

Resource Summary Report

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SEECER

RRID:SCR_005274

Type: Tool

Proper Citation

SEECER (RRID:SCR_005274)

Resource Information

URL: <http://sb.cs.cmu.edu/seecer/>

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Description: Algorithm for sequencing error correction of RNA-seq data sets. SEECER removes mismatch and indel errors from the raw reads and improves downstream analysis of the data.

Abbreviations: SEECER

Synonyms: SEECER - SEquencing Error CorrEction for Rna reads

Resource Type: algorithm resource, data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [PMID:23558750](#)

Keywords: bio.tools

Availability: Free, Available for download

Resource Name: SEECER

Resource ID: SCR_005274

Alternate IDs: OMICS_01236, biotools:seecer

Alternate URLs: <https://bio.tools/seecer>

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260821T193742+0000

Ratings and Alerts

No rating or validation information has been found for SEECER.

No alerts have been found for SEECER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Zhuang Y, et al. (2022) Co-expression network analyses of anthocyanin biosynthesis genes in *Ruellia* (Wild Petunias; Acanthaceae). *BMC ecology and evolution*, 22(1), 27.

Fischer C, et al. (2021) Genome sequences of *Tropheus moorii* and *Petrochromis trewavasae*, two eco-morphologically divergent cichlid fishes endemic to Lake Tanganyika. *Scientific reports*, 11(1), 4309.

Lyll R, et al. (2020) Vegetative desiccation tolerance in the resurrection plant *Xerophyta humilis* has not evolved through reactivation of the seed canonical LAFL regulatory network. *The Plant journal : for cell and molecular biology*, 101(6), 1349.

Liu L, et al. (2019) Identification and Evaluations of Novel Insecticidal Proteins from Plants of the Class Polypodiopsida for Crop Protection against Key Lepidopteran Pests. *Toxins*, 11(7).

Durai DA, et al. (2018) In silico read normalization using set multi-cover optimization. *Bioinformatics (Oxford, England)*, 34(19), 3273.

Chen Q, et al. (2018) Transcriptomic Profiling of Fruit Development in Black Raspberry *Rubus coreanus*. *International journal of genomics*, 2018, 8084032.

Vizueta J, et al. (2017) Evolution of Chemosensory Gene Families in Arthropods: Insight from the First Inclusive Comparative Transcriptome Analysis across Spider Appendages. *Genome biology and evolution*, 9(1), 178.

Jan SZ, et al. (2017) Unraveling transcriptome dynamics in human spermatogenesis. *Development (Cambridge, England)*, 144(20), 3659.

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

Durai DA, et al. (2016) Informed kmer selection for de novo transcriptome assembly. *Bioinformatics (Oxford, England)*, 32(11), 1670.

Wenger Y, et al. (2016) Loss of neurogenesis in *Hydra* leads to compensatory regulation of neurogenic and neurotransmission genes in epithelial cells. *Philosophical transactions*

of the Royal Society of London. Series B, Biological sciences, 371(1685), 20150040.

He X, et al. (2015) De novo ChIP-seq analysis. Genome biology, 16(1), 205.