## **Resource Summary Report**

Generated by <u>dkNET</u> on May 22, 2025

# **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**Description:** Database of information about restriction enzymes and related proteins containing published and unpublished references, recognition and cleavage sites, isoschizomers, commercial availability, methylation sensitivity, crystal, genome, and sequence data.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:** production service resource, analysis service resource, database, data or information resource, service resource, data analysis service, storage service resource, data repository

#### 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

**Availability:** Public, Acknowledgement requested, The community can contribute to this resource

Resource Name: REBASE

Resource ID: SCR\_007886

Alternate IDs: nif-0000-03391

Alternate URLs: http://rebase.neb.com

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

**Record Creation Time:** 20220129T080244+0000

Record Last Update: 20250522T060443+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: <u>SciCrunch Registry</u>

### **Usage and Citation Metrics**

We found 226 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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

Rizzo SM, et al. (2024) GH136-encoding gene (perB) is involved in gut colonization and persistence by Bifidobacterium bifidum PRL2010. Microbial biotechnology, 17(2), e14406.

Dooley D, et al. (2024) Expanded genome and proteome reallocation in a novel, robust Bacillus coagulans strain capable of utilizing pentose and hexose sugars. mSystems, 9(11),

e0095224.

Patakova P, et al. (2024) Whole genome sequencing and characterization of Pantoea agglomerans DBM 3797, endophyte, isolated from fresh hop (Humulus lupulus L.). Frontiers in microbiology, 15, 1305338.

Soto-Serrano A, et al. (2024) Matching excellence: Oxford Nanopore Technologies' rise to parity with Pacific Biosciences in genome reconstruction of non-model bacterium with high G+C content. Microbial genomics, 10(11).

Lu Y, et al. (2024) A novel hierarchical network-based approach to unveil the complexity of functional microbial genome. BMC genomics, 25(1), 786.

Kelleher P, et al. (2024) Phage defence loci of Streptococcus thermophilus-tip of the antiphage iceberg? Nucleic acids research, 52(19), 11853.

Heppert JK, et al. (2024) Analyses of Xenorhabdus griffiniae genomes reveal two distinct sub-species that display intra-species variation due to prophages. BMC genomics, 25(1), 1087.

Dai Q, et al. (2024) Precision DNA methylation typing via hierarchical clustering of Nanopore current signals and attention-based neural network. Briefings in bioinformatics, 25(6).

Flores-Fernández CN, et al. (2024) DNA methylases for site-selective inhibition of type IIS restriction enzyme activity. Applied microbiology and biotechnology, 108(1), 174.

Campbell M, et al. (2024) Comparison of CcrM-dependent methylation in Caulobacter crescentus and Brucella abortus by nanopore sequencing. bioRxiv : the preprint server for biology.

Yang W, et al. (2024) Proxi-RIMS-seq2 applied to native microbiomes uncovers hundreds of known and novel m5C methyltransferase specificities. bioRxiv : the preprint server for biology.

Sterzi L, et al. (2024) Genetic barriers more than environmental associations explain Serratia marcescens population structure. Communications biology, 7(1), 468.

Zhao H, et al. (2024) Genome-wide DNA N6-methyladenosine in Aeromonas veronii and Helicobacter pylori. BMC genomics, 25(1), 161.

Yang Y, et al. (2024) CRISPR-Cas3 and type I restriction-modification team up against blaKPC-IncF plasmid transfer in Klebsiella pneumoniae. BMC microbiology, 24(1), 240.

Chibani Bahi Amar A, et al. (2024) New COI-COII mtDNA Region Haplotypes in the Endemic Honey Bees Apis mellifera intermissa and Apis mellifera sahariensis (Hymenoptera: Apidae) in Algeria. Insects, 15(7).

Gulati P, et al. (2024) Restriction modification systems in archaea: A panoramic outlook. Heliyon, 10(8), e27382.

Park JS, et al. (2024) Development of a web-based high-throughput marker design program: CAPS (cleaved amplified polymorphic sequence) Maker. Plant methods, 20(1), 192.

Reva ON, et al. (2024) Interplay of intracellular and trans-cellular DNA methylation in natural archaeal consortia. Environmental microbiology reports, 16(2), e13258.

Valentin-Alvarado LE, et al. (2024) Complete genomes of Asgard archaea reveal diverse integrated and mobile genetic elements. Genome research, 34(10), 1595.