

Resource Summary Report

Generated by T1D on Aug 2, 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Description: Database of information about restriction enzymes and related proteins containing published and unpublished references, recognition and cleavage sites, isoschizomers, commercial availability, methylation sensitivity, crystal, genome, and sequence data.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

Funding: New England Biolabs Inc ;
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: 20260801T190324+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 246 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

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

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.

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.

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.

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).

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.

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

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

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

G??hmann M, et al. (2025) Diffdigester.uni-jena.de: a tool for optimized selection of restriction enzymes for plasmid identification in cloning procedures. *Nucleic acids research*, 53(W1), W238.

Qiu Y, et al. (2025) The restriction impacts of the Type III restriction-modification system on the transmission dynamics of antimicrobial resistance genes in *Campylobacter jejuni*. *Frontiers in microbiology*, 16, 1496275.

Chen J, et al. (2025) Genomic and metabolomic insights into the antimicrobial compounds and plant growth-promoting potential of *Bacillus velezensis* B115. *Scientific reports*, 15(1), 10666.

Ferrer Obiol J, et al. (2025) Evolutionarily distinct lineages of a migratory bird of prey show divergent responses to climate change. *Nature communications*, 16(1), 3503.

Gottschall W, et al. (2025) The *Helicobacter pylori* orphan ATTAAT-specific methyltransferase M.Hpy99XIX plays a central role in the coordinated regulation of genes involved in iron metabolism. *mBio*, 16(7), e0120925.

Smedile F, et al. (2025) Integrated Analysis of Gene Expression, Protein Synthesis, and Epigenetic Modifications in *Alcanivorax borkumensis* SK2 Under Iron Limitation. *Environmental microbiology reports*, 17(3), e70106.

David E, et al. (2025) Systematic functional assessment of anti-phage systems in their native host. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 380(1934), 20240067.

McDonnell B, et al. (2025) Lactococcal mobile genetic elements harbour a diverse phage defenseome rich in restriction-modification systems. *Nucleic acids research*, 53(17).