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: analysis service resource, data analysis service, production service resource, 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: 20260905T133159+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 151 mentions in open access literature.

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

Kong Z, et al. (2026) AXIN1 Polymorphisms Potentially Modulate Parkinson's Disease Susceptibility: A Cross-Sectional Study in Northern Han Chinese and White Populations. Neurology and therapy, 15(1), 325.

Galvan A, et al. (2026) MiniPromoters Ple384 (TH) and Ple388 (PITX3) for targeting midbrain dopaminergic neurons in mice and monkeys. Scientific reports, 16(1).

Akter S, et al. (2026) Genetic association and computational analysis of CYP2R1 gene polymorphisms rs2060793 and rs12794714 with vitamin D deficiency and acute myocardial infarction in the Bangladeshi population: A case control study. PloS one, 21(6), e0350994.

Y??cedal D, et al. (2026) Growth Hormone Strongly Induces hSMN2 Promoter Driving Construct Gene Expression in Mammalian Cells. Journal of clinical research in pediatric endocrinology, 18(1), 97.

Queeno SR, et al. (2026) Profiling the epigenomic landscape of late embryonic and adult mouse hind limb muscles. Scientific reports, 16(1).

Gross M, et al. (2026) From Gene Copies to Cell Numbers: Advancing Quantitative Approaches in Protistan Ecology Using Digital PCR. Molecular ecology resources, 26(5), e70177.

Bakr NM, et al. (2026) Impact of genetic polymorphisms in the interleukin-18 and interleukin-21 genes on the risk and clinical outcomes of multiple sclerosis. BMC neurology, 26(1).

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.

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.

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

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.

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.

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.

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

Ebrahimi A, et al. (2025) Comparative analysis of butternut (Juglans cinerea) and Japanese walnut (Juglans ailantifolia) chloroplast genomes. BMC plant biology, 26(1), 68.

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.

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.

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.