



## Strain identifier

**BacDive ID:** 24180      **DOI:** 10.13145/bacdive24180.20191129.4.1  
**Type strain:** yes      **Designation:** PG04  
**Culture col. no.:** DSM 25481, ACCC 05759

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## Name and taxonomic classification

<a href="#">Ref.: 21207</a>	<b>Domain</b>	Bacteria
<a href="#">Ref.: 21207</a>	<b>Phylum</b>	Proteobacteria
<a href="#">Ref.: 21207</a>	<b>Class</b>	Alphaproteobacteria
<a href="#">Ref.: 21207</a>	<b>Order</b>	Rhizobiales
<a href="#">Ref.: 21207</a>	<b>Family</b>	Methylocystaceae
<a href="#">Ref.: 21207</a>	<b>Genus</b>	Hansschlegelia
<a href="#">Ref.: 21207</a>	<b>Species</b>	Hansschlegelia beijingensis
<a href="#">Ref.: 21207</a>	<b>Full Scientific Name</b>	Hansschlegelia beijingensis Zou et al. 2013
<a href="#">Ref.: 21207</a>	<b>Designation:</b>	PG04
<a href="#">Ref.: 21207</a>	<b>Type strain:</b>	yes

### **Prokaryotic Nomenclature Up-to-date (PNU)**

<a href="#">Ref.: 20215</a>	<b>Domain</b>	Bacteria
<a href="#">Ref.: 20215</a>	<b>Phylum</b>	Proteobacteria
<a href="#">Ref.: 20215</a>	<b>Class</b>	Alphaproteobacteria
<a href="#">Ref.: 20215</a>	Literature reference	Int. J. Syst. Evol. Microbiol. 56:1
<a href="#">Ref.: 20215</a>	<b>Family</b>	Methylocystaceae
<a href="#">Ref.: 20215</a>	Literature reference	Int. J. Syst. Evol. Microbiol. 56:1
<a href="#">Ref.: 20215</a>	<b>Genus</b>	Hansschlegelia

Ref.: 20215	Taxonomical status	gen. nov. (VL)
Ref.: 20215	Literature reference	Int. J. Syst. Evol. Microbiol. 60:1009
Ref.: 20215	<b>Species</b>	Hansschlegelia beijingensis
Ref.: 20215	Taxonomical status	sp. nov. (VP)
Ref.: 20215	Literature reference	Int. J. Syst. Evol. Microbiol. 63:3715*
Ref.: 20215	<b>Full Scientific Name</b>	Hansschlegelia beijingensis Zou et al. 2013

### Morphology and physiology

Ref.: 31108	<b>Gram stain</b>	negative
Ref.: 31108	<b>Cell length</b>	1.15 µm
Ref.: 31108	<b>Cell width</b>	0.7 µm
Ref.: 31108	<b>Cell shape</b>	rod-shaped

Enzymes	Enzyme	Enzyme activity	EC number
Ref.: 31108	acid phosphatase	+	3.1.3.2
Ref.: 31108	alkaline phosphatase	+	3.1.3.1
Ref.: 31108	catalase	+	1.11.1.6
Ref.: 31108	cytochrome oxidase	+	1.9.3.1
Ref.: 31108	urease	+	3.5.1.5

Metabolite utilization	Chebi ID	Metabolite	Utilization activity	Kind of utilization tested
Ref.: 31108	30751	Formic acid	+	carbon source
Ref.: 31108	28757	Fructose	+	carbon source
Ref.: 31108	32323	Glucuronamide	+	carbon source
Ref.: 31108	17632	Nitrate	+	reduction

Ref.: 31108	<b>Decomposition/lysis</b>	aggregates in clumps
Ref.: 31108	<b>Oxygen tolerance</b>	aerobe

### Culture and growth conditions

Ref.: 21207	<b>Culture medium</b>	YTC MEDIUM (DSMZ Medium 1384), 28°C
Ref.: 21207	<b>Culture medium growth</b>	yes
Ref.: 21207	<b>Culture medium link</b>	<a href="https://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium1384.pdf">https://www.dsmz.de/microorganisms/medium/pdf/DSMZ_Medium1384.pdf</a>

	<b>Temperatures</b>	<b>Kind of temperature</b>	<b>Temperature</b>	
		Ref.: 21207	growth	28 °C
		Ref.: 31108	growth	25-40 °C
		Ref.: 31108	optimum	30 °C

Ref.: 21207	<b>Temperature range</b>	mesophilic
Ref.: 31108	<b>Temperature range</b>	mesophilic

	<b>pH</b>	<b>Kind of pH</b>	<b>pH</b>	
		Ref.: 31108	growth	6.0-9.0
		Ref.: 31108	optimum	7.5

### Isolation, sampling and environmental information

Ref.: 21207	<b>Sample type/isolated from</b>	rhizosphere soil of watermelon
Ref.: 21207	<b>Geographic location (country and/or sea, region)</b>	Daxing district of Beijing
Ref.: 21207	<b>Country</b>	China
Ref.: 21207	<b>Continent</b>	Asia

<b>Isolation sources categories</b>	<b>Cat1</b>	<b>Cat2</b>	<b>Cat3</b>
	#Environmental	#Terrestrial	#Soil
	#Host	#Plants	#Herbaceous plants (Grass,Crops)
	#Host Body-Site	#Plant	#Rhizosphere

### Application and interaction

Ref.: 21207	<b>Biosafety level</b>	1 Risk group (German classification)
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### Molecular biology

Ref.: 21207	<b>GC-content</b>	64.4 mol% thermal denaturation, midpoint method (Tm)
Ref.: 31108	<b>GC-content</b>	64.4 mol%

	<b>Sequence database</b>	<b>Sequence accession description</b>	<b>Sequence accession number</b>	<b>Sequence length(bp)</b>	<b>Associated NCBI tax ID</b>
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Ref.: 21207	16S rRNA gene, Marker Gene (GenBank Direct submission)	Hanschlegelia beijingensis strain PG04 16S ribosomal RNA gene, partial sequence	JQ034346	1459	1133344
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## Strain availability

Ref.: 21207      **Culture collection no.**      DSM 25481, ACCC 05759

Ref.: 21207      **Strain history**      <- J. L. Gao, Beijing Academy of Agriculture and Forestry Science; PG04 <- X. Zou

### **Associated Passport(s) in StrainInfo**

Ref.: 20218      891274 - <http://www.straininfo.net/strains/891274>

Ref.: 20218      891275 - <http://www.straininfo.net/strains/891275>

## References

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.: 21207      Leibniz Institut DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH; Curators of the DSMZ; DSM 25481

Ref.: 31108      Barberan A, Caceres Velazquez H, Jones S, Fierer N. Hiding in Plain Sight: Mining Bacterial Species Records for Phenotypic Trait Information. mSphere 2: None-None 2017 (10.1128/mSphere.00237-17, None) - **originally annotated from #27437**

Ref.: 27437      IJSEM 3715 2013 (10.1099/ijms.0.052308-0)

**\* These References are textmined**

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