0A6N3AEW7
A	283	LEU	-	expression tag	UNP A0A6N3AEW7
A	284	GLU	-	expression tag	UNP A0A6N3AEW7
A	285	HIS	-	expression tag	UNP A0A6N3AEW7
A	286	HIS	-	expression tag	UNP A0A6N3AEW7
A	287	HIS	-	expression tag	UNP A0A6N3AEW7
A	288	HIS	-	expression tag	UNP A0A6N3AEW7
A	289	HIS	-	expression tag	UNP A0A6N3AEW7
A	290	HIS	-	expression tag	UNP A0A6N3AEW7
B	135	LYS	THR	conflict	UNP A0A6N3AEW7
B	278	LYS	-	expression tag	UNP A0A6N3AEW7
B	279	LEU	-	expression tag	UNP A0A6N3AEW7
B	280	ALA	-	expression tag	UNP A0A6N3AEW7
B	281	ALA	-	expression tag	UNP A0A6N3AEW7
B	282	ALA	-	expression tag	UNP A0A6N3AEW7
B	283	LEU	-	expression tag	UNP A0A6N3AEW7
B	284	GLU	-	expression tag	UNP A0A6N3AEW7
B	285	HIS	-	expression tag	UNP A0A6N3AEW7
B	286	HIS	-	expression tag	UNP A0A6N3AEW7
B	287	HIS	-	expression tag	UNP A0A6N3AEW7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	288	HIS	-	expression tag	UNP A0A6N3AEW7
B	289	HIS	-	expression tag	UNP A0A6N3AEW7
B	290	HIS	-	expression tag	UNP A0A6N3AEW7

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	1	0
			10	2	6	2		
2	A	1	Total	C	H	O	1	0
			10	2	6	2		
2	A	1	Total	C	H	O	1	0
			10	2	6	2		
2	A	1	Total	C	H	O	1	0
			10	2	6	2		
2	B	1	Total	C	H	O	1	0
			10	2	6	2		
2	B	1	Total	C	H	O	1	0
			10	2	6	2		
2	B	1	Total	C	H	O	1	0
			10	2	6	2		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



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

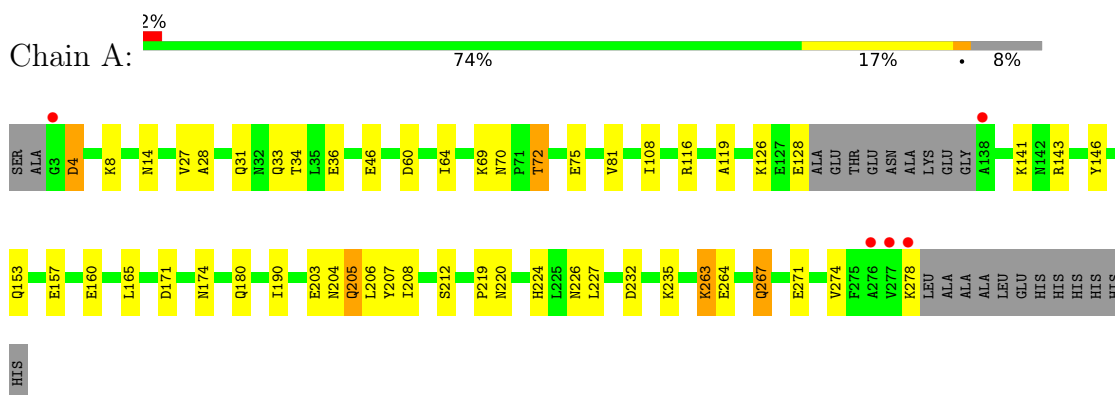
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	106	Total	O	0	0
			106	106		
4	B	81	Total	O	0	0
			81	81		

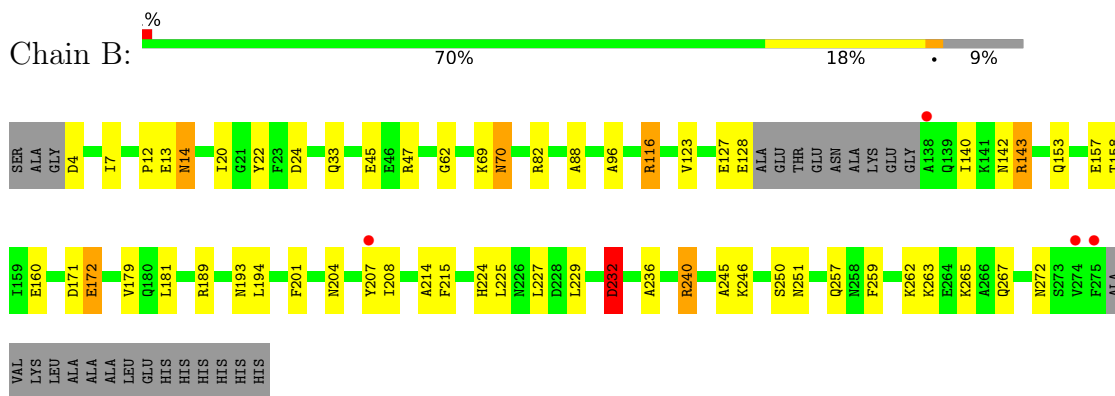
### 3 Residue-property plots [i](#)

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: EfmWxLIP1



#### • Molecule 1: EfmWxLIP1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.54Å 102.72Å 118.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.40 – 1.95 51.40 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.8 (51.40-1.95) 99.8 (51.40-1.95)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.99 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0405	Depositor
R, $R_{free}$	0.192 , 0.247 0.189 , 0.246	Depositor DCC
$R_{free}$ test set	2052 reflections (4.46%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.9	Xtriage
Anisotropy	0.175	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.42 , 39.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.021 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8614	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, 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	A	0.97	1/2135 (0.0%)	1.43	8/2897 (0.3%)
1	B	0.91	1/2114 (0.0%)	1.42	14/2868 (0.5%)
All	All	0.94	2/4249 (0.0%)	1.42	22/5765 (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
1	B	0	6
All	All	0	7

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	224	HIS	CE1-NE2	-5.96	1.26	1.32
1	A	165	LEU	C-O	-5.29	1.17	1.24

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	34	THR	CA-CB-OG1	-7.64	98.14	109.60
1	B	70	ASN	CB-CA-C	-7.03	102.01	111.21
1	A	75	GLU	CB-CA-C	-6.95	97.77	110.63
1	B	259	PHE	CA-CB-CG	6.40	120.20	113.80
1	A	4	ASP	CB-CA-C	-6.05	101.73	111.18

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	143	ARG	Sidechain
1	B	116	ARG	Sidechain
1	B	143	ARG	Sidechain
1	B	47	ARG	Sidechain
1	B	82	ARG	Sidechain

## 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	2098	2094	2087	37	0
1	B	2077	2073	2068	26	0
2	A	20	30	27	9	0
2	B	12	18	17	2	0
3	A	5	0	0	0	0
4	A	106	0	0	8	1
4	B	81	0	0	4	2
All	All	4399	4215	4199	59	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 7.

The worst 5 of 59 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:A:146:TYR:HB3	2:A:305:EDO:O2	1.63	0.98
1:A:267:GLN:NE2	1:A:271:GLU:OE2	1.98	0.95
1:A:4:ASP:HB2	4:A:403:HOH:O	1.69	0.90
1:A:190:ILE:HD11	1:B:140:ILE:HD11	1.63	0.81
1:A:235:LYS:HD2	4:A:494:HOH:O	1.81	0.79

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)
4:B:467:HOH:O	4:B:469:HOH:O[7_444]	2.05	0.15
4:A:432:HOH:O	4:B:466:HOH:O[4_545]	2.06	0.14

## 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	Percentiles	
1	A	263/290 (91%)	254 (97%)	9 (3%)	0	100	100
1	B	259/290 (89%)	250 (96%)	9 (4%)	0	100	100
All	All	522/580 (90%)	504 (97%)	18 (3%)	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	Percentiles	
1	A	234/251 (93%)	221 (94%)	13 (6%)	19	8
1	B	233/251 (93%)	215 (92%)	18 (8%)	12	3
All	All	467/502 (93%)	436 (93%)	31 (7%)	15	5

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	13	GLU
1	B	250	SER

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Mol	Chain	Res	Type
1	B	70	ASN
1	B	267	GLN
1	B	204	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	187	GLN
1	B	224	HIS
1	B	267	GLN
1	B	251	ASN
1	B	213	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

9 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	$\# Z  > 2$
2	EDO	A	301	-	3,3,3	1.94	1 (33%)	2,2,2	0.64	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	EDO	A	303	-	3,3,3	2.21	1 (33%)	2,2,2	0.20	0
2	EDO	A	305	-	3,3,3	0.61	0	2,2,2	0.54	0
2	EDO	B	303	-	3,3,3	1.27	1 (33%)	2,2,2	1.43	1 (50%)
2	EDO	A	306	-	3,3,3	0.59	0	2,2,2	0.84	0
2	EDO	A	302	-	3,3,3	0.64	0	2,2,2	1.81	0
2	EDO	B	302	-	3,3,3	0.43	0	2,2,2	0.36	0
2	EDO	B	301	-	3,3,3	0.64	0	2,2,2	0.98	0
3	SO4	A	304	-	4,4,4	0.32	0	6,6,6	0.12	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	A	301	-	-	1/1/1/1	-
2	EDO	A	303	-	-	1/1/1/1	-
2	EDO	A	305	-	-	0/1/1/1	-
2	EDO	B	303	-	-	1/1/1/1	-
2	EDO	A	306	-	-	1/1/1/1	-
2	EDO	A	302	-	-	1/1/1/1	-
2	EDO	B	302	-	-	0/1/1/1	-
2	EDO	B	301	-	-	1/1/1/1	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	303	EDO	O1-C1	-3.69	1.23	1.42
2	A	301	EDO	O2-C2	-3.24	1.25	1.42
2	B	303	EDO	O1-C1	-2.06	1.31	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	303	EDO	O1-C1-C2	-2.02	96.98	112.39

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
2	A	303	EDO	O1-C1-C2-O2
2	B	301	EDO	O1-C1-C2-O2
2	B	303	EDO	O1-C1-C2-O2
2	A	302	EDO	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	EDO	2	0
2	A	303	EDO	3	0
2	A	305	EDO	4	0
2	B	301	EDO	2	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	A	267/290 (92%)	-0.31	5 (1%) 66 74	31, 46, 75, 99	0
1	B	263/290 (90%)	-0.16	4 (1%) 72 78	32, 51, 85, 115	0
All	All	530/580 (91%)	-0.24	9 (1%) 69 76	31, 48, 81, 115	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	277	VAL	3.9
1	A	138	ALA	2.9
1	A	3	GLY	2.9
1	B	138	ALA	2.5
1	B	207	TYR	2.4

### 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 oligosaccharides 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<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	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SO4	A	304	5/5	0.69	0.11	106,119,134,151	0
2	EDO	B	302	4/4	0.88	0.10	40,60,71,73	1
2	EDO	A	302	4/4	0.88	0.11	44,59,62,62	1
2	EDO	A	306	4/4	0.93	0.12	33,49,55,61	1
2	EDO	A	305	4/4	0.95	0.10	42,68,69,73	1
2	EDO	B	303	4/4	0.95	0.12	25,45,62,67	1
2	EDO	A	303	4/4	0.95	0.10	24,39,59,65	1
2	EDO	B	301	4/4	0.96	0.08	36,46,49,53	1
2	EDO	A	301	4/4	0.97	0.11	31,35,46,53	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.