



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 18, 2020 – 06:04 am BST

PDB ID : 2WE4  
Title : Carbamate kinase from *Enterococcus faecalis* bound to a sulfate ion and two water molecules, which mimic the substrate carbamyl phosphate  
Authors : Ramon-Maiques, S.; Marina, A.; Gil-Ortiz, F.; Rubio, V.  
Deposited on : 2009-03-27  
Resolution : 2.02 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

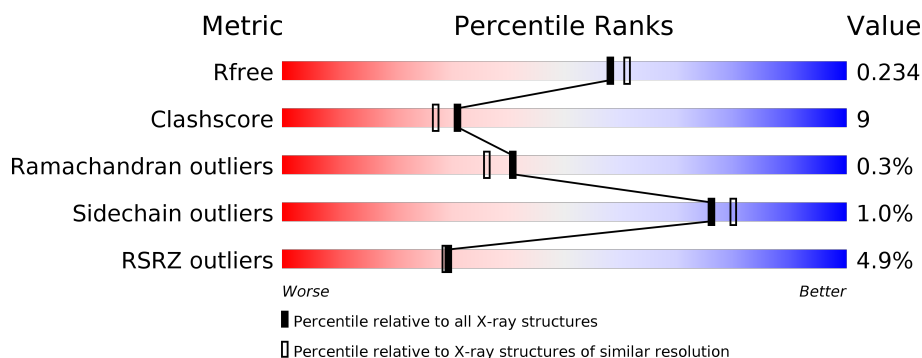
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.02 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))
$R_{free}$	130704	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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 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	310	<div> <div>3%</div> <div> <div></div> <div>82%</div> <div>17%</div> <div>.</div> </div> </div>
1	B	310	<div> <div>4%</div> <div> <div></div> <div>81%</div> <div>18%</div> <div>.</div> </div> </div>
1	C	310	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>11%</div> <div>.</div> </div> </div>
1	D	310	<div> <div>11%</div> <div> <div></div> <div>80%</div> <div>18%</div> <div>.</div> </div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 10190 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 CARBAMATE KINASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	309	Total	C	N	O	S	0	0	0
			2302	1451	390	452	9			
1	B	309	Total	C	N	O	S	0	0	0
			2302	1451	390	452	9			
1	C	309	Total	C	N	O	S	0	0	0
			2302	1451	390	452	9			
1	D	309	Total	C	N	O	S	0	0	0
			2302	1451	390	452	9			

- Molecule 2 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

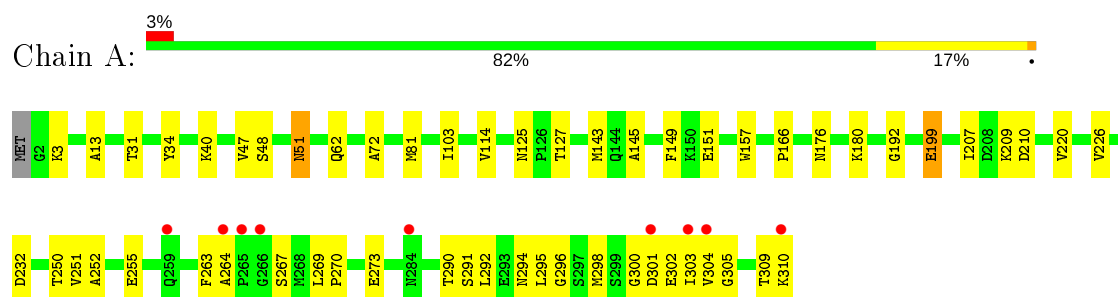
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	252	Total	O	0	0
			252	252		
3	B	200	Total	O	0	0
			200	200		
3	C	254	Total	O	0	0
			254	254		
3	D	201	Total	O	0	0
			201	201		

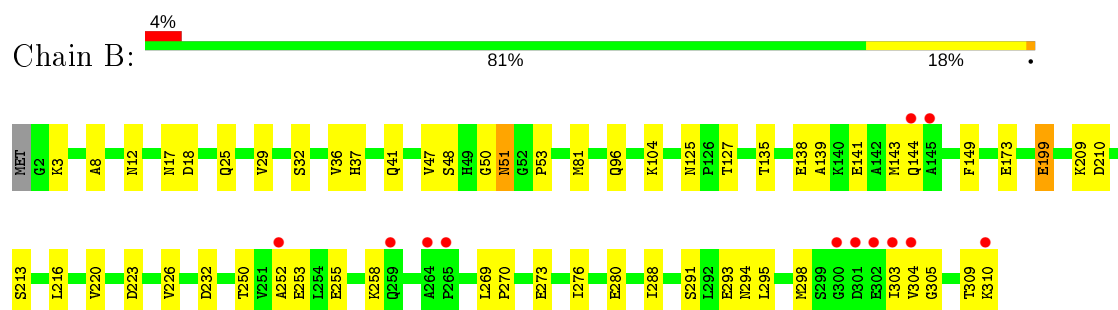
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

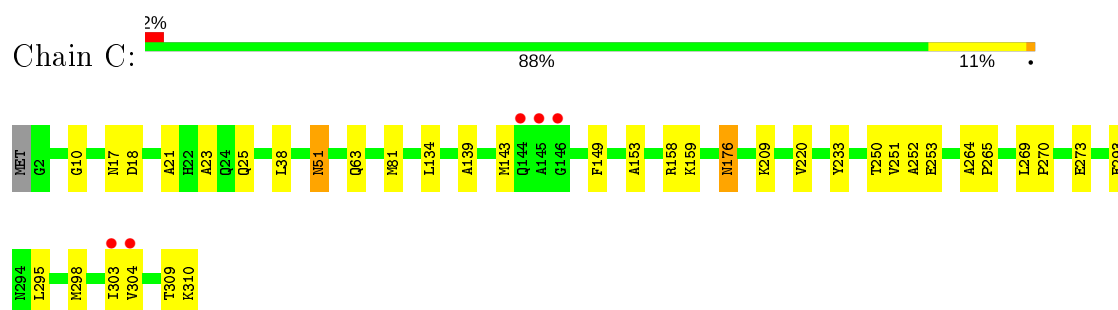
#### • Molecule 1: CARBAMATE KINASE 1



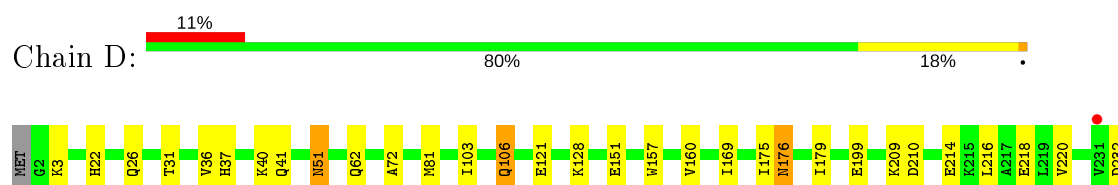
#### • Molecule 1: CARBAMATE KINASE 1



#### • Molecule 1: CARBAMATE KINASE 1



#### • Molecule 1: CARBAMATE KINASE 1



Y233	Y234	C235	I236	N237	Y238	Q239	K240	F241	D242	E243	K244	Q245	L246	T250	V251	A252	E253	L254	E255	E256	Y257	K258	Q259	A260	G261	H262	F263	A264	P265	G266	S267	M268	L269	P270	K271	I272	I276	T290	S291	L292	E293	N294	L295	M298	S299	G300	D301	E302	I303	V304	G305	T309	K310
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.89 Å 172.60 Å 98.63 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.02 49.70 – 2.02	Depositor EDS
% Data completeness (in resolution range)	96.1 (20.00-2.02) 96.2 (49.70-2.02)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.66 (at 2.01 Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.195 , 0.234 0.195 , 0.234	Depositor DCC
$R_{free}$ test set	4450 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.2	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 52.4	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	0.94	EDS
Total number of atoms	10190	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	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 23.45 % 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 4.6544e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [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	A	0.29	0/2337	0.57	0/3171
1	B	0.28	0/2337	0.53	0/3171
1	C	0.29	0/2337	0.56	0/3171
1	D	0.28	0/2337	0.55	0/3171
All	All	0.29	0/9348	0.55	0/12684

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	A	2302	0	2337	43	0
1	B	2302	0	2337	48	0
1	C	2302	0	2337	32	0
1	D	2302	0	2337	50	0
2	A	20	0	0	0	0
2	B	20	0	0	1	0
2	C	15	0	0	0	0
2	D	20	0	0	0	0
3	A	252	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	200	0	0	2	0
3	C	254	0	0	3	0
3	D	201	0	0	0	0
All	All	10190	0	9348	169	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 9.

The worst 5 of 169 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:D:176:ASN:HD21	1:D:220:VAL:HA	1.21	1.04
1:A:31:THR:HG23	1:A:292:LEU:HD21	1.39	1.01
1:D:251:VAL:HB	1:D:310:LYS:HD3	1.45	0.99
1:A:252:ALA:HB2	1:A:310:LYS:HE3	1.49	0.94
1:B:252:ALA:HB2	1:B:310:LYS:HE3	1.51	0.90

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	Allowed	Outliers	Percentiles	
1	A	307/310 (99%)	299 (97%)	6 (2%)	2 (1%)	22	15
1	B	307/310 (99%)	295 (96%)	12 (4%)	0	100	100
1	C	307/310 (99%)	296 (96%)	10 (3%)	1 (0%)	41	36
1	D	307/310 (99%)	297 (97%)	9 (3%)	1 (0%)	41	36
All	All	1228/1240 (99%)	1187 (97%)	37 (3%)	4 (0%)	41	36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	153	ALA
1	D	263	PHE
1	A	263	PHE
1	A	300	GLY

### 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	
1	A	248/249 (100%)	246 (99%)	2 (1%)	81	85
1	B	248/249 (100%)	246 (99%)	2 (1%)	81	85
1	C	248/249 (100%)	246 (99%)	2 (1%)	81	85
1	D	248/249 (100%)	244 (98%)	4 (2%)	62	66
All	All	992/996 (100%)	982 (99%)	10 (1%)	76	80

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	51	ASN
1	C	176	ASN
1	D	106	GLN
1	B	199	GLU
1	D	51	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	294	ASN
1	C	12	ASN
1	D	51	ASN
1	B	144	GLN
1	B	248	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

15 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	SO4	B	1312	-	4,4,4	1.86	2 (50%)	6,6,6	0.90	0
2	SO4	A	1314	-	4,4,4	1.88	2 (50%)	6,6,6	0.90	0
2	SO4	A	1313	-	4,4,4	1.87	2 (50%)	6,6,6	0.92	0
2	SO4	B	1311	-	4,4,4	1.83	2 (50%)	6,6,6	0.87	0
2	SO4	A	1311	-	4,4,4	1.83	2 (50%)	6,6,6	0.92	0
2	SO4	D	1311	-	4,4,4	1.84	2 (50%)	6,6,6	0.87	0
2	SO4	C	1312	-	4,4,4	1.88	2 (50%)	6,6,6	0.90	0
2	SO4	B	1314	-	4,4,4	1.87	2 (50%)	6,6,6	0.91	0
2	SO4	A	1312	-	4,4,4	1.89	2 (50%)	6,6,6	0.91	0
2	SO4	D	1314	-	4,4,4	1.87	2 (50%)	6,6,6	0.90	0
2	SO4	C	1311	-	4,4,4	1.85	2 (50%)	6,6,6	0.90	0
2	SO4	B	1313	-	4,4,4	1.83	2 (50%)	6,6,6	0.90	0
2	SO4	C	1313	-	4,4,4	1.83	2 (50%)	6,6,6	0.88	0
2	SO4	D	1313	-	4,4,4	1.86	2 (50%)	6,6,6	0.89	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	D	1312	-	4,4,4	1.89	2 (50%)	6,6,6	0.91	0

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1312	SO4	O1-S	3.15	1.63	1.46
2	A	1314	SO4	O1-S	3.13	1.63	1.46
2	A	1312	SO4	O1-S	3.13	1.62	1.46
2	C	1312	SO4	O1-S	3.10	1.62	1.46
2	B	1314	SO4	O1-S	3.09	1.62	1.46

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1311	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	A	309/310 (99%)	0.21	9 (2%) 51 51	13, 24, 46, 60	0
1	B	309/310 (99%)	0.32	12 (3%) 39 39	14, 27, 50, 73	0
1	C	309/310 (99%)	0.05	5 (1%) 72 71	13, 22, 43, 65	0
1	D	309/310 (99%)	0.36	34 (11%) 5 5	13, 24, 65, 80	0
All	All	1236/1240 (99%)	0.24	60 (4%) 29 29	13, 24, 52, 80	0

The worst 5 of 60 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	303	ILE	9.0
1	D	241	PRO	6.8
1	A	303	ILE	5.4
1	D	301	ASP	5.2
1	D	239	GLY	5.2

### 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. 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
2	SO4	C	1312	5/5	0.80	0.25	86,87,87,87	0
2	SO4	D	1312	5/5	0.90	0.19	62,62,62,63	0
2	SO4	A	1312	5/5	0.92	0.14	66,67,67,68	0
2	SO4	B	1312	5/5	0.94	0.14	80,80,80,80	0
2	SO4	D	1314	5/5	0.94	0.25	72,73,73,73	0
2	SO4	B	1314	5/5	0.94	0.16	69,70,70,70	0
2	SO4	A	1314	5/5	0.95	0.14	55,56,57,57	0
2	SO4	D	1313	5/5	0.97	0.13	49,49,50,51	0
2	SO4	A	1313	5/5	0.97	0.12	34,35,37,40	0
2	SO4	B	1311	5/5	0.99	0.12	26,27,29,31	0
2	SO4	C	1311	5/5	0.99	0.11	21,24,26,27	0
2	SO4	B	1313	5/5	0.99	0.16	39,40,40,41	0
2	SO4	A	1311	5/5	0.99	0.13	22,23,24,24	0
2	SO4	D	1311	5/5	0.99	0.11	19,23,24,26	0
2	SO4	C	1313	5/5	1.00	0.09	21,23,23,24	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.