

Resource Summary Report

Generated by [RRID](#) on Sep 21, 2026

NECAT

RRID:SCR_025350

Type: Tool

Proper Citation

NECAT (RRID:SCR_025350)

Resource Information

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

Proper Citation: NECAT (RRID:SCR_025350)

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

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

Defining Citation: [PMID:33397900](#)

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

Funding: Guangdong Basic and Applied Basic Research Foundation ;
National Natural Science Foundation of China ;
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: 20260919T200022+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 27 mentions in open access literature.

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

Fiesinger A, et al. (2026) The genome of the reef-building coral *Porites harrisoni* from the southern Persian/Arabian Gulf. GigaByte (Hong Kong, China), 2026, gigabyte174.

Guo T, et al. (2026) Chromosome-scale reference genome assembly and annotation of *Prunus scopulorum*. Scientific data, 13(1).

Peng S, et al. (2026) Development and Assessment of Heavy Oil-Degrading Fungal Consortia (*Aspergillus* and *Alternaria*) for Soil Bioremediation. Journal of fungi (Basel, Switzerland), 12(3).

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.

Duan Z, et al. (2025) Draft genome sequence of the medicinal fungus *Rigidoporus glomeratus* isolated from Gaoligong mountain. BMC genomic data, 27(1), 19.

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).

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).

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.

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

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

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

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.

Jiu S, et al. (2024) Chromosome-level genome assembly provides insights into the genetic diversity, evolution, and flower development of *Prunus conradinae*. *Molecular horticulture*, 4(1), 25.

Fu Z, et al. (2024) Unveiling biosynthetic potential of an Arctic marine-derived strain *Aspergillus sydowii* MNP-2. *BMC genomics*, 25(1), 603.

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.

Li S, et al. (2024) Chromosome-Level Assembly Reveals a Fifteen-Chromosome Aneuploid Genome and Environmental Adaptation Strategy of Chinese Traditional Medical Fungus *Wolfiporia hoelen*. *International journal of molecular sciences*, 25(16).

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.