Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 13, 2025

HiTEC

RRID:SCR_011826
Type: Tool

Proper Citation

HiTEC (RRID:SCR_011826)

Resource Information

URL: http://www.csd.uwo.ca/~ilie/HiTEC/

Proper Citation: HiTEC (RRID:SCR_011826)

Description: Accurate error correction in high-throughput sequencing data.

Abbreviations: HiTEC

Resource Type: software resource

Funding:

Resource Name: HiTEC

Resource ID: SCR_011826

Alternate IDs: OMICS_01105

Record Creation Time: 20220129T080306+0000

Record Last Update: 20250410T070208+0000

Ratings and Alerts

No rating or validation information has been found for HiTEC.

No alerts have been found for HiTEC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Fukuhara A, et al. (2024) Rethinking the four-wing problem in plesiosaur swimming using bio-inspired decentralized control. Scientific reports, 14(1), 25333.

Kong J, et al. (2019) GAAP: A Genome Assembly + Annotation Pipeline. BioMed research international, 2019, 4767354.

Laehnemann D, et al. (2016) Denoising DNA deep sequencing data-high-throughput sequencing errors and their correction. Briefings in bioinformatics, 17(1), 154.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Sarkar A, et al. (2015) Attributes of carbapenemase encoding conjugative plasmid pNDM-SAL from an extensively drug-resistant Salmonella enterica Serovar Senftenberg. Frontiers in microbiology, 6, 969.

El-Metwally S, et al. (2013) Next-generation sequence assembly: four stages of data processing and computational challenges. PLoS computational biology, 9(12), e1003345.