



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 06:45 am GMT

PDB ID : 2FU7
Title : Zinc-beta-lactamase L1 from *Stenotrophomonas maltophilia* (Cu-substituted form)
Authors : Nauton, L.; Garau, G.; Kahn, R.; Dideberg, O.
Deposited on : 2006-01-26
Resolution : 1.85 Å (reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

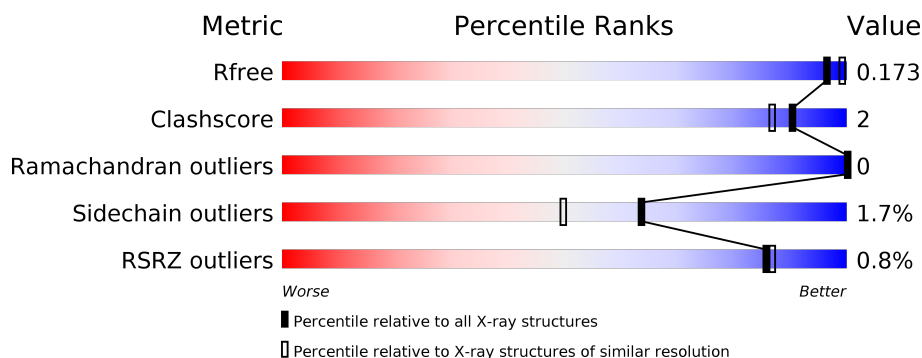
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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}	111664	2111 (1.86-1.86)
Clashscore	122126	2258 (1.86-1.86)
Ramachandran outliers	120053	2234 (1.86-1.86)
Sidechain outliers	120020	2234 (1.86-1.86)
RSRZ outliers	108989	2075 (1.86-1.86)

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 ≥ 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	A	269	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 90%; height: 10px; background-color: green;"></div> <div style="width: 9%; height: 10px; background-color: yellow;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> % 90% 9% .. </div> </div>
1	B	269	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 94%; height: 10px; background-color: green;"></div> <div style="width: 4%; height: 10px; background-color: yellow;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> <div style="display: flex; justify-content: space-between; font-size: 0.8em;"> % 94% </div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4530 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 Metallo-beta-lactamase L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	0	0
			2001	1258	360	375	8			
1	B	266	Total	C	N	O	S	0	0	0
			2001	1258	360	375	8			

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

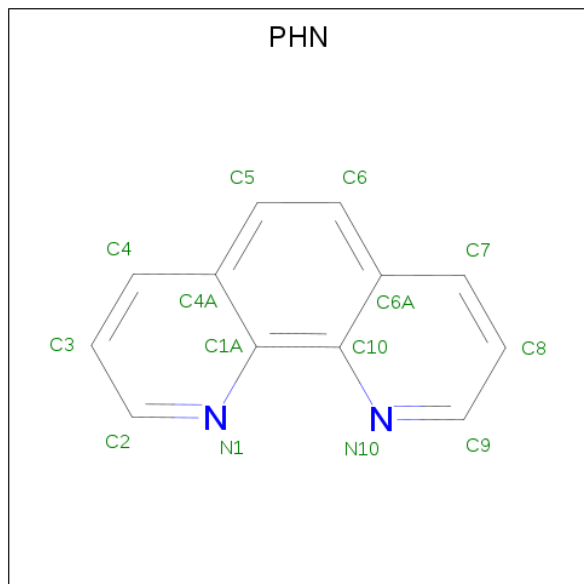
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	Cu	0	0
			3	3		
2	A	3	Total	Cu	0	0
			3	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 4 is 1,10-PHENANTHROLINE (three-letter code: PHN) (formula: $C_{12}H_8N_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N 14 12 2	0	0
4	B	1	Total C N 14 12 2	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		

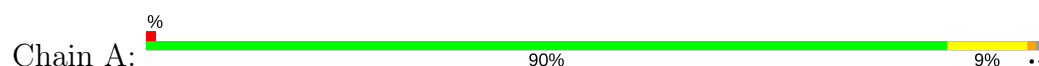
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	224	Total	O	0	4
			226	226		
6	B	223	Total	O	0	3
			226	226		

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: Metallo-beta-lactamase L1



• Molecule 1: Metallo-beta-lactamase L1



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	105.35Å 105.35Å 196.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.37 – 1.85 46.41 – 1.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.37-1.85) 100.0 (46.41-1.85)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.28 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.163 , 0.195 0.175 , 0.173	Depositor DCC
R_{free} test set	2773 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	15.1	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4530	wwPDB-VP
Average B, all atoms (Å ²)	17.0	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 74.08 % 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 1.6322e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GOL, SO4, CU, PHN

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	0.79	5/2051 (0.2%)	0.86	8/2801 (0.3%)
1	B	0.85	5/2051 (0.2%)	0.89	5/2801 (0.2%)
All	All	0.82	10/4102 (0.2%)	0.87	13/5602 (0.2%)

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	3
1	B	0	1
All	All	0	4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	276	ARG	C-N	14.61	1.67	1.34
1	B	157	GLY	C-N	13.79	1.65	1.34
1	A	157	GLY	C-N	12.13	1.61	1.34
1	A	87	MET	C-N	9.16	1.51	1.34
1	A	276	ARG	C-N	8.63	1.53	1.34
1	B	87	MET	C-N	7.58	1.48	1.34
1	B	191	PHE	C-N	6.29	1.48	1.34
1	A	57	THR	C-N	5.45	1.46	1.34
1	A	222	LEU	C-N	5.30	1.46	1.34
1	B	166	PRO	C-N	5.19	1.46	1.34

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	157	GLY	O-C-N	-12.36	102.93	122.70
1	A	301	ASP	CB-CG-OD2	6.71	124.34	118.30
1	B	160	ASP	CB-CG-OD2	6.59	124.24	118.30
1	A	308	ASP	CB-CG-OD2	5.99	123.69	118.30
1	B	171	ASP	CB-CG-OD2	5.82	123.54	118.30
1	B	191	PHE	O-C-N	5.71	131.83	122.70
1	B	78	ASP	CB-CG-OD2	5.69	123.42	118.30
1	A	160	ASP	CB-CG-OD2	5.37	123.13	118.30
1	A	166	PRO	O-C-N	-5.28	114.26	122.70
1	A	152	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	171	ASP	CB-CG-OD2	5.13	122.91	118.30
1	A	102	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	A	78	ASP	CB-CG-OD2	5.03	122.83	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	157	GLY	Mainchain
1	A	24	GLU	Peptide
1	A	57	THR	Mainchain
1	B	166	PRO	Mainchain

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	A	2001	0	1958	8	0
1	B	2001	0	1958	4	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	20	0	0	0	0
3	B	10	0	0	0	0
4	A	14	0	8	0	0
4	B	14	0	8	0	0
5	A	12	0	16	5	0
6	A	226	0	0	6	0
6	B	226	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4530	0	3948	15	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 2.

All (15) 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:B:276:ARG:C	1:B:289:ALA:N	1.67	1.47
1:A:268:ASN:CB	6:A:584:HOH:O	2.45	0.64
1:B:276:ARG:C	1:B:289:ALA:CA	2.67	0.60
5:A:7:GOL:H31	6:A:551:HOH:O	2.02	0.59
1:A:252:ARG:HD2	5:A:8:GOL:H12	1.84	0.58
1:A:268:ASN:CG	6:A:584:HOH:O	2.41	0.58
1:A:268:ASN:HB3	6:A:584:HOH:O	2.05	0.56
1:B:276:ARG:CA	1:B:289:ALA:N	2.65	0.56
5:A:8:GOL:H12	6:A:538:HOH:O	2.07	0.54
5:A:7:GOL:C3	6:A:551:HOH:O	2.58	0.49
1:A:252:ARG:HD2	5:A:8:GOL:C1	2.44	0.46
1:B:76:THR:HB	1:B:77:PRO:HD2	1.98	0.46
1:A:83:LEU:O	1:A:84:ASP:HB2	2.16	0.46
1:A:76:THR:HB	1:A:77:PRO:HD2	1.99	0.44
1:A:138:ALA:O	1:A:173:ILE:HA	2.18	0.44

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	264/269 (98%)	255 (97%)	9 (3%)	0	100	100
1	B	264/269 (98%)	256 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	528/538 (98%)	511 (97%)	17 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	201/202 (100%)	198 (98%)	3 (2%)	67	56
1	B	201/202 (100%)	197 (98%)	4 (2%)	58	43
All	All	402/404 (100%)	395 (98%)	7 (2%)	63	50

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	107	ARG
1	A	212	LYS
1	A	237	TYR
1	B	78	ASP
1	B	100	LYS
1	B	107	ARG
1	B	237	TYR

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

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 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	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	A	1	-	4,4,4	0.28	0	6,6,6	0.13	0
3	SO4	A	3	-	4,4,4	0.35	0	6,6,6	0.48	0
3	SO4	A	4	-	4,4,4	0.29	0	6,6,6	0.39	0
4	PHN	A	410	2	16,16,16	1.75	2 (12%)	22,22,22	1.16	2 (9%)
3	SO4	A	6	-	4,4,4	0.09	0	6,6,6	0.40	0
5	GOL	A	7	-	5,5,5	0.53	0	5,5,5	0.66	0
5	GOL	A	8	-	5,5,5	0.54	0	5,5,5	0.77	0
3	SO4	B	2	-	4,4,4	0.18	0	6,6,6	0.33	0
4	PHN	B	410	2	16,16,16	1.58	2 (12%)	22,22,22	1.65	4 (18%)
3	SO4	B	5	-	4,4,4	0.18	0	6,6,6	0.61	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	A	1	-	-	0/0/0/0	0/0/0/0
3	SO4	A	3	-	-	0/0/0/0	0/0/0/0
3	SO4	A	4	-	-	0/0/0/0	0/0/0/0
4	PHN	A	410	2	-	0/0/0/0	0/3/3/3
3	SO4	A	6	-	-	0/0/0/0	0/0/0/0
5	GOL	A	7	-	-	0/4/4/4	0/0/0/0
5	GOL	A	8	-	-	0/4/4/4	0/0/0/0
3	SO4	B	2	-	-	0/0/0/0	0/0/0/0
4	PHN	B	410	2	-	0/0/0/0	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	B	5	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	410	PHN	C4A-C1A	3.39	1.48	1.41
4	B	410	PHN	C6A-C10	3.63	1.48	1.41
4	A	410	PHN	C6A-C10	4.02	1.49	1.41
4	A	410	PHN	C4A-C1A	4.05	1.49	1.41

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	410	PHN	C4-C3-C2	2.11	121.70	118.92
4	B	410	PHN	C9-N10-C10	2.13	120.84	117.10
4	A	410	PHN	C7-C8-C9	2.17	121.79	118.92
4	B	410	PHN	C2-N1-C1A	2.40	121.31	117.10
4	B	410	PHN	C1A-C10-N10	3.78	122.89	118.23
4	B	410	PHN	C10-C1A-N1	3.93	123.07	118.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	7	GOL	2	0
5	A	8	GOL	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	2

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Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	276:ARG	C	289:ALA	N	1.67
1	B	157:GLY	C	160:ASP	N	1.65
1	A	157:GLY	C	160:ASP	N	1.61

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, 95th 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 ²)	Q<0.9
1	A	266/269 (98%)	-0.49	2 (0%) 86 87	9, 14, 26, 40	0
1	B	266/269 (98%)	-0.44	2 (0%) 86 87	10, 16, 27, 42	0
All	All	532/538 (98%)	-0.46	4 (0%) 86 87	9, 15, 27, 42	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	24	GLU	5.5
1	A	24	GLU	3.6
1	A	275	ALA	2.9
1	B	317	GLY	2.2

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, 95th 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(Å ²)	Q<0.9
5	GOL	A	8	6/6	0.77	0.25	35,38,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	GOL	A	7	6/6	0.85	0.22	25,25,25,27	6
3	SO4	B	5	5/5	0.85	0.17	33,34,35,36	5
4	PHN	B	410	14/14	0.88	0.45	15,17,18,18	14
3	SO4	A	6	5/5	0.90	0.18	36,37,38,39	5
3	SO4	A	4	5/5	0.91	0.12	32,32,35,37	5
3	SO4	A	3	5/5	0.91	0.18	34,36,36,37	5
4	PHN	A	410	14/14	0.96	0.10	18,19,20,20	14
3	SO4	B	2	5/5	0.98	0.08	31,36,36,36	0
2	CU	B	403	1/1	0.99	0.02	33,33,33,33	1
3	SO4	A	1	5/5	0.99	0.07	23,24,26,27	0
2	CU	A	401	1/1	1.00	0.08	14,14,14,14	0
2	CU	B	402	1/1	1.00	0.05	16,16,16,16	0
2	CU	A	403	1/1	1.00	0.18	5,5,5,5	1
2	CU	A	402	1/1	1.00	0.06	16,16,16,16	0
2	CU	B	401	1/1	1.00	0.08	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.