Resource Summary Report

Generated by T1D on Aug 1, 2026

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, service resource, production service resource, analysis service resource

Defining Citation: PMID:12824395

Keywords: bio.tools, FASEB list

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: 20260801T042709+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 142 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Roshan S, et al. (2025) Identification of an in-frame insertion in ACKR1 in five individuals from Agri community, India. Hematology, transfusion and cell therapy, 48(1), 106075.

Yuan M, et al. (2025) Wheat TaNADPO Promotes Spot Blotch Resistance. Molecular plant pathology, 26(6), e70103.

Javaid M, et al. (2025) Immunotherapeutic Approach for Improving the Efficacy of a Novel Subunit Vaccine Against SARS-CoV-2 by Cytotoxic T-Lymphocytes (CTL) Epitopes. Scientifica, 2025, 6025826.

DeYoung V, et al. (2025) Development of a protease-resistant ADAMTS13 to improve stability against proteolytic degradation. Blood advances, 9(11), 2695.

Girma S, et al. (2025) Genetic variation of cutaneous leishmaniasis causative species in Ethiopia. Scientific reports, 15(1), 44039.

Gharbi W, et al. (2025) Functional genetic variants in immune-checkpoint molecules and susceptibility to Nasopharyngeal carcinoma in a Tunisian case-control study. Molecular biology reports, 53(1), 230.

Naumann N, et al. (2025) Multiplex detection of seven transgenes for human gene doping analysis. Scientific reports, 15(1), 20219.

Khazaei S, et al. (2025) Designing and Evaluation of a Plasmid Encoding Immunogenic Epitopes From Echinococcus granulosus Eg95-1-6, P29, and GST Against Hydatid Cyst in BALB/c Mice. Journal of parasitology research, 2025, 1655679.

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).

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

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

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 wollebaeki). Ecology and evolution, 14(11), e70596.

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.

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.

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

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

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

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.

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.