

Resource Summary Report

Generated by [NIF](#) on Aug 28, 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 SERVICE. 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: data or information resource, database

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 SERVICE.

Resource Name: DEG - Database of Essential Genes

Resource ID: SCR_012929

Alternate IDs: r3d100012052, nif-0000-02745

Record Creation Time: 20220129T080313+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 64 mentions in open access literature.

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

Bai G, et al. (2026) LARS promotes osteosarcoma proliferation through leucine-dependent PRIM2 translation and DNA replication activation. Journal of experimental & clinical cancer research : CR, 45(1).

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.

Bedree JK, et al. (2025) Identifying essential genes in Schaalialia 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.

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.

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.

Shah M, et al. (2023) Proteome level analysis of drug-resistant Prevotella melaninogenica for the identification of novel therapeutic candidates. Frontiers in microbiology, 14, 1271798.

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

Khan T, et al. (2022) Subtractive proteomics assisted therapeutic targets mining and designing ensemble vaccine against Candida auris for immune response induction.

Computers in biology and medicine, 145, 105462.

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.

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

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.

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.