Resource Summary Report

Generated by dkNET on Sep 16, 2026

REBASE

RRID:SCR_007886
Type: Tool

Proper Citation

REBASE (RRID:SCR_007886)

Resource Information

URL: http://rebase.neb.com/rebase/

Proper Citation: REBASE (RRID:SCR_007886)

Description: Database of information about restriction enzymes and related proteins containing published and unpublished references, recognition and cleavage sites, isoschizomers, commercial availability, methylation sensitivity, crystal, genome, and sequence data. DNA methyltransferases, homing endonucleases, nicking enzymes, specificity subunits and control proteins are also included. Several tools are available including REBsites, BLAST against REBASE, NEBcutter and REBpredictor. Putative DNA methyltransferases and restriction enzymes, as predicted from analysis of genomic sequences, are also listed. REBASE is updated daily and is constantly expanding. Users may submit new enzyme and/or sequence information, recommend references, or send them corrections to existing data. The contents of REBASE may be browsed from the web and selected compilations can be downloaded by ftp (ftp.neb.com). Additionally, monthly updates can be requested via email.,

Abbreviations: REBASE

Synonyms: The Restriction Enzyme Database, Restriction Enzyme Database

Resource Type: data or information resource, database

Defining Citation: PMID:19846593, PMID:17202163

Keywords: endonuclease, enzyme, genome, archaeal, bacterial, cleavage, crystal, dna, individual protein family databases, isochizomer, methylation, methyltransferase, modification, protein, recognition, restriction, restriction enzyme, sensitivity, sequence, site, methylase, cleavage site, restriction-modification, blast, FASEB list

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NLM LM04971

Resource Name: REBASE

Resource ID: SCR_007886

Alternate IDs: r3d100012171, nif-0000-03391

Alternate URLs: http://rebase.neb.com, https://doi.org/10.17616/R3J930

Old URLs: http://www.neb.com/rebase

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260912T195657+0000

Ratings and Alerts

No rating or validation information has been found for REBASE.

No alerts have been found for REBASE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 261 mentions in open access literature.

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

Wang M, et al. (2026) Comprehensive Genomics and Functional Validation Reveal Evolutionary Insights into Xanthan Gum Biosynthesis and Pathogenesis of Xanthomonas campestris pv. campestris. Journal of agricultural and food chemistry, 74(16), 13302.

Schlaiß C, et al. (2026) Genetic modification of Clostridium kluyveri for heterologous n-butanol and n-hexanol production. Applied and environmental microbiology, 92(4), e0005826.

Figueroa W, et al. (2026) Immune-deficient bacteria serve as gateways to genetic exchange and microbial evolution. Nature communications, 17(1).

Koong J, et al. (2026) Variations in plasmid transfer in Acinetobacter baumannii: insights from epigenetics, strain properties, and experimental conditions. Microbiology spectrum, 14(6), e0348725.

White K, et al. (2026) Diversity and prevalence of dairy streptococcal phages in two European dairy fermentation facilities over a one-year period. Microbial genomics, 12(5).

Martínez-Alvarez L, et al. (2026) Diversity and evolution of archaeal immune strategies. Nucleic acids research, 54(5).

Arévalo-Lalanne A, et al. (2026) Genetic engineering of gut commensals: heterologous protein expression in Bifidobacterium animalis subsp. lactis CECT8145. Current research in microbial sciences, 10, 100591.

Zeng Y, et al. (2026) Tail spike protein evolution enables phage Psm140 to target Salmonella ShdA and overcome host resistance. Poultry science, 105(6), 106791.

Pearl S, et al. (2025) Genomic landscape of nosocomial Acinetobacter baumannii: A comprehensive analysis of the resistome, virulome, and mobilome. Scientific reports, 15(1), 18203.

Takahashi M, et al. (2025) Host-encoded DNA methyltransferases modify the epigenome and host tropism of invading phages. iScience, 28(4), 112264.

Born P, et al. (2025) Complete genome sequence data of Clostridium isatidis BK32, a lignocellulose-degrading bacterium isolated from compost. Data in brief, 61, 111874.

Koong J, et al. (2025) Genomic characteristics of the multiresistant Acinetobacter baumannii global clone 1 reference strain A297/RUH875. The Journal of antimicrobial chemotherapy, 80(7), 1988.

Leprince A, et al. (2025) Strengthening phage resistance of Streptococcus thermophilus by leveraging complementary defense systems. Nature communications, 16(1), 7142.

Shin D, et al. (2025) RECAP-seq: restriction enzyme-based CpG-methylated fragment amplification for early cancer detection. Scientific reports, 15(1), 40892.

Sloboda S, et al. (2025) Methylation of foreign DNA overcomes the restriction barrier of Flavobacterium psychrophilum and allows efficient genetic manipulation. Applied and environmental microbiology, 91(2), e0144824.

Chen Z, et al. (2025) Identifying DNA methylation types and methylated base positions from bacteria using nanopore sequencing with multi-scale neural network. Bioinformatics (Oxford, England), 41(8).

Truchon AR, et al. (2025) Epigenome analysis of an algae-infecting giant virus reveals a unique methylation motif catalogue. PloS one, 20(12), e0330887.

Catalano Gonzaga O, et al. (2025) Gene-trait matching among Bifidobacterium dentium strains reveals various glycan metabolism loci including a strain-specific fucosyllactose utilization cluster. Frontiers in microbiology, 16, 1584694.

Korotetskiy IS, et al. (2025) Epigenetic background of lineage-specific gene expression landscapes of four Staphylococcus aureus hospital isolates. PloS one, 20(5), e0322006.

Ni M, et al. (2025) Epigenetic phase variation in the gut microbiome enhances bacterial adaptation. bioRxiv : the preprint server for biology.