# Resource Summary Report

Generated by ASWG on Aug 5, 2026

## DEG - Database of Essential Genes

RRID:SCR_012929
Type: Tool

### Proper Citation

DEG - Database of Essential Genes (RRID:SCR_012929)

### Resource Information

**URL:** http://tubic.tju.edu.cn/deg

**Proper Citation:** DEG - Database of Essential Genes (RRID:SCR_012929)

**Description:** THIS RESOURCE IS NO LONGER IN SEVICE. Documented on August 19,2019.It hosts records of currently available essential genes among a wide range of organisms. For prokaryotes, DEG contains essential genes in more than 10 bacteria, such as E. coli, B. subtilis, H. pylori, S. pneumoniae, M. genitalium and H. influenzae, whereas for eukaryotes, DEG contains those in yeast, humans, mice, worms, fruit flies, zebra fish and the plant A. thaliana. Users can Blast query sequences against DEG, and can also search for essential genes by their functions and names. Essential gene products comprise excellent targets for antibacterial drugs. Essential genes in a bacterium constitute a minimal genome, forming a set of functional modules, which play key roles in the emerging field, synthetic biology.

**Abbreviations:** DEG

**Synonyms:** Database of Essential Genes

**Resource Type:** database, data or information resource

**Keywords:** e. coli, essential gene, eukaryote essential gene, fruit fly, a. thaliana, b. subtilis, h. influenzae, h. pylori, human, m. genitalium, mice, prokaryote essential gene, s. pneumoniae, worm, yeast, zebra fish, FASEB list

**Availability:** THIS RESOURCE IS NO LONGER IN SEVICE.

**Resource Name:** DEG - Database of Essential Genes

**Resource ID:** SCR_012929

**Alternate IDs:** r3d100012052, nif-0000-02745

**Record Creation Time:** 20220129T080313+0000

**Record Last Update:** 20260805T044306+0000

## Ratings and Alerts

No rating or validation information has been found for DEG - Database of Essential Genes.

No alerts have been found for DEG - Database of Essential Genes.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 61 mentions in open access literature.

**Listed below are recent publications.** The full list is available at ASWG .


Basharat Z, et al. (2025) Proteome mining of Yersinia Enterocolitica for drug targets and computational inhibitor identification with ADMET, anti-inflammation potential and formulation characteristics. BioData mining, 18(1), 68.

Riaz R, et al. (2025) Combatting antibiotic resistance in Gardnerella vaginalis: A comparative in silico investigation for drug target identification. PloS one, 20(3), e0314465.

Bedree JK, et al. (2025) Identifying essential genes in Schaalia odontolytica using a saturated transposon library. Journal of bacteriology, 207(8), e0016425.

Yan W, et al. (2025) A hybrid machine learning model with attention mechanism and multidimensional multivariate feature coding for essential gene prediction. BMC biology, 23(1), 108.

Rahman S, et al. (2024) Prediction of potential drug targets and key inhibitors (ZINC67974679, ZINC67982856, and ZINC05668040) against Rickettsia felis using integrated computational approaches. Frontiers in veterinary science, 11, 1507496.

Khan S, et al. (2022) Identification of a Potential Vaccine against Treponema pallidum Using Subtractive Proteomics and Reverse-Vaccinology Approaches. Vaccines, 11(1).

Zhang X, et al. (2022) In silico Methods for Identification of Potential Therapeutic Targets. Interdisciplinary sciences, computational life sciences, 14(2), 285.

Pun FW, et al. (2022) Hallmarks of aging-based dual-purpose disease and age-associated targets predicted using PandaOmics AI-powered discovery engine. Aging, 14(6), 2475.

Basharat Z, et al. (2021) Pan-genomics, drug candidate mining and ADMET profiling of natural product inhibitors screened against Yersinia pseudotuberculosis. Genomics, 113(1 Pt 1), 238.

Baraquet C, et al. (2021) Transposon sequencing analysis of Bradyrhizobium diazoefficiens 110spc4. Scientific reports, 11(1), 13211.

Chowdhury UF, et al. (2021) Subtractive proteomics approach to Unravel the druggable proteins of the emerging pathogen Waddlia chondrophila and drug repositioning on its MurB protein. Heliyon, 7(6), e07320.

Xiong K, et al. (2021) An optimized genome-wide, virus-free CRISPR screen for mammalian cells. Cell reports methods, 1(4).

Jalal K, et al. (2021) Identification of a Novel Therapeutic Target against XDR Salmonella Typhi H58 Using Genomics Driven Approach Followed Up by Natural Products Virtual Screening. Microorganisms, 9(12).

Zhang F, et al. (2020) Engineering of a genome-reduced strain Bacillus amyloliquefaciens for enhancing surfactin production. Microbial cell factories, 19(1), 223.

Muir A, et al. (2020) Construction of a complete set of Neisseria meningitidis mutants and its use for the phenotypic profiling of this human pathogen. Nature communications, 11(1), 5541.

Zhang X, et al. (2020) DeepHE: Accurately predicting human essential genes based on deep learning. PLoS computational biology, 16(9), e1008229.

Mahmud A, et al. (2019) Identification of novel drug targets for humans and potential vaccine targets for cattle by subtractive genomic analysis of Brucella abortus strain 2308. Microbial pathogenesis, 137, 103731.

Rashid MI, et al. (2019) Fishing for vaccines against Vibrio cholerae using in silico pan-proteomic reverse vaccinology approach. PeerJ, 7, e6223.

Ireland PM, et al. (2019) Global Analysis of Genes Essential for Francisella tularensis Schu S4 Growth In Vitro and for Fitness during Competitive Infection of Fischer 344 Rats. Journal of bacteriology, 201(7).

Ain QU, et al. (2018) Subtractive proteomics and immunoinformatics revealed novel B-cell derived T-cell epitopes against Yersinia enterocolitica: An etiological agent of Yersiniosis. Microbial pathogenesis, 125, 336.