## **Resource Summary Report**

Generated by <u>dkNET</u> on May 16, 2025

# **KBase**

RRID:SCR\_022162 Type: Tool

**Proper Citation** 

KBase (RRID:SCR\_022162)

#### **Resource Information**

URL: https://www.kbase.us/

Proper Citation: KBase (RRID:SCR\_022162)

**Description:** Data science platform for predicting and designing biological function. Platform to model plant and microbial physiology and community dynamics. Knowledge creation and discovery environment for biologists and bioinformaticians. Integrates variety of data and analysis tools from US Department of Energy and other public services into platform that leverages scalable computing infrastructure and performs systems biology analyses. Enables scientists to analyze their own data within context of public data and share findings across system.

**Synonyms:** DOE Systems Biology Knowledgebase, Department of Energy Systems Biology Knowledgebase, The Department of Energy Systems Biology Knowledgebase

Resource Type: data or information resource, portal

Defining Citation: DOI:10.1038/nbt.4163

**Keywords:** Energy Systems Biology Knowledgebase, systems biology analyses, model plant and microbial physiology, predicting and designing biological function, data science

**Funding:** U.S. Department of Energy ; Office of Science ; Office of Biological and Environmental Research

Availability: Free, Freely available

Resource Name: KBase

**Resource ID:** SCR\_022162

Record Creation Time: 20220421T050139+0000

Record Last Update: 20250516T054244+0000

### **Ratings and Alerts**

No rating or validation information has been found for KBase.

No alerts have been found for KBase.

### Data and Source Information

Source: SciCrunch Registry

### **Usage and Citation Metrics**

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Campos-Avelar I, et al. (2025) Bacillus cabrialesii subsp. cabrialesii Strain TE5: A Promising Biological Control Bacterium Against the Causal Agent of Spot Blotch in Wheat. Plants (Basel, Switzerland), 14(2).

Price MN, et al. (2024) Interactive tools for functional annotation of bacterial genomes. Database : the journal of biological databases and curation, 2024.

Hossain MS, et al. (2024) Whole genome analysis of 26 bacterial strains reveals aromatic and hydrocarbon degrading enzymes from diverse environmental soil samples. Scientific reports, 14(1), 30685.

Zhang M, et al. (2024) Comparative Phylogenetic Analysis and Protein Prediction Reveal the Taxonomy and Diverse Distribution of Virulence Factors in Foodborne Clostridium Strains. Evolutionary bioinformatics online, 20, 11769343241294153.

Dzhuraeva M, et al. (2024) The metagenomic landscape of a high-altitude geothermal spring in Tajikistan reveals a novel Desulfurococcaceae member, Zestomicrobium tamdykulense gen. nov., sp. nov. MicrobiologyOpen, 13(5), e70004.

Alnaimat SM, et al. (2024) Comparative genomic characterization of Cellulosimicrobium funkei isolate RVMD1 from Ma'an desert rock varnish challenges Cellulosimicrobium systematics. Frontiers in microbiology, 15, 1445943.

Imai S, et al. (2024) Complete genome sequence of Luteolibacter sp. strain Populi, a

member of phylum Verrucomicrobiota isolated from the Populus trichocarpa rhizosphere. Microbiology resource announcements, 13(11), e0080124.

Chávez-Luzanía RA, et al. (2024) Transdisciplinary approaches for the study of cyanobacteria and cyanotoxins. Current research in microbial sciences, 7, 100289.

Contarini PE, et al. (2024) A novel open-source cultivation system helps establish the first full cycle chemosynthetic symbiosis model system involving the giant ciliate Zoothamnium niveum. Frontiers in microbiology, 15, 1491485.

Riesco R, et al. (2024) Update on the proposed minimal standards for the use of genome data for the taxonomy of prokaryotes. International journal of systematic and evolutionary microbiology, 74(3).

Gunathilake KMD, et al. (2024) Diversity of Salmonella enterica phages isolated from chicken farms in Kenya. Microbiology spectrum, 12(1), e0272923.

Burch-Konda J, et al. (2024) EF-hand calcium sensor, EfhP, controls transcriptional regulation of iron uptake by calcium in Pseudomonas aeruginosa. mBio, 15(11), e0244724.

Das R, et al. (2024) Probiotic yeast characterization and fungal amplicon metagenomics analysis of fermented bamboo shoot products from Arunachal Pradesh, northeast India. Heliyon, 10(20), e39500.

Prescott RD, et al. (2023) Bridging Place-Based Astrobiology Education with Genomics, Including Descriptions of Three Novel Bacterial Species Isolated from Mars Analog Sites of Cultural Relevance. Astrobiology, 23(12), 1348.

Mourão J, et al. (2023) From Farm to Fork: Persistence of Clinically Relevant Multidrug-Resistant and Copper-Tolerant Klebsiella pneumoniae Long after Colistin Withdrawal in Poultry Production. Microbiology spectrum, 11(4), e0138623.

Jawaharraj K, et al. (2023) Transcriptome-wide marker gene expression analysis of stressresponsive sulfate-reducing bacteria. Scientific reports, 13(1), 16181.

Losey NA, et al. (2023) Draft genomes of two rhizosphere associated bacterial isolates from Tims Branch, a heavy metal contaminated wetland. Microbiology resource announcements, 12(12), e0058223.

Carneiro J, et al. (2023) Mapping human pathogens in wastewater using a metatranscriptomic approach. Environmental research, 231(Pt 1), 116040.

Hay MC, et al. (2023) Metagenome-assembled genomes from High Arctic glaciers highlight the vulnerability of glacier-associated microbiota and their activities to habitat loss. Microbial genomics, 9(11).