

Resource Summary Report

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NEBcutter

RRID:SCR_010664

Type: Tool

Proper Citation

NEBcutter (RRID:SCR_010664)

Resource Information

URL: <http://tools.neb.com/NEBcutter2/>

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Description: This tool will take a DNA sequence and find the large, non-overlapping open reading frames using the E.coli genetic code and the sites for all Type II and commercially available Type III restriction enzymes that cut the sequence just once. By default, only enzymes available from NEB are used, but other sets may be chosen. Just enter your sequence and submit. Further options will appear with the output. The maximum size of the input file is 1 MByte, and the maximum sequence length is 300 KBases. NEBcutter produces a variety of outputs including restriction enzyme maps, theoretical digests and links into the restriction enzyme database, REBASE (<http://rebase.neb.com/rebase/rebase.html>). Importantly, its table of recognition sites is updated daily from REBASE and it marks all sites that are potentially affected by DNA methylation (Dam, Dcm, etc.). Many options exist to choose the enzymes used for digestion, including all known specificities, subsets of those that are commercially available or sets of enzymes that produce compatible termini.

Resource Type: data analysis service, production service resource, analysis service resource, service resource

Defining Citation: [PMID:12824395](#)

Keywords: bio.tools, FASEB list

Funding:

Resource Name: NEBcutter

Resource ID: SCR_010664

Alternate IDs: biotools:nebcutter, nlx_71778

Alternate URLs: <https://bio.tools/nebcutter>

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250420T015621+0000

Ratings and Alerts

No rating or validation information has been found for NEBcutter.

No alerts have been found for NEBcutter.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 134 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Sousa GSM, et al. (2024) Identification of Chromoblastomycosis and Phaeohyphomycosis Agents through ITS-RFLP. Journal of fungi (Basel, Switzerland), 10(2).

Valizadeh Osalo M, et al. (2024) The prevalence of ADSL (rs3788579) and CYP1A2 (rs17861162) polymorphisms in female breast cancer patients in North-West Iran. Discover. Oncology, 15(1), 59.

Amos BK, et al. (2024) Discovery and Characterization of Fluopipamine, a Putative Cellulose Synthase 1 Antagonist within Arabidopsis. Journal of agricultural and food chemistry, 72(6), 3171.

Livingston IG, et al. (2024) Molecular Discovery of Filarial Nematode DNA in an Endangered Wild Pinniped (Galapagos Sea Lion, Zalophus wolfebaeki). Ecology and evolution, 14(11), e70596.

Khan J, et al. (2024) Designing multi-epitope vaccines against Echinococcus granulosus: an in-silico study using immuno-informatics. BMC molecular and cell biology, 25(1), 29.

Asadbeigi A, et al. (2024) Protection of animals against devastating RNA viruses using CRISPR-Cas13s. Molecular therapy. Nucleic acids, 35(3), 102235.

Materniak-Kornas M, et al. (2024) Identification of New Single Nucleotide Polymorphisms

Potentially Related to Small Ruminant Lentivirus Infection Susceptibility in Goats Based on Data Selected from High-Throughput Sequencing. *Pathogens* (Basel, Switzerland), 13(10).

Koni E, et al. (2024) Overexpression of CXCL17 increases migration and invasion of A549 lung adenocarcinoma cells. *Frontiers in pharmacology*, 15, 1306273.

Zhang G, et al. (2024) An innovative molecular approach towards the cost-effective entomological authentication of honey. *NPJ science of food*, 8(1), 24.

Tate NM, et al. (2024) Sequence Analysis of Six Candidate Genes in Miniature Schnauzers with Primary Hypertriglyceridemia. *Genes*, 15(2).

Decewicz P, et al. (2023) Structure and functions of a multireplicon genome of Antarctic *Psychrobacter* sp. ANT_H3: characterization of the genetic modules suitable for the construction of the plasmid-vectors for cold-active bacteria. *Journal of applied genetics*, 64(3), 545.

Muselmani W, et al. (2023) A Multimodal Approach towards Genomic Identification of Protein Inhibitors of Uracil-DNA Glycosylase. *Viruses*, 15(6).

Heydari A, et al. (2023) Molecular Characterization of *Paederus* Spp (Coleoptera: Staphylinidae, Paederinae) the Agent of Human Linear Dermatitis in the Caspian Sea Coast, North of Iran. *Journal of arthropod-borne diseases*, 17(1), 94.

Sritong N, et al. (2023) Development of an Integrated Sample Amplification Control for Salivary Point-of-Care Pathogen Testing. *medRxiv : the preprint server for health sciences*.

Zanet S, et al. (2023) The Dangerous Side of Being a Predator: *Toxoplasma gondii* and *Neospora caninum* in Birds of Prey. *Pathogens* (Basel, Switzerland), 12(2).

Panda M, et al. (2022) Nanobody-peptide-conjugate (NPC) for passive immunotherapy against SARS-CoV-2 variants of concern (VoC): a prospective pan-coronavirus therapeutics. *Molecular diversity*, 1.

Ye C, et al. (2022) Use of a Bacterial Artificial Chromosome to Generate Recombinant SARS-CoV-2 Expressing Robust Levels of Reporter Genes. *Microbiology spectrum*, 10(6), e0273222.

Deka P, et al. (2022) A study of risk factors associated with Newcastle disease and molecular characterization of genotype XIII Newcastle disease virus in backyard and commercial poultry in Assam, India. *Research in veterinary science*, 150, 122.

Žák A, et al. (2022) FADS Polymorphisms Affect the Clinical and Biochemical Phenotypes of Metabolic Syndrome. *Metabolites*, 12(6).

Chen CY, et al. (2022) Sequence analysis and plasmid mobilization of a 6.6-kb kanamycin resistance plasmid, pSNC3-Kan, from a *Salmonella enterica* serotype Newport isolate. *PloS one*, 17(7), e0268502.