



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:38 PM UTC

PDB ID : 6MS2 / pdb_00006ms2
Title : Crystal structure of the GH43 BIXynB protein from Bacillus licheniformis
Authors : Zanphorlin, L.M.; Morais, M.A.B.; Diogo, J.A.; Murakami, M.T.
Deposited on : 2018-10-16
Resolution : 2.49 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 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
Xtrriage (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

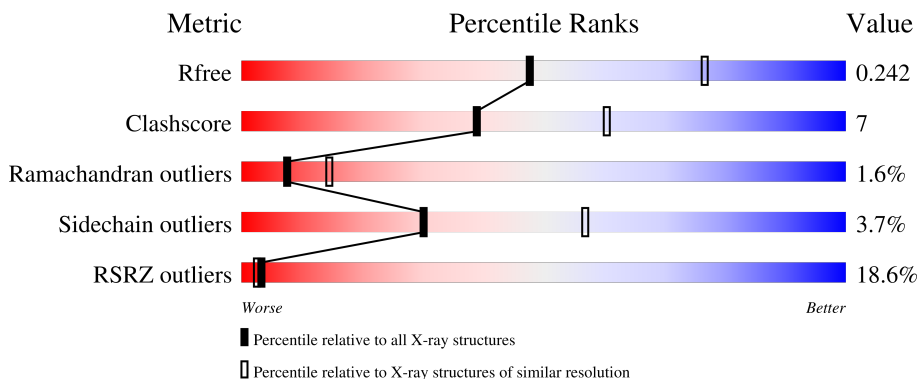
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	538	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4132 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 Glycoside Hydrolase Family 43.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	511	4073	2590	706	765	12	0	0	0

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	initiating methionine	UNP Q65MB6
A	-21	GLY	-	expression tag	UNP Q65MB6
A	-20	SER	-	expression tag	UNP Q65MB6
A	-19	SER	-	expression tag	UNP Q65MB6
A	-18	HIS	-	expression tag	UNP Q65MB6
A	-17	HIS	-	expression tag	UNP Q65MB6
A	-16	HIS	-	expression tag	UNP Q65MB6
A	-15	HIS	-	expression tag	UNP Q65MB6
A	-14	HIS	-	expression tag	UNP Q65MB6
A	-13	HIS	-	expression tag	UNP Q65MB6
A	-12	SER	-	expression tag	UNP Q65MB6
A	-11	SER	-	expression tag	UNP Q65MB6
A	-10	GLY	-	expression tag	UNP Q65MB6
A	-9	LEU	-	expression tag	UNP Q65MB6
A	-8	VAL	-	expression tag	UNP Q65MB6
A	-7	PRO	-	expression tag	UNP Q65MB6
A	-6	ARG	-	expression tag	UNP Q65MB6
A	-5	GLY	-	expression tag	UNP Q65MB6
A	-4	SER	-	expression tag	UNP Q65MB6
A	-3	HIS	-	expression tag	UNP Q65MB6
A	-2	MET	-	expression tag	UNP Q65MB6
A	-1	ALA	-	expression tag	UNP Q65MB6
A	0	SER	-	expression tag	UNP Q65MB6

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	58	Total O 58 58	0	0

4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	152.86Å 41.90Å 71.81Å 90.00° 91.70° 90.00°	Depositor
Resolution (Å)	33.31 – 2.49 33.31 – 2.49	Depositor EDS
% Data completeness (in resolution range)	87.8 (33.31-2.49) 77.9 (33.31-2.49)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.06 (at 2.48Å)	Xtrriage
Refinement program	PHENIX 1.10_2148	Depositor
R, R_{free}	0.197 , 0.242 0.198 , 0.242	Depositor DCC
R_{free} test set	1604 reflections (9.89%)	wwPDB-VP
Wilson B-factor (Å ²)	24.5	Xtrriage
Anisotropy	0.544	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.055 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	4132	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.59% 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: CA

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	0.14	0/4200	0.47	4/5712 (0.1%)

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	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	162	GLU	N-CA-C	11.06	124.71	111.33
1	A	162	GLU	CA-C-N	9.14	138.15	121.70
1	A	162	GLU	C-N-CA	9.14	138.15	121.70
1	A	162	GLU	CA-C-O	-5.36	114.84	120.63

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	178	THR	Peptide

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	4073	0	3863	54	0
2	A	1	0	0	0	0
3	A	58	0	0	0	0
All	All	4132	0	3863	54	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 7.

All (54) 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:446:ILE:HG13	1:A:451:ARG:HG2	1.72	0.70
1:A:65:LEU:HD12	1:A:66:ASP:H	1.60	0.67
1:A:499:SER:O	1:A:501:ARG:N	2.27	0.65
1:A:45:HIS:HB2	1:A:55:ILE:HD13	1.79	0.65
1:A:161:ASN:HD21	1:A:165:THR:HG22	1.66	0.61
1:A:167:ILE:HG22	1:A:169:GLY:H	1.66	0.61
1:A:33:SER:HB3	1:A:78:ALA:H	1.65	0.60
1:A:214:ARG:NH1	1:A:287:ASP:O	2.30	0.59
1:A:371:GLU:OE1	1:A:451:ARG:NH2	2.36	0.59
1:A:162:GLU:N	1:A:163:GLU:HB3	2.19	0.58
1:A:116:SER:HB2	1:A:123:TYR:HA	1.87	0.56
1:A:181:ARG:HD2	1:A:181:ARG:H	1.71	0.56
1:A:161:ASN:C	1:A:163:GLU:HB3	2.30	0.56
1:A:361:ILE:HD12	1:A:401:THR:HG21	1.88	0.56
1:A:131:GLU:OE2	1:A:133:SER:OG	2.25	0.55
1:A:204:THR:O	1:A:242:ARG:NH2	2.39	0.54
1:A:287:ASP:OD1	1:A:287:ASP:N	2.37	0.54
1:A:10:PRO:HG2	1:A:13:THR:HG22	1.89	0.53
1:A:63:GLU:HB3	1:A:125:LYS:HA	1.92	0.52
1:A:22:ILE:HG21	1:A:82:SER:HA	1.91	0.52
1:A:88:PHE:CZ	1:A:119:PRO:HG3	2.47	0.49
1:A:114:ILE:HB	1:A:123:TYR:HB3	1.95	0.48
1:A:261:LEU:HD13	1:A:275:ARG:HD2	1.95	0.48
1:A:46:SER:HB2	1:A:52:TRP:CD2	2.49	0.48
1:A:256:TRP:CD1	1:A:284:TRP:HE1	2.31	0.48
1:A:21:ILE:H	1:A:247:LYS:HD3	1.79	0.47
1:A:360:ASP:OD2	1:A:361:ILE:N	2.48	0.47
1:A:187:HIS:HB2	1:A:198:ILE:HB	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:ASP:OD1	1:A:321:ASP:N	2.45	0.47
1:A:101:VAL:HA	1:A:105:ARG:O	2.15	0.46
1:A:137:PRO:HA	1:A:150:LEU:O	2.16	0.46
1:A:256:TRP:CG	1:A:284:TRP:HE1	2.34	0.46
1:A:176:GLU:OE2	1:A:176:GLU:N	2.38	0.45
1:A:337:HIS:HA	1:A:340:TRP:CD1	2.52	0.45
1:A:172:VAL:HG11	1:A:219:TYR:CE1	2.52	0.44
1:A:14:GLY:HA2	1:A:273:VAL:HG13	1.99	0.44
1:A:322:GLU:H	1:A:322:GLU:CD	2.24	0.44
1:A:63:GLU:HB3	1:A:126:PRO:HD3	2.00	0.43
1:A:77:TRP:C	1:A:77:TRP:CD1	2.96	0.43
1:A:341:SER:HG	1:A:344:GLU:HG3	1.83	0.43
1:A:496:ASN:O	1:A:498:GLY:HA3	2.17	0.43
1:A:61:GLU:OE2	1:A:337:HIS:NE2	2.44	0.43
1:A:206:TYR:CE2	1:A:242:ARG:HD3	2.55	0.42
1:A:142:ASP:HB3	1:A:144:ASP:OD1	2.19	0.42
1:A:497:GLY:HA3	1:A:498:GLY:HA3	1.68	0.42
1:A:15:PHE:HB3	1:A:370:ARG:HG2	2.01	0.42
1:A:386:PRO:HB2	1:A:411:TYR:HB2	2.02	0.42
1:A:356:TRP:HB2	1:A:363:ALA:HA	2.02	0.41
1:A:181:ARG:HD2	1:A:181:ARG:N	2.33	0.41
1:A:194:TYR:CE1	1:A:214:ARG:HD3	2.56	0.40
1:A:134:GLY:HA3	1:A:152:SER:O	2.21	0.40
1:A:441:PHE:HB2	1:A:456:SER:HB3	2.03	0.40
1:A:40:ALA:HB3	1:A:59:ILE:HB	2.02	0.40
1:A:65:LEU:HD12	1:A:66:ASP:N	2.33	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	509/538 (95%)	480 (94%)	21 (4%)	8 (2%)	7 14

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	163	GLU
1	A	15	PHE
1	A	64	GLY
1	A	103	ASN
1	A	500	GLY
1	A	170	GLU
1	A	41	ILE
1	A	180	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	432/454 (95%)	416 (96%)	16 (4%)	30 57

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	SER
1	A	66	ASP
1	A	102	ILE
1	A	115	LYS
1	A	133	SER
1	A	162	GLU
1	A	165	THR
1	A	181	ARG
1	A	214	ARG
1	A	273	VAL
1	A	287	ASP
1	A	315	LYS
1	A	321	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	325	LEU
1	A	327	LEU
1	A	361	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	ASN
1	A	71	ASN
1	A	359	HIS
1	A	427	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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 [i](#)

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, 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	511/538 (94%)	1.26	95 (18%) 3 2	20, 37, 61, 83	8 (1%)

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	162	GLU	5.5
1	A	193	GLY	4.1
1	A	77	TRP	4.1
1	A	181	ARG	4.0
1	A	64	GLY	3.7
1	A	222	TYR	3.7
1	A	500	GLY	3.7
1	A	206	TYR	3.6
1	A	205	GLY	3.6
1	A	324	THR	3.5
1	A	158	PHE	3.5
1	A	161	ASN	3.4
1	A	284	TRP	3.4
1	A	361	ILE	3.2
1	A	393	ALA	3.2
1	A	163	GLU	3.1
1	A	176	GLU	3.1
1	A	267	GLN	3.0
1	A	221	PRO	2.9
1	A	387	SER	2.9
1	A	154	ALA	2.8
1	A	167	ILE	2.8
1	A	191	LYS	2.8
1	A	216	THR	2.8
1	A	104	GLY	2.8
1	A	290	PHE	2.8
1	A	84	HIS	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	165	THR	2.7
1	A	207	SER	2.6
1	A	60	THR	2.6
1	A	204	THR	2.6
1	A	227	TYR	2.6
1	A	219	TYR	2.6
1	A	287	ASP	2.5
1	A	175	TRP	2.5
1	A	286	ASP	2.5
1	A	156	THR	2.5
1	A	171	PRO	2.5
1	A	498	GLY	2.5
1	A	172	VAL	2.4
1	A	210	ILE	2.4
1	A	410	ILE	2.4
1	A	325	LEU	2.4
1	A	182	ALA	2.4
1	A	223	GLU	2.4
1	A	487	GLY	2.4
1	A	65	LEU	2.4
1	A	67	LEU	2.3
1	A	237	ASP	2.3
1	A	63	GLU	2.3
1	A	356	TRP	2.3
1	A	438	GLY	2.3
1	A	78	ALA	2.3
1	A	309	GLN	2.3
1	A	313	ASP	2.3
1	A	323	ASP	2.3
1	A	317	PHE	2.3
1	A	502	LYS	2.3
1	A	439	PRO	2.3
1	A	117	SER	2.2
1	A	300	LEU	2.2
1	A	434	HIS	2.2
1	A	76	ILE	2.2
1	A	505	ALA	2.2
1	A	75	GLY	2.2
1	A	177	GLY	2.2
1	A	288	GLY	2.2
1	A	105	ARG	2.2
1	A	494	ALA	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	169	GLY	2.2
1	A	349	LEU	2.2
1	A	303	ARG	2.2
1	A	5	HIS	2.1
1	A	194	TYR	2.1
1	A	74	HIS	2.1
1	A	62	ASN	2.1
1	A	100	THR	2.1
1	A	180	ARG	2.1
1	A	386	PRO	2.1
1	A	38	PHE	2.1
1	A	289	TRP	2.1
1	A	188	LEU	2.1
1	A	511	ARG	2.1
1	A	314	GLU	2.1
1	A	138	SER	2.1
1	A	244	GLY	2.1
1	A	501	ARG	2.1
1	A	195	TYR	2.1
1	A	179	GLY	2.0
1	A	268	GLY	2.0
1	A	159	PRO	2.0
1	A	346	PRO	2.0
1	A	155	CYS	2.0
1	A	302	GLN	2.0
1	A	427	GLN	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 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(\AA^2)	Q<0.9
2	CA	A	601	1/1	0.83	0.13	73,73,73,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.