



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2WRS / pdb_00002wrs
Title : Crystal Structure of the Mono-Zinc Metallo-beta-lactamase VIM-4 from *Pseudomonas aeruginosa*
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Deposited on : 2009-09-02
Resolution : 2.79 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 ⓘ 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 ⓘ](#)) 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

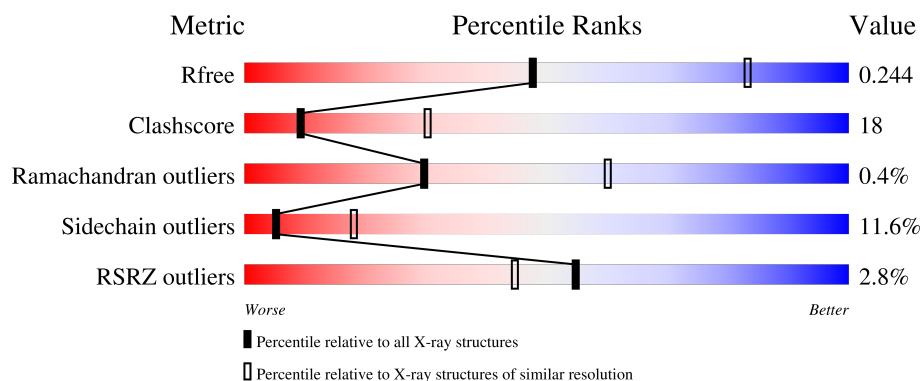
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.79 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 $\leq 5\%$. 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	230	 65% 31% 5% 1% 1%
1	B	230	 5% 63% 33% 1% 1%

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
3	FLC	A	1263	-	-	X	-
4	CIT	A	1264	-	-	X	-
4	CIT	A	1265	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3546 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.

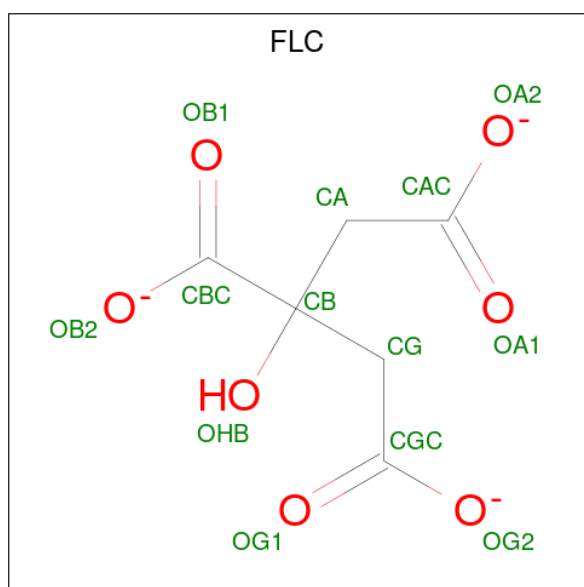
- Molecule 1 is a protein called BETA-LACTAMASE VIM-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	1	0
			1738	1091	306	340	1			
1	B	230	Total	C	N	O	S	0	0	0
			1727	1085	302	339	1			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

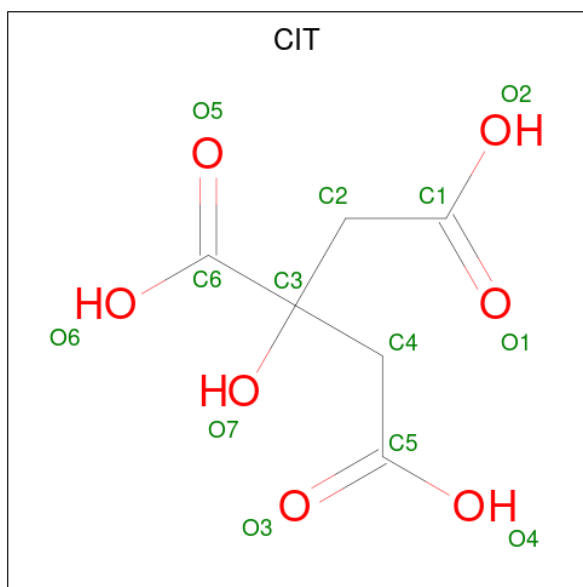
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is CITRATE ANION (CCD ID: FLC) (formula: C₆H₅O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	6	7		
4	A	1	Total	C	O	0	0
			13	6	7		

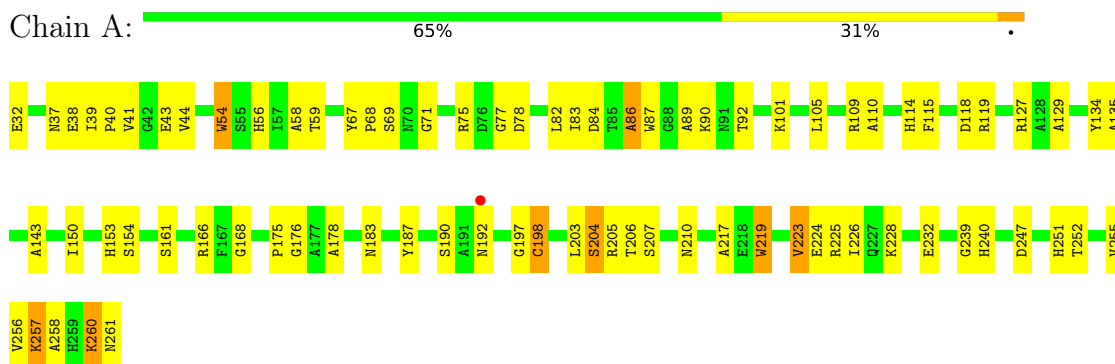
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	26	Total	O	0	0
			26	26		
5	B	1	Total	O	0	0
			1	1		

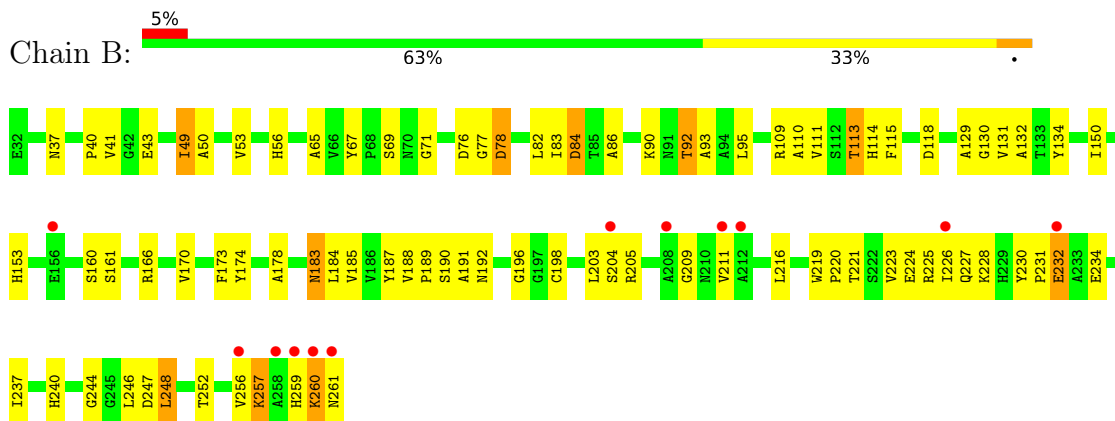
3 Residue-property plots

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: BETA-LACTAMASE VIM-4



• Molecule 1: BETA-LACTAMASE VIM-4



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	140.13Å 45.67Å 105.03Å 90.00° 105.41° 90.00°	Depositor
Resolution (Å)	43.27 – 2.79 43.27 – 2.79	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.27-2.79) 98.9 (43.27-2.79)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.199 , 0.253 0.194 , 0.244	Depositor DCC
R_{free} test set	806 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3546	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.43% of the height of the origin peak. No significant pseudotranslation is detected.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FLC, ZN, CIT

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	1.28	5/1778 (0.3%)	1.25	13/2431 (0.5%)
1	B	1.09	1/1767 (0.1%)	1.16	3/2417 (0.1%)
All	All	1.19	6/3545 (0.2%)	1.21	16/4848 (0.3%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	127	ARG	C-O	-6.42	1.16	1.24
1	A	135	ALA	CA-CB	-6.27	1.43	1.53
1	A	89	ALA	CA-CB	-6.19	1.43	1.53
1	A	92	THR	CA-CB	-5.46	1.44	1.53
1	B	92	THR	CA-CB	-5.35	1.45	1.53

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	150	ILE	N-CA-C	8.02	116.18	107.60
1	B	78	ASP	N-CA-CB	-7.18	100.69	110.67
1	A	78	ASP	N-CA-C	-6.86	105.46	114.31
1	B	115	PHE	N-CA-C	6.78	121.55	113.28
1	B	78	ASP	N-CA-C	-6.67	105.43	113.97

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	1738	0	1685	55	0
1	B	1727	0	1672	65	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	13	0	5	8	0
3	B	13	0	5	3	0
4	A	26	0	10	11	0
5	A	26	0	0	4	0
5	B	1	0	0	0	0
All	All	3546	0	3377	125	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 18.

The worst 5 of 125 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:40:PRO:HG2	1:A:43:GLU:OE2	1.51	1.08
1:A:198:CYS:SG	3:A:1263:FLC:OB1	2.13	1.06
1:B:49:ILE:HD12	1:B:237:ILE:HD11	1.44	0.99
4:A:1264:CIT:C6	4:A:1264:CIT:O4	2.13	0.96
1:A:109:ARG:HH12	4:A:1264:CIT:H41	1.28	0.95

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	229/230 (100%)	212 (93%)	17 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	228/230 (99%)	196 (86%)	30 (13%)	2 (1%)	14	41
All	All	457/460 (99%)	408 (89%)	47 (10%)	2 (0%)	30	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	77	GLY
1	B	84	ASP

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	182/181 (101%)	160 (88%)	22 (12%)	5	16
1	B	181/181 (100%)	161 (89%)	20 (11%)	6	20
All	All	363/362 (100%)	321 (88%)	42 (12%)	5	18

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	160	SER
1	B	232	GLU
1	B	166	ARG
1	B	216	LEU
1	B	246	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	254	ASN
1	B	227	GLN
1	B	48	GLN
1	A	254	ASN
1	B	114	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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$
4	CIT	A	1265	-	12,12,12	2.11	6 (50%)	17,17,17	2.52	5 (29%)
4	CIT	A	1264	-	12,12,12	1.83	5 (41%)	17,17,17	1.58	4 (23%)
3	FLC	A	1263	2	12,12,12	1.19	1 (8%)	17,17,17	1.27	2 (11%)
3	FLC	B	1263	2	12,12,12	1.10	0	17,17,17	1.51	3 (17%)

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
4	CIT	A	1265	-	-	10/16/16/16	-
4	CIT	A	1264	-	-	8/16/16/16	-
3	FLC	A	1263	2	-	7/16/16/16	-
3	FLC	B	1263	2	-	11/16/16/16	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1265	CIT	O7-C3	3.88	1.50	1.43
4	A	1265	CIT	C4-C3	3.00	1.57	1.54
4	A	1264	CIT	O1-C1	2.87	1.31	1.22
4	A	1265	CIT	O1-C1	2.81	1.31	1.22
4	A	1264	CIT	O5-C6	2.72	1.30	1.22

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1265	CIT	O5-C6-C3	-5.89	110.69	122.09
4	A	1265	CIT	O6-C6-C3	5.39	123.47	113.14
4	A	1264	CIT	O6-C6-C3	4.00	120.81	113.14
3	B	1263	FLC	OB2-CBC-CB	3.40	119.67	113.14
4	A	1265	CIT	C4-C3-C6	-3.20	102.95	110.03

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1263	FLC	CG-CB-CBC-OB1
3	A	1263	FLC	CG-CB-CBC-OB2
3	A	1263	FLC	OHB-CB-CBC-OB1
3	A	1263	FLC	OHB-CB-CBC-OB2
3	A	1263	FLC	CBC-CB-CG-CGC

There are no ring outliers.

4 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1265	CIT	3	0
4	A	1264	CIT	8	0
3	A	1263	FLC	8	0
3	B	1263	FLC	3	0

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	230/230 (100%)	-0.39	1 (0%) 88 84	5, 22, 49, 76	1 (0%)
1	B	230/230 (100%)	0.33	12 (5%) 33 25	16, 47, 86, 104	0
All	All	460/460 (100%)	-0.03	13 (2%) 55 45	5, 33, 82, 104	1 (0%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	204	SER	3.3
1	B	259	HIS	2.9
1	B	208	ALA	2.7
1	A	192	ASN	2.5
1	B	261	ASN	2.5

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, 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($\text{\AA}^2$)	Q<0.9
4	CIT	A	1265	13/13	0.76	0.25	22,25,31,31	0
4	CIT	A	1264	13/13	0.83	0.23	22,24,28,32	0
3	FLC	B	1263	13/13	0.89	0.12	69,70,71,71	0
3	FLC	A	1263	13/13	0.94	0.09	55,62,63,64	0
2	ZN	B	1262	1/1	0.99	0.07	58,58,58,58	0
2	ZN	A	1262	1/1	1.00	0.02	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.