



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:27 AM GMT

PDB ID : 3LVZ  
Title : New refinement of the crystal structure of BJP-1, a subclass B3 metallo-beta-lactamase of *Bradyrhizobium japonicum*  
Authors : Docquier, J.D.; Benvenuti, M.; Calderone, V.; Stoczko, M.; Rossolini, G.M.; Mangani, S.  
Deposited on : 2010-02-23  
Resolution : 1.40 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

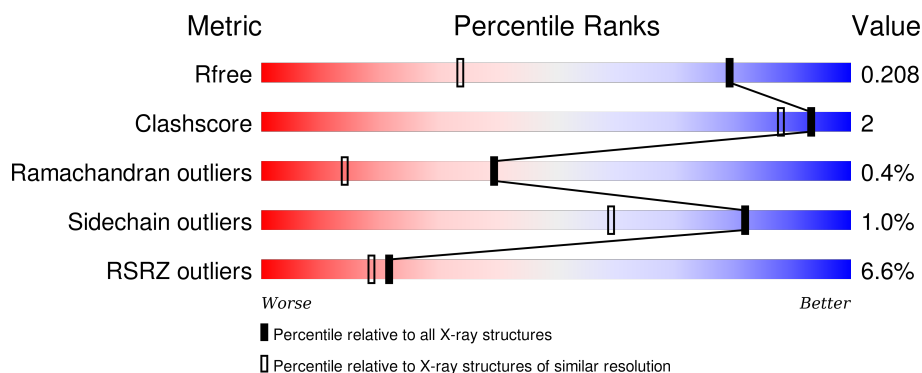
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.40 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))
$R_{free}$	91344	1199 (1.40-1.40)
Clashscore	102246	1295 (1.40-1.40)
Ramachandran outliers	100387	1259 (1.40-1.40)
Sidechain outliers	100360	1258 (1.40-1.40)
RSRZ outliers	91569	1198 (1.40-1.40)

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. 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	294	<div> <div>4%</div> <div>84%</div> <div>7% • 7%</div> </div>
1	B	294	<div> <div>8%</div> <div>84%</div> <div>9% 7%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4656 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 Blr6230 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	272	Total	C	N	O	S	0	4	0
			2071	1322	343	396	10			
1	B	273	Total	C	N	O	S	0	6	0
			2097	1342	349	395	11			

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

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

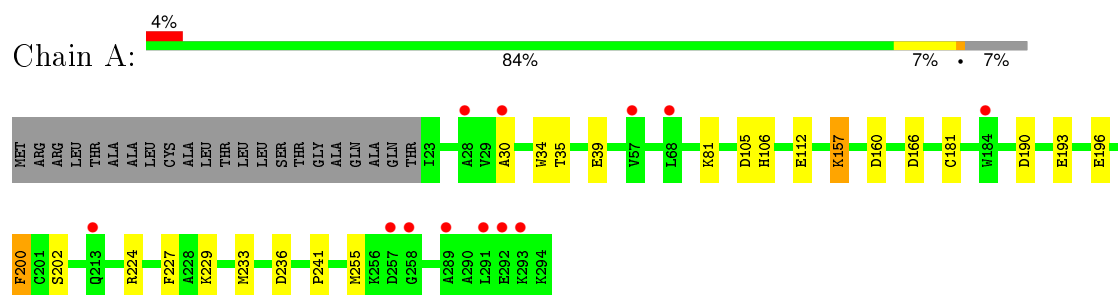
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	256	Total	O	0	0
			256	256		
3	B	226	Total	O	0	0
			226	226		

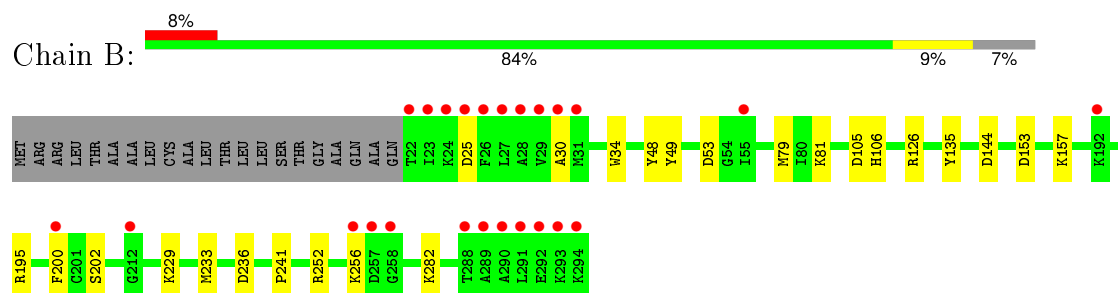
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ( $\text{RSRZ} > 2$ ). 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: Blr6230 protein



#### • Molecule 1: Blr6230 protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	42.50Å 44.77Å 76.97Å 78.92° 89.51° 61.91°	Depositor
Resolution (Å)	32.24 – 1.40 32.24 – 1.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (32.24-1.40) 84.3 (32.24-1.40)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.27 (at 1.40Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.162 , 0.193 0.178 , 0.208	Depositor DCC
$R_{free}$ test set	8006 reflections (10.06%)	DCC
Wilson B-factor (Å <sup>2</sup> )	13.3	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 43.1	EDS
Estimated twinning fraction	0.018 for h,h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 87608 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4656	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	12.0	wwPDB-VP

Xtriage'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.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN

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	1.25	10/2126 (0.5%)	1.17	10/2884 (0.3%)
1	B	1.19	4/2158 (0.2%)	1.16	10/2923 (0.3%)
All	All	1.22	14/4284 (0.3%)	1.16	20/5807 (0.3%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	181	CYS	CB-SG	-6.71	1.70	1.82
1	A	112	GLU	CD-OE1	6.59	1.32	1.25
1	A	39	GLU	CG-CD	6.54	1.61	1.51
1	A	196	GLU	CD-OE2	-6.30	1.18	1.25
1	A	200	PHE	CE1-CZ	5.85	1.48	1.37
1	B	135	TYR	CG-CD1	5.47	1.46	1.39
1	B	48	TYR	CE2-CZ	-5.46	1.31	1.38
1	A	196	GLU	CG-CD	5.33	1.59	1.51
1	A	81	LYS	CD-CE	-5.29	1.38	1.51
1	B	81	LYS	CD-CE	-5.18	1.38	1.51
1	A	224[A]	ARG	CG-CD	-5.09	1.39	1.51
1	A	224[B]	ARG	CG-CD	-5.09	1.39	1.51
1	A	227	PHE	CE2-CZ	-5.04	1.27	1.37
1	B	49	TYR	CG-CD1	-5.01	1.32	1.39

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	255	MET	CG-SD-CE	-13.58	78.47	100.20
1	A	224[A]	ARG	NE-CZ-NH2	-8.24	116.18	120.30
1	A	224[B]	ARG	NE-CZ-NH2	-8.24	116.18	120.30
1	B	144	ASP	CB-CG-OD1	7.97	125.47	118.30
1	B	79[A]	MET	CG-SD-CE	-7.60	88.05	100.20

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	79[B]	MET	CG-SD-CE	-7.60	88.05	100.20
1	B	53	ASP	CB-CG-OD1	6.58	124.22	118.30
1	B	252	ARG	NE-CZ-NH2	-6.49	117.06	120.30
1	B	236	ASP	CB-CG-OD2	6.36	124.02	118.30
1	A	166	ASP	CB-CG-OD2	6.22	123.90	118.30
1	A	236	ASP	CB-CG-OD2	5.98	123.68	118.30
1	B	195	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	A	181	CYS	CA-CB-SG	5.62	124.12	114.00
1	A	255	MET	CA-CB-CG	5.56	122.76	113.30
1	A	196	GLU	OE1-CD-OE2	-5.51	116.68	123.30
1	B	153	ASP	CB-CG-OD2	5.44	123.20	118.30
1	A	255	MET	CB-CA-C	5.17	120.74	110.40
1	B	105	ASP	CB-CG-OD1	5.16	122.95	118.30
1	B	282	LYS	CD-CE-NZ	5.07	123.36	111.70
1	A	105	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

## 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	2071	0	2044	9	0
1	B	2097	0	2095	7	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	256	0	0	0	0
3	B	226	0	0	1	0
All	All	4656	0	4139	16	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 (16) 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:229:LYS:HE3	1:B:233:MET:CE	2.09	0.82
1:A:190:ASP:O	1:A:193[B]:GLU:HG2	1.88	0.73
1:A:229:LYS:HE3	1:A:233:MET:CE	2.32	0.59
1:A:200:PHE:O	1:A:241:PRO:HD3	2.03	0.58
1:B:200:PHE:O	1:B:241:PRO:HD3	2.05	0.57
1:B:229:LYS:HE3	1:B:233:MET:HE1	1.89	0.52
1:A:106:HIS:CE1	1:A:241:PRO:HB2	2.46	0.49
1:A:229:LYS:HE3	1:A:233:MET:HE1	1.94	0.49
1:A:229:LYS:HE3	1:A:233:MET:HE3	1.96	0.48
1:B:106:HIS:CE1	1:B:241:PRO:HB2	2.49	0.48
1:B:126:ARG:NE	3:B:479:HOH:O	2.49	0.46
1:A:157:LYS:HE3	1:A:160:ASP:OD2	2.17	0.45
1:B:229:LYS:O	1:B:233:MET:HG3	2.19	0.42
1:A:30:ALA:O	1:A:35:THR:HG23	2.20	0.42
1:A:30:ALA:HA	1:A:34:TRP:HB2	2.03	0.40
1:B:30:ALA:HA	1:B:34:TRP:HB2	2.04	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	274/294 (93%)	264 (96%)	9 (3%)	1 (0%)	39	14
1	B	277/294 (94%)	265 (96%)	11 (4%)	1 (0%)	39	14
All	All	551/588 (94%)	529 (96%)	20 (4%)	2 (0%)	39	14

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	202	SER
1	B	202	SER

### 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	213 / 235 (91%)	212 (100%)	1 (0%)	92	78
1	B	216 / 235 (92%)	213 (99%)	3 (1%)	74	45
All	All	429 / 470 (91%)	425 (99%)	4 (1%)	82	63

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	157	LYS
1	B	25	ASP
1	B	157	LYS
1	B	256	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	213	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	272/294 (92%)	0.37	12 (4%) 38 35	6, 10, 21, 29	0
1	B	273/294 (92%)	0.53	24 (8%) 12 10	5, 10, 25, 36	0
All	All	545/588 (92%)	0.45	36 (6%) 22 19	5, 10, 22, 36	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	22	THR	6.6
1	A	258	GLY	6.5
1	B	28	ALA	6.2
1	B	30	ALA	5.4
1	B	291	LEU	5.1
1	B	31	MET	4.9
1	B	258	GLY	4.1
1	B	23	ILE	4.0
1	B	27	LEU	3.9
1	A	291	LEU	3.4
1	B	24	LYS	3.0
1	B	257	ASP	2.9
1	B	293	LYS	2.8
1	B	290	ALA	2.7
1	B	26	PHE	2.7
1	A	292	GLU	2.7
1	B	25	ASP	2.6
1	B	256	LYS	2.6
1	A	257	ASP	2.6
1	A	293	LYS	2.6
1	B	294	LYS	2.6
1	A	184	TRP	2.4
1	B	212	GLY	2.4
1	B	289	ALA	2.3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	29	VAL	2.3
1	B	200	PHE	2.2
1	B	288	THR	2.2
1	B	55	ILE	2.2
1	A	213	GLN	2.2
1	A	289	ALA	2.1
1	B	192	LYS	2.1
1	A	68	LEU	2.1
1	A	30	ALA	2.1
1	B	292	GLU	2.1
1	A	28	ALA	2.0
1	A	57	VAL	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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	B	297	1/1	1.00	0.11	-0.15	15,15,15,15	0
2	ZN	A	297	1/1	1.00	0.09	-0.48	16,16,16,16	0
2	ZN	A	296	1/1	1.00	0.03	-4.85	7,7,7,7	0
2	ZN	B	295	1/1	1.00	0.03	-5.99	8,8,8,8	0
2	ZN	A	295	1/1	1.00	0.05	-	10,10,10,10	0
2	ZN	B	296	1/1	1.00	0.03	-	9,9,9,9	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.