

Close

Print

◀ [ 1 ] ▶

**Record 1 of 1**

**Title:** High quality draft genome sequence of the slightly halophilic bacterium *Halomonas zhanjiangensis* type strain JSM 078169(T) (DSM 21076(T)) from a sea urchin in southern China

**Author(s):** Zhou, Y (Zhou, Yu); Li, R (Li, Rui); Gao, XY (Gao, Xiao-Yang); Lapidus, A (Lapidus, Alla); Han, J (Han, James); Haynes, M (Haynes, Matthew); Lobos, E (Lobos, Elizabeth); Huntemann, M (Huntemann, Marcel); Pati, A (Pati, Amrita); Ivanova, NN (Ivanova, Natalia N.); Rohde, M (Rohde, Manfred); Mavromatis, K (Mavromatis, Konstantinos); Tindall, BJ (Tindall, Brian J.); Markowitz, V (Markowitz, Victor); Woyke, T (Woyke, Tanja); Klenk, HP (Klenk, Hans-Peter); Kyrpides, NC (Kyrpides, Nikos C.); Li, WJ (Li, Wen-Jun)

**Source:** STANDARDS IN GENOMIC SCIENCES **Volume:** 9 **Issue:** 3 **DOI:** 10.4056/sigs.5449586 **Published:** 2014

**Times Cited in Web of Science Core Collection:** 1

**Total Times Cited:** 1

**Usage Count (Last 180 days):** 3

**Usage Count (Since 2013):** 13

**Cited Reference Count:** 60

**Abstract:** *Halomonas zhanjiangensis* Chen et al. 2009 is a member of the genus *Halomonas*, family Halomonadaceae, class Gammaproteobacteria. Representatives of the genus *Halomonas* are a group of halophilic bacteria often isolated from salty environments. The type strain *H. zhanjiangensis* JSM 078169(T) was isolated from a sea urchin (*Hemicentrotus pulcherrimus*) collected from the South China Sea. The genome of strain JSM 078169 T is the fourteenth sequenced genome in the genus *Halomonas* and the fifteenth in the family Halomonadaceae. The other thirteen genomes from the genus *Halomonas* are *H. halocynthiae*, *H. venusta*, *H. alkaliphila*, *H. lutea*, *H. anticariensis*, *H. jeotgali*, *H. titanicae*, *H. desiderata*, *H. smyrnensis*, *H. salifodinae*, *H. boliviensis*, *H. elongata* and *H. stevensii*. Here, we describe the features of strain JSM 078169(T), together with the complete genome sequence and annotation from a culture of DSM 21076(T). The 4,060,520 bp long draft genome consists of 17 scaffolds with the 3,659 protein-coding and 80 RNA genes and is a part of Genomic Encyclopedia of Type Strains, Phase I: the one thousand microbial genomes (KMG) project.

**Accession Number:** WOS:000338995000024

**PubMed ID:** 25197480

**Language:** English

**Document Type:** Article

**Author Keywords:** strictly aerobic; motile Gram-negative; chemoorganotrophic; slightly halophilic; Halomonadaceae

**KeyWords Plus:** STANDARD OPERATING PROCEDURE; ET-AL. 1989; SP NOV.; FAMILY HALOMONADACEAE; EMENDED DESCRIPTION; MICROBIAL GENOMES; FRANZMANN 1996; SOLAR SALTERN; GEN. NOV.; PHYLOGENY

**Addresses:** [Zhou, Yu; Li, Wen-Jun] Yunnan Univ, Key Lab Microbial Divers Southwest China, Minist Educ, Kunming, Peoples R China.

[Zhou, Yu; Li, Wen-Jun] Yunnan Univ, Lab Conservat & Utilizat Bioresources, Yunnan Inst Microbiol, Kunming, Peoples R China.

[Zhou, Yu; Li, Rui] State Key Lab Breeding Base Zhejiang Sustainable, Hangzhou, Zhejiang, Peoples R China.

[Zhou, Yu; Li, Rui] Zhejiang Acad Agr Sci, Inst Qual & Standard Agroprod, Hangzhou, Zhejiang, Peoples R China.

[Gao, Xiao-Yang; Li, Wen-Jun] Chinese Acad Sci, Key Lab Biogeog & Bioresource Arid Land, Xinjiang Inst Ecol & Geog, Urumqi, Peoples R China.

[Gao, Xiao-Yang] Univ Chinese Acad Sci, Beijing, Peoples R China.

[Lapidus, Alla] St Petersburg State Univ, Theodosius Dobzhansky Ctr Genome Bionformat, St Petersburg 199034, Russia.

[Lapidus, Alla] St Petersburg Acad Univ, Algorithm Biol Lab, St Petersburg, Russia.

[Han, James; Haynes, Matthew; Lobos, Elizabeth; Huntemann, Marcel; Pati, Amrita; Ivanova, Natalia N.; Mavromatis, Konstantinos; Woyke, Tanja; Kyrpides, Nikos C.] US DOE, Joint Genome Inst, Walnut Creek, CA USA.

[Rohde, Manfred] HZI Helmholtz Ctr Infect Res, Braunschweig, Germany.

[Tindall, Brian J.; Klenk, Hans-Peter] Leibniz Inst DSMZ German Collect Microorganisms &, Braunschweig, Germany.

[Markowitz, Victor] Univ Calif Berkeley, Lawrence Berkeley Natl Lab, Biol Data Management & Technol Ctr, Berkeley, CA 94720 USA.

[Kyrpides, Nikos C.] King Abdulaziz Univ, Dept Biol Sci, Jeddah 21413, Saudi Arabia.

**Reprint Address:** Li, WJ (reprint author), Yunnan Univ, Key Lab Microbial Divers Southwest China, Minist Educ, Kunming, Peoples R China.

**E-mail Addresses:** hpk@dsMZ.de; wjli@ynu.edu.cn

**Author Identifiers:**

Author	ResearcherID Number	ORCID Number
Kyrpides, Nikos	A-6305-2014	0000-0002-6131-0462
Lapidus, Alla	I-4348-2013	0000-0003-0427-8731
Fac Sci, KAU, Biol Sci Dept	L-4228-2013	
Ivanova, Natalia		0000-0002-5802-9485

**Publisher:** BIOMED CENTRAL LTD

**Publisher Address:** 236 GRAYS INN RD, FLOOR 6, LONDON WC1X 8HL, ENGLAND

**Web of Science Categories:** Genetics & Heredity; Microbiology

**Research Areas:** Genetics & Heredity; Microbiology

**IDS Number:** AL2ZQ

**ISSN:** 1944-3277

**29-char Source Abbrev.:** STAND GENOMIC SCI

**ISO Source Abbrev.:** Stand. Genomic Sci.

**Source Item Page Count:** 14

**Funding:**

Funding Agency	Grant Number
US Department of Energy Office of Science, Biological and Environmental Research Program	
University of California, Lawrence Berkeley National Laboratory	DE-AC02-05CH11231
Lawrence Livermore National Laboratory	DE-AC52-07NA27344
National Basic Research Program of China	2010CB833801
Chinese Academy of Sciences	
Russian Ministry of Science	11.G34.31.0068

The authors gratefully acknowledge the assistance of Susanne Schneider for growing *H. zhanjiangensis* cultures and Evelyne-Marie Brambilla for DNA extraction and quality control (both at the DSMZ). This work was performed under the auspices of the US Department of Energy Office of Science, Biological and Environmental Research Program, and by the University of California, Lawrence Berkeley National Laboratory under contract No. DE-AC02-05CH11231, Lawrence Livermore National Laboratory under Contract No. DE-AC52-07NA27344 Genome analysis was supported by the National Basic Research Program of China (No. 2010CB833801). W-J Li was also supported by 'Hundred Talents Program' of the Chinese Academy of Sciences. A. L. was supported in part by Russian Ministry of Science Mega-grant no. 11.G34.31.0068 (PI. Dr Stephen J O'Brien)

**Open Access:** gold

**Output Date:** 2017-08-01

Close

Print

◀ [ 1 ] ▶

