

Resource Summary Report

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KBase

RRID:SCR_022162

Type: Tool

Proper Citation

KBase (RRID:SCR_022162)

Resource Information

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

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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](https://doi.org/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

Resource Name: KBase

Resource ID: SCR_022162

Record Creation Time: 20220421T050139+0000

Record Last Update: 20260811T043702+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 63 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Luzmore A, et al. (2026) Seasonal frost improves probiotic and nutrient availability in fermented vegetables. NPJ science of food, 10(1).

Zhou H, et al. (2026) Two Novel Thiosulfate-Oxidizing Species from Coastal Sediments Reveal Distinct Ecological Strategies: *Pseudothioclava alba* sp. nov. and *Terasakiella sediminum* sp. nov. Microorganisms, 14(2).

Butarelli ACdA, et al. (2026) Genomic insights into a versatile deep-sea methanotroph constituting the rare biosphere of a Brazilian carbonate mound complex. mSystems, 11(2), e0131125.

Shahid I, et al. (2026) Comparative genome analysis of *Pseudomonas chlororaphis* strains reveals biosynthetic diversity underlying plant growth promotion and soil health improvement. BMC genomics, 27(1).

Onumanyi V, et al. (2026) PacBio HiFi sequencing datasets of culture-enriched airborne microbial cave communities from dolomitic Sudwala Caves, South Africa. Data in brief, 67, 112970.

Ghevondyan D, et al. (2026) Genomic and chemical insights into a human lectin-binding extracellular polysaccharides from *Parageobacillus toebii* strain H-70. PloS one, 21(1), e0340423.

Giovannini M, et al. (2026) Modelling *Fusobacterium* lifestyles transitions by integrating transcriptomics and growth data. Current research in microbial sciences, 10, 100573.

Maumela P, et al. (2026) In vitro and in silico analysis of the fungicidal potential of secondary metabolites from a bacterial endophyte against *Botrytis cinerea*. BMC biotechnology, 26(1).

Roopnarain A, et al. (2026) Plant growth promoting traits of selected psychrotolerant bacteria: a genomic basis of biocontrol, nutrient acquisition and stress tolerance. World journal of microbiology & biotechnology, 42(6).

Ogola HJO, et al. (2025) Hydrological regime and niche partitioning drive fungal community structure and function in arid wetlands sediments of South Africa. *Environmental science and pollution research international*, 32(25), 15217.

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).

Shimada S, et al. (2025) Characterization of *Mycobacterium antarcticum* sp. nov., a psychrotolerant member of the genus *Mycobacterium* isolated from Antarctic soil. *Scientific reports*, 15(1), 34231.

El Hafi B, et al. (2025) *Pseudomonas aeruginosa* supports the survival of *Prevotella melaninogenica* in a cystic fibrosis lung polymicrobial community through metabolic cross-feeding. *mBio*, 16(10), e0159425.

Qiu QT, et al. (2025) Spatial chromosome organization and adaptation of the radiation-resistant extremophile *Deinococcus radiodurans*. *The Journal of biological chemistry*, 301(1), 108068.

Elmanzalawi M, et al. (2025) DFAST_QC: quality assessment and taxonomic identification tool for prokaryotic Genomes. *BMC bioinformatics*, 26(1), 3.

Islam MS, et al. (2025) Characterization of *Congregicoccus parvus* gen. nov., sp. nov., a novel slow-growing ultramicrobacterium of the phylum Verrucomicrobiota. *PloS one*, 20(6), e0326734.

Ghevondyan D, et al. (2025) Production, characterization, and genomic insights of a human lectin-binding exopolysaccharide from *Haloarcula japonica* strain SST1. *Scientific reports*, 15(1), 34727.

Wang N, et al. (2025) *Flagellimonas algicida* sp. Nov.: A Novel Broad-Spectrum Algicidal Bacterium Targeting Harmful Algal Bloom Species and Genomic Insights into Its Secondary Metabolites. *Microorganisms*, 13(9).

Huda N-U, et al. (2025) Complete genome of *Lactococcus lactis* isolate S11-599 from the brain of a silver carp (*Hypophthalmichthys molitrix*) during a mass mortality event in the Mississippi river. *Microbiology resource announcements*, 14(10), e0050325.

Gichure J, et al. (2025) Exploring the Genetic Diversity, Virulence and Antimicrobial Resistance of Diarrhoeagenic *Escherichia coli* From Southern Africa Using Whole-Genome Data. *Public health challenges*, 4(3), e70098.