

Strain identifier

BacDive ID: 598 **DOI:** 10.13145/bacdive598.20191129.4.1
Type strain: yes **Designation:** F Fukumoto strain F
Culture col. no.: DSM 7, ATCC 23350, CCUG 28519, NRRL B-14393

Sections

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Name and taxonomic classification

Ref.: 2015	Domain	Bacteria
Ref.: 2015	Phylum	Firmicutes
Ref.: 2015	Class	Bacilli
Ref.: 2015	Order	Bacillales
Ref.: 2015	Family	Bacillaceae
Ref.: 2015	Genus	Bacillus
Ref.: 2015	Species	<i>Bacillus amyloliquefaciens</i>
Ref.: 2015	Full Scientific Name	<i>Bacillus amyloliquefaciens</i> subsp. <i>amyloliquefaciens</i> Borris (ex Fukumoto 1943) Priest et al. 1987
Ref.: 2015	Designation:	F Fukumoto strain F
Ref.: 2015	Type strain:	yes

Prokaryotic Nomenclature Up-to-date (PNU)

Ref.: 20215	Domain	Bacteria
Ref.: 20215	Phylum	Firmicutes
Ref.: 20215	Class	Bacilli
Ref.: 20215	Literature reference	Int. J. Syst. Bacteriol. 38:220
Ref.: 20215	Family	Bacillaceae
Ref.: 20215	Literature reference	Int. J. Syst. Bacteriol. 30:225
Ref.: 20215	Genus	Bacillus

Ref.: 20215	Taxonomical status	genus (AL)
Ref.: 20215	Literature reference	Int. J. Syst. Bacteriol. 30:225
Ref.: 20215	Species	Bacillus amyloliquefaciens
Ref.: 20215	Taxonomical status	sp. nov. (VP)
Ref.: 20215	Literature reference	Int. J. Syst. Bacteriol. 37:69*
Ref.: 20215	Full Scientific Name	Bacillus amyloliquefaciens (ex Fukumoto 1943) Priest et al. 1987 emend. Wang et al. 2008
Ref.: 20215	Synonym	Bacillus amyloliquefaciens subsp. amyloliquefaciens

Morphology and physiology

Ref.: 24474	Gram stain	positive
Ref.: 24474	Cell length	1.8-3.0 µm
Ref.: 24474	Cell width	0.7-0.9 µm
Ref.: 24474	Cell shape	rod-shaped
Ref.: 24474	Motility	yes
Ref.: 24474	Flagellum arrangement	peritrichous
Ref.: 24474	Cultivation medium used	medium of Gordon et al.

Ref.: 2015	Name of produced compound	alpha amylase
Ref.: 2015	Name of produced compound	1 desoxynojirimycin
Ref.: 2015	Name of produced compound	inhibitors for glycoside hydrolases
Ref.: 2015	Name of produced compound	restriction endonuclease <i>BamFI</i> (<i>BamHI</i>)
Ref.: 24474	Name of produced compound	Acetoin

Ref.: 24474	Enzymes	<table border="1"> <thead> <tr> <th>Enzyme</th> <th>Enzyme activity</th> <th>EC number</th> </tr> </thead> <tbody> <tr> <td>arginine dihydrolase</td> <td>-</td> <td>3.5.3.6</td> </tr> </tbody> </table>			Enzyme	Enzyme activity	EC number	arginine dihydrolase	-	3.5.3.6
		Enzyme	Enzyme activity	EC number						
arginine dihydrolase	-	3.5.3.6								

Ref.: 24474 Ref.: 24474	Halophily	<table border="1"> <thead> <tr> <th>Salt</th> <th>Tested relation</th> <th>Salt conc.</th> </tr> </thead> <tbody> <tr> <td>NaCl</td> <td>growth</td> <td>5 %(w/v)</td> </tr> <tr> <td>NaCl</td> <td>growth</td> <td>10 %</td> </tr> </tbody> </table>			Salt	Tested relation	Salt conc.	NaCl	growth	5 %(w/v)	NaCl	growth	10 %
		Salt	Tested relation	Salt conc.									
		NaCl	growth	5 %(w/v)									
NaCl	growth	10 %											

Metabolite production	<table border="1"> <thead> <tr> <th>Chebi ID</th> <th>Metabolite</th> <th>Production</th> </tr> </thead> <tbody> <tr> <td> </td> <td> </td> <td> </td> </tr> </tbody> </table>			Chebi ID	Metabolite	Production			
	Chebi ID	Metabolite	Production						

Ref.: 24474

15688	Acetoin	yes
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Physiological tests

Ref.: 24474

Chebi ID	Metabolite	Voges-Proskauer-test
15688	Acetoin	+

Metabolite utilization

Ref.: 24474

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Chebi ID	Metabolite	Utilization activity	Kind of utilization tested
15688	Acetoin	+	other
16708	Adenine	-	other
16708	Adenine	-	degradation
15676	Allantoin	-	hydrolysis
17925	alpha-D-Glucose	+	builds acid from
17716	alpha-D-Lactose	+	builds acid from
18305	Arbutin	+	hydrolysis
85146	Carboxymethylcellulose	-	degradation
	Casein	+	other
	Casein	+	degradation
17057	Cellobiose	+	builds acid from
62968	Cellulose	-	other
30769	Citric acid	+	growth
30769	Citric acid	+	carbon source
16991	DNA	+/-	degradation
4767	Elastin	+	other
4767	Elastin	+	degradation
4853	Esculin	+	hydrolysis
28757	Fructose	+	builds acid from
5291	Gelatin	+	other
17234	Glucose	+	builds acid from
17754	Glycerol	+	builds acid from
16235	Guanine	-	other
16235	Guanine	-	degradation
17368	Hypoxanthine	-	other
17368	Hypoxanthine	-	degradation
17716	Lactose	+	builds acid from
17306	Maltose	+	builds acid from
29864	Mannitol	+	builds acid from
37684	Mannose	+	builds acid from

Ref.: 24474	17632	Nitrate	+	reduction
Ref.: 24474	17309	Pectin	-	degradation
Ref.: 24474	16634	Raffinose	+	builds acid from
Ref.: 24474	17814	Salicin	+	builds acid from
Ref.: 24474	30911	Sorbitol	+	builds acid from
Ref.: 24474	28017	Starch	+	other
Ref.: 24474	28017	Starch	+	degradation
Ref.: 24474	17992	Sucrose	+	builds acid from
Ref.: 24474	17347	Testosterone	-	other
Ref.: 24474	17347	Testosterone	-	degradation
Ref.: 24474	27082	Trehalose	+	builds acid from
Ref.: 24474	35020	Tributyryn	+	other
Ref.: 24474	35020	Tributyryn	+	degradation
Ref.: 24474	53424	Tween 20	+	other
Ref.: 24474	53424	Tween 20	+	degradation
Ref.: 24474	53423	Tween 40	+	other
Ref.: 24474	53423	Tween 40	+	degradation
Ref.: 24474	53425	Tween 60	+	other
Ref.: 24474	53425	Tween 60	+	degradation
Ref.: 24474	18186	Tyrosine	-	other
Ref.: 24474	18186	Tyrosine	-	degradation
Ref.: 24474	16199	Urea	-	other
Ref.: 24474	16199	Urea	-	hydrolysis
Ref.: 24474	15318	Xanthine	-	other
Ref.: 24474	15318	Xanthine	-	degradation

Ref.: 24474	Spore description	central or paracentral
Ref.: 24474	Type of spore	spore
Ref.: 24474	Ability of spore formation	yes

Culture and growth conditions

Ref.: 24474	Culture medium	medium of Gordon et al.
Ref.: 24474	Culture medium growth	yes
Ref.: 35323	Culture medium	MEDIUM 3 - Columbia agar
Ref.: 35323	Culture medium growth	yes

Ref.: 35323	Culture medium composition	Columbia agar (39.000 g);distilled water (1000.000 ml)
Ref.: 2015	Culture medium	NUTRIENT AGAR (DSMZ Medium 1), 30°C
Ref.: 2015	Culture medium growth	yes
Ref.: 2015	Culture medium link	https://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium1.pdf

	Temperatures	
Ref.: 24474		
Ref.: 24474		
Ref.: 24474		
Ref.: 2015		
Ref.: 35323		

Kind of temperature	Temperature
growth	<15 °C
growth	>50 °C
optimum	30-40 °C
growth	30 °C
growth	30 °C

Ref.: 24474	Temperature range	psychrophilic
Ref.: 24474	Temperature range	thermophilic
Ref.: 2015	Temperature range	mesophilic
Ref.: 35323	Temperature range	mesophilic

Isolation, sampling and environmental information

Ref.: 24474	Sample type/isolated from	soil and industrial amylase fermentations
Ref.: 49266	Sample type/isolated from	Soil
Ref.: 2015	Sample type/isolated from	soil

Isolation sources categories	Cat1	Cat2	Cat3
	#Engineered	#Industrial	#Industrial production
	#Environmental	#Terrestrial	#Soil

Application and interaction

Ref.: 2015	Biosafety level	1 Risk group (German classification)
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Molecular biology



Bacillus amyloliquefaciens

Ref.: 24474 **GC-content** 44.6 mol%
Ref.: 2015 **GC-content** 46.2 mol% thermal denaturation, midpoint method (Tm)
Ref.: 2015 **GC-content** 44.5 mol% Buoyant density centrifugation (BD)

	Sequence database	Sequence accession description	Sequence accession number	Sequence length(bp)	Associated NCBI tax ID	
Ref.: 20218	Marker Gene (GenBank Direct submission)	Bacillus amyloliquefaciens replication terminator protein (rtp) gene, complete cds	AF045057	479	692420	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Bacillus amyloliquefaciens clone BamyloDH3R 16S ribosomal RNA gene, partial sequence; 16S-23S internal transcribed spacer, complete sequence; and 23S ribosomal RNA gene, partial sequence	AF478077	408	692420	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Bacillus amyloliquefaciens clone DH-19 16S ribosomal RNA gene, partial sequence; 16S-23S internal transcribed spacer, complete sequence; and 23S ribosomal RNA gene, partial sequence	AF478078	466	692420	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Bacillus amyloliquefaciens clone DH-11-1 16S ribosomal RNA gene, partial sequence; 16S-23S internal transcribed spacer, complete sequence; tRNA-Ile and tRNA-Ala genes, complete sequence; and 23S ribosomal RNA gene, partial sequence	AF478079	584	692420	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Bacillus amyloliquefaciens strain DSM7 (F) 16S ribosomal RNA gene, partial sequence	AY055225	500	692420	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Bacillus amyloliquefaciens strain DSMZ 7 histidine kinase (cheA) gene, partial cds	AY212964	591	692420	*
Ref.: 20218	INSDC Sequence	Neutral protease gene of B.amyloliquefaciens and its early region	E00450	954	1390	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Bacillus amyloliquefaciens strain DSM 7 small acid-soluble spore protein gamma-type (sspE) gene, complete cds	EF433927	189	692420	*

Ref.: 20218	Marker Gene (EMBL Direct submission)	TPA: Bacillus amyloliquefaciens DSM 7 transfer-messenger mRNA Bacil_amylo_7, single chain mature transcript	HG781813	363	692420	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Bacillus amyloliquefaciens strain MPA 1034 16S ribosomal RNA gene, partial sequence	HQ231913	1448	1390	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Bacillus amyloliquefaciens DSM 7 strain ATCC 23350 surfactin (srfA) gene, partial cds	JF279530	220	692420	*
Ref.: 20218	Marker Gene (GenBank Direct submission)	Zhouia sp. DSM7 16S ribosomal RNA gene, partial sequence	KC439236	910	1343290	*
Ref.: 20218	INSDC Sequence	B.amyloliquefaciens neutral protease gene, complete cds	M36723	1888	1390	*
Ref.: 20218	Marker Gene (EMBL Direct submission)	B.amyloliquefaciens 16S ribosomal RNA	X60605	1427	692420	*
Ref.: 2015	complete genome, Marker Gene (EMBL Direct submission)	Bacillus amyloliquefaciens DSM7 complete genome	FN597644	3980199	692420	
Ref.: 2015	16S rRNA gene, Marker Gene (DDBJ Direct submission)	Bacillus amyloliquefaciens gene for 16S rRNA, partial sequence	AB006920	274	692420	

Strain availability

Ref.: 2015 **Culture collection no.** DSM 7, ATCC 23350, CCUG 28519, NRRL B-14393

Ref.: 2015 **Strain history** <- ATCC <- L.L. Campbell, F (*Bacillus subtilis*)

Associated Passport(s) in StrainInfo

Ref.: 20218 4420 - <http://www.straininfo.net/strains/4420>

Ref.: 20218 4417 - <http://www.straininfo.net/strains/4417>

References

Ref.: 2015 Leibniz Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH; Curators of the DSMZ; DSM 7

- [Ref.: 20215](#) D.Gleim, M.Kracht, N.Weiss et. al.: Prokaryotic Nomenclature Up-to-date - compilation of all names of Bacteria and Archaea, validly published according to the Bacteriological Code since 1. Jan. 1980, and validly published nomenclatural changes since.
- [Ref.: 20218](#) Verslyppe, B., De Smet, W., De Baets, B., De Vos, P., Dawyndt P. StrainInfo introduces electronic passports for microorganisms.. Syst Appl Microbiol. 37: 42-50 2014 (10.1016/j.syapm.2013.11.002, 24321274)
- [Ref.: 24474](#) F. G. Priest, M. Goodfellow, L. A. Shute, R. C. W. Berkeley *Bacillus amyloliquefaciens* sp. nov., nom. rev.. IJSEM 37: 69-71 1987 (10.1099/00207713-37-1-69, None)
- [Ref.: 35323](#) None; Curators of the CIP; None
- [Ref.: 49266](#) Culture Collection University of Gothenburg (CCUG); Curators of the CCUG; CCUG 28519

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