

Resource Summary Report

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NECAT

RRID:SCR_025350

Type: Tool

Proper Citation

NECAT (RRID:SCR_025350)

Resource Information

URL: <https://github.com/xiaochuanle/NECAT>

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Description: Software error correction and de-novo assembly tool for Nanopore long noisy reads. Nanopore data assembler.

Resource Type: software application, data processing software, source code, data analysis software, software resource

Defining Citation: [PMID:33397900](#)

Keywords: Nanopore, data assembler, Nanopore long noisy reads, de-novo assembly, error correction,

Funding: National Natural Science Foundation of China ;
Guangdong Basic and Applied Basic Research Foundation ;
US National Institute of Food and Agriculture ;
US National Science Foundation

Availability: Free, Available for download, Freely available

Resource Name: NECAT

Resource ID: SCR_025350

Record Creation Time: 20240521T053244+0000

Record Last Update: 20260804T043908+0000

Ratings and Alerts

No rating or validation information has been found for NECAT.

No alerts have been found for NECAT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Schell T, et al. (2025) Establishing genome sequencing and assembly for non-model and emerging model organisms: a brief guide. *Frontiers in zoology*, 22(1), 7.

Lei Y, et al. (2025) Population sequencing of cherry accessions unravels the evolution of *Cerasus* species and the selection of genetic characteristics in edible cherries. *Molecular horticulture*, 5(1), 6.

Kang Z, et al. (2025) Genomic and Multi-Omics Analysis of *Phlebopus portentosus*: Effects of Cultivation on Secondary Metabolites. *Journal of fungi (Basel, Switzerland)*, 11(4).

Tang Y, et al. (2025) The biocontrol effects and mechanisms of mycoparasitic *Alternaria alternata* against Chinese rose powdery mildew. *Frontiers in microbiology*, 16, 1598458.

Luo CY, et al. (2025) Whole genome sequencing and analysis of the symbiotic *Armillaria gallica* M3 with *Gastrodia elata*. *BMC genomics*, 26(1), 324.

Deng K, et al. (2025) Decoding Pecan's Fungal Foe: A Genomic Insight into *Colletotrichum plurivorum* Isolate W-6. *Journal of fungi (Basel, Switzerland)*, 11(3).

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. *GigaScience*, 14.

Jiang M, et al. (2025) The telomere-to-telomere gap-free reference genome and taxonomic reassessment of *Siniperca roulei*. *GigaScience*, 14.

Restrepo-Benavides M, et al. (2024) Unveiling potential virulence determinants in *Vibrio* isolates from *Anadara tuberculosa* through whole genome analyses. *Microbiology spectrum*, 12(2), e0292823.

Sugimura Y, et al. (2024) Impact of rice GENERAL REGULATORY FACTOR14h (GF14h) on low-temperature seed germination and its application to breeding. *PLoS genetics*, 20(8), e1011369.

Xie X, et al. (2024) Genome-wide characterization and metabolite profiling of *Cyathus olla*: insights into the biosynthesis of medicinal compounds. *BMC genomics*, 25(1), 618.

Yin D, et al. (2024) Telomere-to-telomere gap-free genome assembly of the endangered Yangtze finless porpoise and East Asian finless porpoise. *GigaScience*, 13.

Yang H, et al. (2024) High-quality assembly of the T2T genome for *Isodon rubescens* f. *lushanensis* reveals genomic structure variations between 2 typical forms of *Isodon rubescens*. *GigaScience*, 13.