



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 2, 2021 – 12:06 PM EDT

PDB ID : 6WPX  
Title : Crystal structure of Bacillus licheniformis lipase BIEst2 in propetide form  
Authors : Nakamura, A.M.; Godoy, A.S.; Kadowaki, M.A.S.; Polikarpov, I.  
Deposited on : 2020-04-28  
Resolution : 2.00 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

<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  
Xtriage (Phenix) : 1.13  
EDS : 2.19  
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) : 2.19

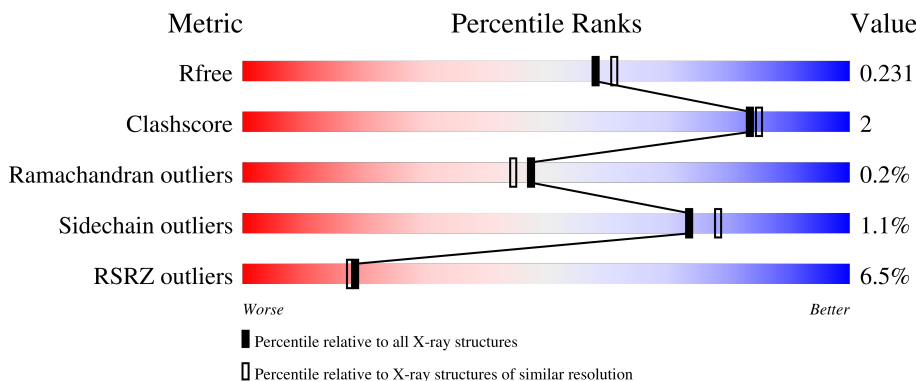
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 of 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	487	
1	B	487	

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
2	IOD	A	505	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7489 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 BIEst2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	450	3504	2233	604	660	7	0	1	0
1	B	451	3519	2243	610	659	7	0	1	0

- Molecule 2 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	13	Total	I	0	0
			13	13		
2	B	11	Total	I	0	0
			11	11		

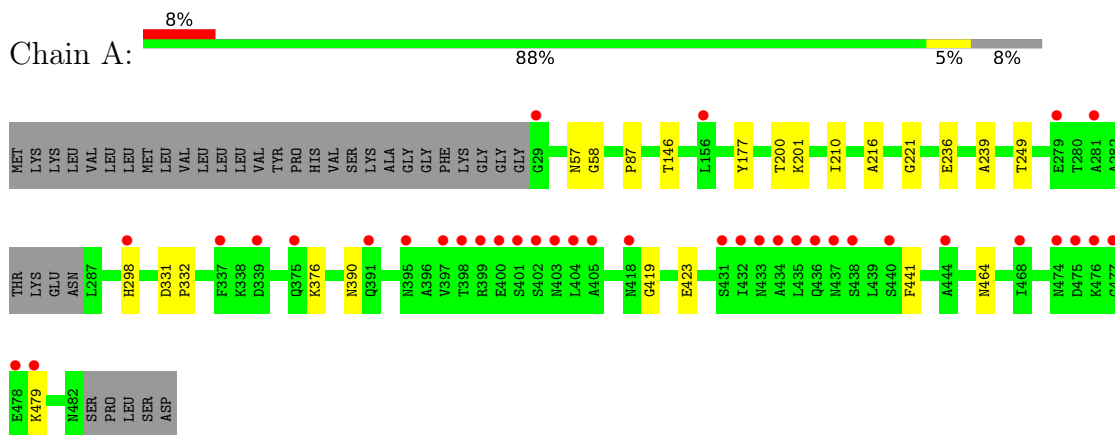
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	213	Total	O	0	0
			213	213		
3	B	229	Total	O	0	0
			229	229		

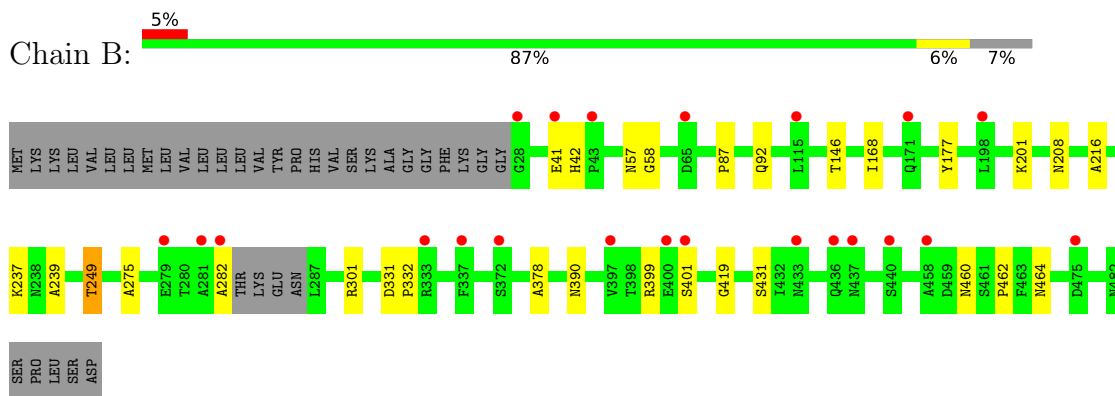
### 3 Residue-property plots [i](#)

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: BIEst2



- Molecule 1: BIEst2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.89Å 78.31Å 166.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.16 – 2.00 29.81 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.16-2.00) 99.6 (29.81-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.67 (at 2.00Å)	Xtrriage
Refinement program	BUSTER 2.10.3	Depositor
R, $R_{free}$	0.196 , 0.228 0.199 , 0.231	Depositor DCC
$R_{free}$ test set	1989 reflections (3.32%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.8	Xtrriage
Anisotropy	0.279	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 48.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7489	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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, 0.333 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: IOD

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	0.52	0/3597	0.67	0/4873
1	B	0.55	0/3612	0.68	0/4889
All	All	0.54	0/7209	0.68	0/9762

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	3504	0	3379	15	0
1	B	3519	0	3413	18	0
2	A	13	0	0	5	0
2	B	11	0	0	4	0
3	A	213	0	0	0	0
3	B	229	0	0	1	0
All	All	7489	0	6792	33	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 (33) 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:390:ASN:HB3	2:A:505:IOD:I	2.35	0.96
1:B:390:ASN:HB3	2:B:502:IOD:I	2.43	0.88
1:B:216:ALA:O	2:B:509:IOD:I	2.73	0.77
1:A:331:ASP:HB2	1:A:332:PRO:CD	2.30	0.61
1:B:41:GLU:HG2	1:B:42:HIS:CD2	2.37	0.59
1:B:41:GLU:HG2	1:B:42:HIS:NE2	2.17	0.58
1:A:216:ALA:O	2:A:511:IOD:I	2.92	0.58
1:B:58:GLY:HA3	2:B:507:IOD:I	2.73	0.58
1:A:390:ASN:CB	2:A:505:IOD:I	3.20	0.55
1:B:146:THR:O	1:B:239:ALA:HA	2.07	0.55
1:B:41:GLU:HG2	1:B:42:HIS:CE1	2.42	0.55
1:A:58:GLY:HA3	2:A:504:IOD:I	2.78	0.54
1:A:146:THR:O	1:A:239:ALA:HA	2.07	0.53
1:B:208:ASN:ND2	1:B:249:THR:HG23	2.23	0.52
1:B:57:ASN:HA	1:B:87:PRO:HB2	1.94	0.50
1:B:208:ASN:HD22	1:B:249:THR:CG2	2.26	0.49
1:B:237:LYS:HE3	1:B:282:ALA:HB3	1.96	0.48
1:A:331:ASP:HB2	1:A:332:PRO:HD2	1.96	0.47
1:A:441:PHE:HB2	1:A:479:LYS:HE3	1.97	0.47
1:B:92:GLN:HA	2:B:508:IOD:I	2.85	0.47
1:A:57:ASN:HA	1:A:87:PRO:HB2	1.97	0.46
1:B:331:ASP:HB2	1:B:332:PRO:CD	2.46	0.46
1:A:177:TYR:CE2	1:A:419:GLY:HA2	2.52	0.45
1:A:331:ASP:CB	1:A:332:PRO:CD	2.94	0.45
1:B:168:ILE:HD11	1:B:378:ALA:HB3	1.99	0.44
1:B:208:ASN:ND2	1:B:249:THR:CG2	2.80	0.44
1:A:423:GLU:HG2	2:A:510:IOD:I	2.89	0.43
1:B:177:TYR:CE2	1:B:419:GLY:HA2	2.54	0.43
1:B:201:LYS:HE2	1:B:275:ALA:O	2.19	0.42
1:A:298:HIS:CD2	1:A:376:LYS:HG3	2.55	0.42
1:A:236:GLU:HG3	1:A:249:THR:OG1	2.20	0.41
1:B:462:PRO:HD2	3:B:620:HOH:O	2.20	0.41
1:A:210:ILE:HB	1:A:221:GLY:HA3	2.04	0.40

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	447/487 (92%)	439 (98%)	8 (2%)	0	100	100
1	B	448/487 (92%)	436 (97%)	10 (2%)	2 (0%)	34	30
All	All	895/974 (92%)	875 (98%)	18 (2%)	2 (0%)	47	44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	401	SER
1	B	399	ARG

### 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	365/400 (91%)	362 (99%)	3 (1%)	81	86
1	B	367/400 (92%)	362 (99%)	5 (1%)	67	72
All	All	732/800 (92%)	724 (99%)	8 (1%)	73	78

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	200	THR
1	A	201	LYS
1	A	464	ASN
1	B	249	THR

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	301	ARG
1	B	431	SER
1	B	460	ASN
1	B	464	ASN

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

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 24 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 [i](#)

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	450/487 (92%)	0.32	37 (8%) <b>11</b> <b>11</b>	12, 28, 58, 78	0
1	B	451/487 (92%)	0.28	22 (4%) <b>29</b> <b>28</b>	11, 24, 50, 75	0
All	All	901/974 (92%)	0.30	59 (6%) <b>18</b> <b>18</b>	11, 26, 54, 78	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	401	SER	6.9
1	A	401	SER	6.0
1	A	432	ILE	5.6
1	A	399	ARG	5.5
1	A	431	SER	5.4
1	A	435	LEU	5.4
1	B	28	GLY	5.3
1	B	281	ALA	5.3
1	A	437	ASN	4.8
1	A	433	ASN	4.8
1	B	437	ASN	4.5
1	B	171	GLN	4.2
1	A	400	GLU	4.0
1	A	438	SER	3.9
1	B	337	PHE	3.9
1	A	404	LEU	3.8
1	A	434	ALA	3.5
1	B	333	ARG	3.4
1	B	433	ASN	3.3
1	A	398	THR	3.3
1	A	440	SER	3.2
1	B	198	LEU	3.2
1	B	41	GLU	3.2
1	A	436	GLN	3.2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	475	ASP	3.1
1	A	476	LYS	3.1
1	A	29	GLY	3.1
1	A	418	ASN	3.0
1	B	43	PRO	2.9
1	B	282	ALA	2.9
1	A	397	VAL	2.9
1	A	403	ASN	2.9
1	A	337	PHE	2.8
1	A	339	ASP	2.8
1	A	156	LEU	2.8
1	B	436	GLN	2.8
1	A	405	ALA	2.7
1	A	281	ALA	2.7
1	B	400	GLU	2.7
1	A	402	SER	2.6
1	B	440	SER	2.4
1	A	444	ALA	2.4
1	B	475	ASP	2.3
1	B	279	GLU	2.3
1	B	372	SER	2.3
1	A	468	ILE	2.3
1	B	115	LEU	2.3
1	A	474	ASN	2.3
1	A	479	LYS	2.2
1	B	397	VAL	2.2
1	A	395	ASN	2.2
1	A	477	GLY	2.2
1	A	279	GLU	2.2
1	A	478	GLU	2.2
1	A	375	GLN	2.1
1	B	458	ALA	2.0
1	A	391	GLN	2.0
1	A	298	HIS	2.0
1	B	65	ASP	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 monosaccharides 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(Å <sup>2</sup> )	Q<0.9
2	IOD	A	505	1/1	0.92	0.13	57,57,57,57	0
2	IOD	A	513	1/1	0.92	0.10	68,68,68,68	0
2	IOD	A	510	1/1	0.94	0.15	71,71,71,71	0
2	IOD	B	509	1/1	0.95	0.16	67,67,67,67	0
2	IOD	B	511	1/1	0.95	0.21	67,67,67,67	0
2	IOD	A	507	1/1	0.96	0.15	64,64,64,64	0
2	IOD	A	511	1/1	0.97	0.13	55,55,55,55	0
2	IOD	A	512	1/1	0.97	0.12	72,72,72,72	0
2	IOD	A	504	1/1	0.97	0.16	57,57,57,57	0
2	IOD	B	504	1/1	0.97	0.07	52,52,52,52	0
2	IOD	B	505	1/1	0.97	0.10	55,55,55,55	0
2	IOD	B	506	1/1	0.97	0.10	58,58,58,58	0
2	IOD	A	508	1/1	0.97	0.11	54,54,54,54	0
2	IOD	A	502	1/1	0.97	0.10	45,45,45,45	0
2	IOD	B	501	1/1	0.98	0.07	45,45,45,45	0
2	IOD	B	507	1/1	0.98	0.14	50,50,50,50	0
2	IOD	A	506	1/1	0.98	0.13	56,56,56,56	0
2	IOD	B	510	1/1	0.98	0.17	66,66,66,66	0
2	IOD	A	509	1/1	0.98	0.21	72,72,72,72	0
2	IOD	B	503	1/1	0.99	0.11	46,46,46,46	0
2	IOD	B	508	1/1	0.99	0.09	47,47,47,47	0
2	IOD	A	503	1/1	0.99	0.17	49,49,49,49	0
2	IOD	A	501	1/1	0.99	0.07	48,48,48,48	0
2	IOD	B	502	1/1	0.99	0.07	47,47,47,47	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.