



Full wwPDB X-ray Structure Validation Report i

Sep 12, 2014 – 03:18 AM EDT

PDB ID : 4C1G
Title : Crystal structure of the metallo-beta-lactamaseIMP-1 with D-captopril
Authors : Zollman, D.; Brem, J.; McDonough, M.A.; vanBerkel, S.S.; Schofield, C.J.
Deposited on : 2013-08-12
Resolution : 1.71 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

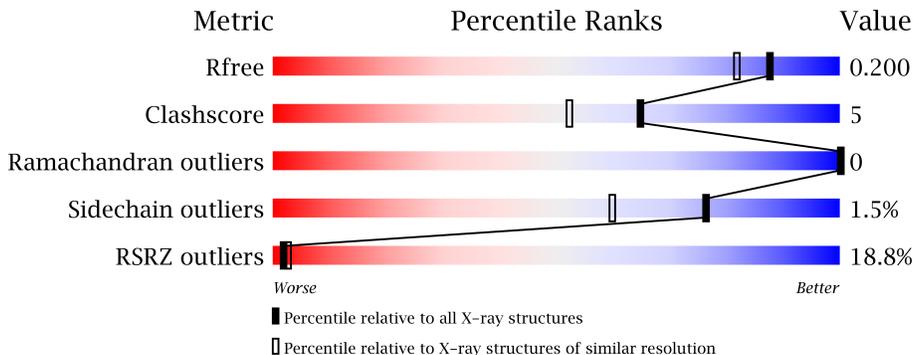
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable23489
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23489

1 Overall quality at a glance

The reported resolution of this entry is 1.71 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}	66092	2979 (1.74-1.70)
Clashscore	79885	3506 (1.74-1.70)
Ramachandran outliers	78287	3449 (1.74-1.70)
Sidechain outliers	78261	3449 (1.74-1.70)
RSRZ outliers	66119	2979 (1.74-1.70)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	228	
1	B	228	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	ZN	A	300	-	X
3	MCO	A	305	-	X
4	SO4	A	310	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3522 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

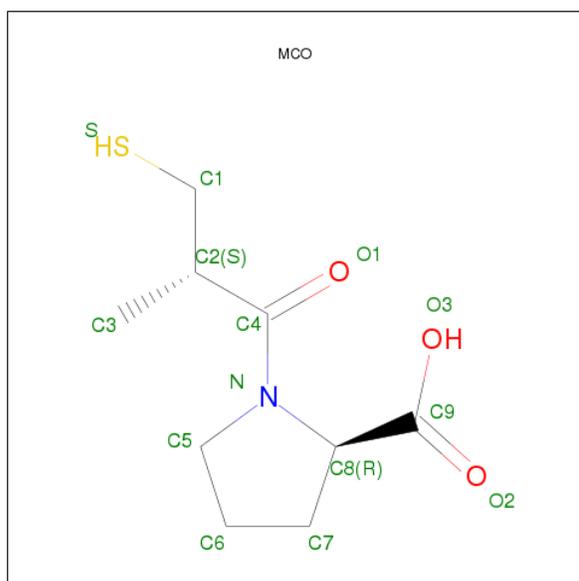
- Molecule 1 is a protein called BETA-LACTAMASE IMP-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	219	Total 1726	C 1118	N 281	O 326	S 1	0	4	0
1	B	217	Total 1553	C 1006	N 254	O 292	S 1	0	0	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

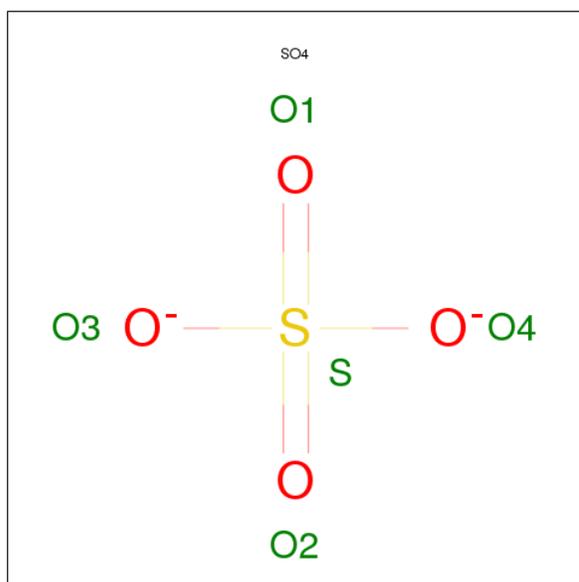
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total 2	Zn 2	0	0
2	A	2	Total 2	Zn 2	0	0

- Molecule 3 is 1-(3-MERCAPTO-2-METHYL-PROPIONYL)-PYRROLIDINE-2-CARBOXYLICACID (three-letter code: MCO) (formula: C₉H₁₅NO₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	14	9	1	3	1	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	201	201	201	0	0
5	B	14	14	14	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

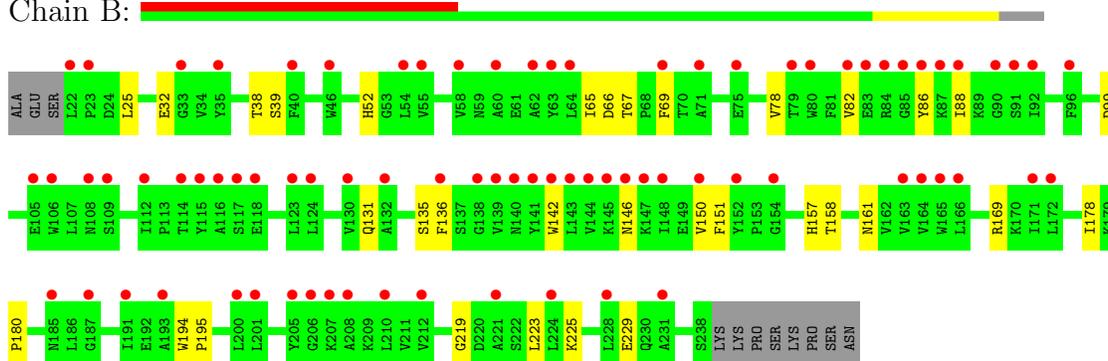
- Molecule 1: BETA-LACTAMASE IMP-1

Chain A:



- Molecule 1: BETA-LACTAMASE IMP-1

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.22Å 54.57Å 194.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	52.54 – 1.71 52.54 – 1.71	Depositor EDS
% Data completeness (in resolution range)	99.9 (52.54-1.71) 96.5 (52.54-1.71)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 1.71Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.145 , 0.176 0.170 , 0.200	Depositor DCC
R_{free} test set	1964 reflections (3.45%)	DCC
Wilson B-factor (Å ²)	21.2	Xtrriage
Anisotropy	0.465	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.7	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Outliers	0 of 58423 reflections	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3522	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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: MCO, ZN, 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	0/1773	0.82	0/2409
1	B	0.60	0/1597	0.62	0/2197
All	All	0.82	0/3370	0.73	0/4606

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1726	0	1708	11	0
1	B	1553	0	1380	22	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	14	0	13	5	0
4	A	10	0	0	0	0
5	A	201	0	0	3	0
5	B	14	0	0	1	0
All	All	3522	0	3101	34	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (34) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:142:TRP:HZ3	1:B:146:ASN:HA	1.53	0.73
1:B:65:ILE:O	1:B:66:ASP:HB2	1.95	0.66
1:A:179:LYS:NZ	3:A:305:MCO:O3	2.30	0.65
1:A:179:LYS:NZ	3:A:305:MCO:C9	2.61	0.64
1:A:179:LYS:NZ	3:A:305:MCO:O2	2.30	0.64
1:A:179:LYS:HZ1	3:A:305:MCO:C9	2.10	0.64
1:B:25:LEU:HG	1:B:38:THR:O	1.98	0.63
1:B:25:LEU:HD12	1:B:39:SER:HB3	1.82	0.60
1:B:219:GLY:HA3	1:B:223:LEU:HD11	1.84	0.59
1:A:65:ILE:O	1:A:66:ASP:HB2	2.03	0.58
1:B:142:TRP:CZ3	1:B:146:ASN:HA	2.35	0.58
1:B:131:GLN:NE2	5:B:2009:HOH:O	2.41	0.54
1:A:38:THR:OG1	1:A:52:HIS:HD2	1.91	0.53
1:B:142:TRP:HZ3	1:B:146:ASN:CA	2.20	0.53
1:A:122:GLU:HG3	5:A:2118:HOH:O	2.08	0.53
5:A:2024:HOH:O	1:B:52:HIS:HE1	1.93	0.52
1:A:69:PHE:CE2	1:A:99:ASP:HB3	2.45	0.52
1:B:32:GLU:O	1:B:169:ARG:NE	2.43	0.51
1:B:142:TRP:CZ3	1:B:146:ASN:N	2.79	0.50
1:B:82:VAL:HA	1:B:86:TYR:O	2.12	0.49
1:B:69:PHE:CE1	1:B:99:ASP:HB3	2.49	0.48
1:B:178:ILE:HG22	1:B:180:PRO:HD3	1.96	0.47
1:B:157:HIS:CD2	1:B:158:THR:HG23	2.51	0.46
1:B:150:VAL:HG12	1:B:151:PHE:N	2.31	0.45
1:A:78:VAL:HG13	1:A:88:ILE:HG13	1.98	0.45
1:B:78:VAL:HG22	1:B:88:ILE:HG13	1.99	0.44
3:A:305:MCO:C6	3:A:305:MCO:O3	2.64	0.44
1:A:213:PRO:HD2	5:A:2035:HOH:O	2.19	0.43
1:B:225:LYS:O	1:B:229:GLU:HG3	2.19	0.42
1:B:194:TRP:N	1:B:195:PRO:HD2	2.35	0.41
1:A:194:TRP:HB3	1:A:195:PRO:HD3	2.01	0.41
1:B:142:TRP:CZ3	1:B:146:ASN:CA	3.01	0.41
1:B:219:GLY:CA	1:B:223:LEU:HD11	2.50	0.41
1:B:135:SER:OG	1:B:136:PHE:N	2.53	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	221/228 (97%)	217 (98%)	4 (2%)	0	100	100
1	B	215/228 (94%)	205 (95%)	10 (5%)	0	100	100
All	All	436/456 (96%)	422 (97%)	14 (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	187/196 (95%)	184 (98%)	3 (2%)	75	58
1	B	143/196 (73%)	141 (99%)	2 (1%)	78	62
All	All	330/392 (84%)	325 (98%)	5 (2%)	76	60

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	92	ILE
1	A	95	HIS
1	A	161	ASN
1	B	67	THR
1	B	161	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	HIS
1	A	131	GLN
1	B	52	HIS

5.3.3 RNA [i](#)

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 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	MCO	A	305	2	14,14,14	2.25	3 (21%)	19,19,19	1.50	4 (21%)
4	SO4	A	310	-	4,4,4	0.57	0	6,6,6	1.33	1 (16%)
4	SO4	A	311	-	4,4,4	1.48	1 (25%)	6,6,6	0.84	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	MCO	A	305	2	-	0/14/24/24	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SO4	A	310	-	-	0/0/0/0	0/0/0/0
4	SO4	A	311	-	-	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)
3	A	305	MCO	C4-N	5.39	1.45	1.34
3	A	305	MCO	C8-C9	-3.89	1.45	1.52
3	A	305	MCO	C8-N	-2.21	1.42	1.47
4	A	311	SO4	O1-S	2.02	1.54	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	305	MCO	C7-C8-C9	-3.09	106.38	111.44
4	A	310	SO4	O2-S-O1	-2.90	100.19	109.50
3	A	305	MCO	C2-C1-S	-2.86	110.45	114.14
3	A	305	MCO	C5-N-C8	-2.61	108.13	111.98
3	A	305	MCO	C9-C8-N	-2.33	107.26	111.93

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	219/228 (96%)	0.16	2 (0%) 81 87	14, 22, 40, 67	0
1	B	217/228 (95%)	1.86	80 (36%) 1 2	58, 77, 97, 118	0
All	All	436/456 (95%)	1.00	82 (18%) 2 3	14, 59, 93, 118	0

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	171	ILE	8.2
1	B	33	GLY	6.6
1	B	106	TRP	6.3
1	B	112	ILE	5.9
1	B	55	VAL	5.8
1	B	143	LEU	5.7
1	B	60	ALA	5.6
1	B	90	GLY	5.5
1	B	166	LEU	5.3
1	B	200	LEU	5.2
1	B	63	TYR	5.1
1	B	139	VAL	5.1
1	B	141	TYR	5.1
1	B	144	VAL	5.0
1	B	148	ILE	4.9
1	B	82	VAL	4.8
1	B	62	ALA	4.7
1	B	116	ALA	4.7
1	B	205	TYR	4.7
1	B	142	TRP	4.6
1	B	88	ILE	4.5
1	B	163	VAL	4.4
1	B	115	TYR	4.2
1	B	147	LYS	4.2

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Mol	Chain	Res	Type	RSRZ
1	B	35	TYR	4.0
1	B	136	PHE	4.0
1	B	165	TRP	3.6
1	B	91	SER	3.6
1	B	207	LYS	3.6
1	B	193	ALA	3.5
1	A	92	ILE	3.5
1	B	224	LEU	3.5
1	B	80	TRP	3.4
1	B	152	TYR	3.3
1	B	64	LEU	3.3
1	B	210	LEU	3.3
1	B	138	GLY	3.3
1	B	201	LEU	3.3
1	B	118	GLU	3.2
1	B	69	PHE	3.2
1	B	208	ALA	3.2
1	B	79	THR	3.1
1	B	85	GLY	3.1
1	B	87	LYS	3.1
1	B	185	ASN	3.1
1	B	228	LEU	3.1
1	B	221	ALA	3.1
1	B	22	LEU	3.1
1	B	124	LEU	3.1
1	B	154	GLY	3.0
1	B	46	TRP	3.0
1	B	132	ALA	3.0
1	B	75	GLU	2.9
1	B	105	GLU	2.9
1	B	117	SER	2.9
1	B	83	GLU	2.8
1	B	58	VAL	2.8
1	B	23	PRO	2.8
1	B	164	VAL	2.8
1	B	231	ALA	2.7
1	A	21	SER	2.7
1	B	109	SER	2.6
1	B	140	ASN	2.6
1	B	86	TYR	2.6
1	B	108	ASN	2.6
1	B	206	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	84	ARG	2.6
1	B	172	LEU	2.4
1	B	212	VAL	2.4
1	B	54	LEU	2.4
1	B	40	PHE	2.3
1	B	146	ASN	2.3
1	B	123	LEU	2.2
1	B	92	ILE	2.2
1	B	145	LYS	2.2
1	B	114	THR	2.2
1	B	96	PHE	2.2
1	B	187	GLY	2.1
1	B	130	VAL	2.1
1	B	150	VAL	2.1
1	B	71	ALA	2.0
1	B	191	ILE	2.0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q < 0.9
3	MCO	A	305	14/14	0.28	10.76	24,31,35,40	0
2	ZN	A	300	1/1	0.13	2.75	19,19,19,19	0
4	SO4	A	310	5/5	0.14	2.16	59,60,64,65	0
4	SO4	A	311	5/5	0.11	0.82	19,32,34,35	5
2	ZN	A	301	1/1	0.11	0.10	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	ZN	B	300	1/1	0.05	-2.21	63,63,63,63	0
2	ZN	B	301	1/1	0.05	-2.37	61,61,61,61	0

6.5 Other polymers

There are no such residues in this entry.