



# Draft genome sequence of *Thermoactinomyces* sp. Gus2-1 isolated from the hot-spring Gusikha in Bargusín Valley (Baikal Rift Zone, Russia)



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## ABSTRACT

The *Thermoactinomyces* sp. strain Gus2-1 was isolated from hot-spring sediments sample from the hot-spring Gusikha in Bargusín Valley (Baikal Rift Zone, Russia). The sequenced and annotated genome is 2,623,309 bp and encodes 2513 genes. The draft genome sequence of the *Thermoactinomyces* sp. strain Gus2-1 has been deposited at DDBJ/EMBL/GenBank under the accession JPZM01000000 and the sequences could be found at the site <https://www.ncbi.nlm.nih.gov/nucore/JPZM01000000>.

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## Specifications

Organism/cell line/tissue	<i>Thermoactinomyces</i> sp. Gus2-1
Sex	–
Sequencer or array type	Ion PGM™ Template OT2 400 kits
Data format	Processed
Experimental factors	Bacteria
Experimental features	Whole genome sequence of <i>N. lepida</i> , assembly and annotation
Consent	Level of consent allowed for reuse if applicable
Sample source location	The hot-spring Gusikha (60 °C) in Bargusín Valley (Baikal Rift Zone, Russia)

## 1. Direct link to deposited data

<https://www.ncbi.nlm.nih.gov/nucore/JPZM01000000>.

## 2. Introduction

The genus *Thermoactinomyces* is one of the earliest known Actinomycete taxa, and the type species of this genus is *Thermoactinomyces vulgaris* [1]. The members of this genus are aerobic, endospore-forming, Gram-positive bacteria belonging to the order *Bacillales* [2]. They produce endospores that are formed endogenously inside the aerial and substrate hyphae of the bacteria [3]. Currently, researchers are finding new species belonging to this genus [4].

## 3. Strain isolation

The strain Gus2-1 was isolated from sediments sample from the hot-spring Gusikha (60 °C) in Bargusín Valley (Baikal Rift Zone, Russia). *Thermoactinomyces* sp. Gus2-1 culture was cultivated in liquid medium containing 1% trypton, 0.5% yeast extract, and 3.5 M of NaCl. Eight ml of cell culture were pelleted by centrifugation and resuspended in 75 µl of H<sub>2</sub>O by intense pipetting.

## 4. DNA isolation and sequencing

DNA was isolated using the DNA Purification Kit (Fermentas). Ion PGM™ Template OT2 400 and Ion PGM™ Template OT2 400 kits were used to create libraries for genome sequencing. Genome sequencing was performed on an IonTorrent platform (Applied Biosystems) using Ion PGM™ Sequencing 400 Kit in the SBRAS Sequencing Center.

## 5. Genome assembly and annotation

*De novo* assembly of short reads into contigs was performed using MIRA v. 4. Contigs shorter than 1000 bp were deleted. A total of 92 contigs yielded a genome sequence 2,623,309 bp long, and the G + C content is 48.01%. ORF prediction and automatic annotation was performed using NCBI PGAAP ([http://www.ncbi.nlm.nih.gov/genome/annotation\\_prok](http://www.ncbi.nlm.nih.gov/genome/annotation_prok)). The complete genome sequence contained 2513 genes, 2315 CDS, 14 rRNAs (5S, 16S, 23S), 76 tRNAs, one ncRNA.

## 6. Phylogenetic analysis

Phylogenetic analysis was performed using 16S rRNA sequences with the UPGMA algorithm implemented in MEGA v.6. 16S rRNA

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sequences of *Thermoactinomyces* type strains were found using the StrainInfo ([www.straininfo.net](http://www.straininfo.net)) and GenBank ([www.ncbi.nlm.nih.gov/nucleotide](http://www.ncbi.nlm.nih.gov/nucleotide)) databases. According to phylogenetic analysis, the *Thermoactinomyces* sp. strain Gus2-1 is most closely related to *Thermoactinomyces vulgaris*.

### 7. Nucleotide sequence accession numbers

The draft genome sequence for *Thermoactinomyces* sp. strain Gus2-1 has been deposited in DDBJ/EMBL/Genbank under the accession no. JPZM01000000. The 92 contigs have been deposited under accession no. JPZM01000001-JPZM01000092.

### Conflict of interest

The authors declare that there is no conflict of interests with respect to the work published in this paper.

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