

Resource Summary Report

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Rcorrector

RRID:SCR_022011

Type: Tool

Proper Citation

Rcorrector (RRID:SCR_022011)

Resource Information

URL: <https://github.com/mourisl/Rcorrector>

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Description: Software tool as kmer based error correction method for RNAseq data. Can also be applied to other types of sequencing data where read coverage is nonuniform, such as single cell sequencing. Used for error correction for Illumina RNAseq reads.

Synonyms: RNA-seq error CORRECTOR

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

Defining Citation: [DOI:10.1186/s13742-015-0089-y](https://doi.org/10.1186/s13742-015-0089-y)

Keywords: RNA-seq, k-mer, random sequencing errors correction, kmer based error correction, RNA-seq data, sequencing data, nonuniform read coverage, Illumina RNAseq reads error correction

Funding: NSF ABI1159078;
NSF ABI1356078

Availability: Free, Available for download, Freely available

Resource Name: Rcorrector

Resource ID: SCR_022011

License: GPL v 3.0

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260813T055239+0000

Ratings and Alerts

No rating or validation information has been found for Rcorrector.

No alerts have been found for Rcorrector.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Park S, et al. (2026) Structural variation and evolutionary dynamics of plastid genomes in the subgenus *Lychnis* (*Silene*, Caryophyllaceae): insights from genome rearrangements and substitution rates. *BMC plant biology*, 26(1), 266.

Douglas AJ, et al. (2026) The *Rana sylvatica* skin-secreted antimicrobial peptide (AMP) gene repertoire highlights broader patterns in anuran AMP evolution. *Scientific reports*, 16(1).

Vajs V, et al. (2026) Integrated transcriptomic and proteomic analysis of cancer-suppressive *Mesocestoides corti* larvae. *Parasites & vectors*, 19(1).

Chen L, et al. (2026) Integrative utilization of genomic resources for improved phylogenetic resolution in *Sonerileae* (*Melastomataceae*). *American journal of botany*, 113(6), e70216.

Salgado-Roa FC, et al. (2026) Gene Expression and Structural Differences Underpinning Black and White Colouration in Spiders. *Molecular ecology*, 35(12), e70433.

Kotagal S, et al. (2026) Insights into the functional and genetic basis of heteranthery in *Arthrostemma ciliatum* Pav. ex D.Don (*Melastomataceae*). *BMC plant biology*, 26(1).

Picciani N, et al. (2025) Comparative Analysis of Convergent Jellyfish Eyes Reveals Extensive Differences in Expression of Vision-Related Genes. *Ecology and evolution*, 15(7), e71784.

Ortiz R, et al. (2025) Skin transcriptomics of invasive Coqui frogs: stress responses, parasite signatures, and antimicrobial peptides. *PloS one*, 20(7), e0328623.

Ramanauskas K, et al. (2025) Rapid detection of RNase-based self-incompatibility in *Lysimachia monelli* (*Primulaceae*). *American journal of botany*, 112(1), e16449.

Balasubrahmaniam N, et al. (2025) Exposure to elevated relative humidity in laboratory chambers alters fungal gene expression in dust from the International Space Station (ISS). *Scientific reports*, 15(1), 28366.

Martín-Díaz A, et al. (2025) De novo transcriptome assembly of the plant *Helianthemum marifolium* for the study of adaptive mechanisms. *Scientific data*, 12(1), 515.

Paris JR, et al. (2025) Gene Expression Shifts in Emperor Penguin Adaptation to the Extreme Antarctic Environment. *Molecular ecology*, 34(15), e17552.

Fischer M, et al. (2025) p53 reveals principles of chromatin remodeling and enhancer activation. *Nucleic acids research*, 53(11).

Winter S, et al. (2025) Chromosome-Level genome assembly and transcriptome analysis of the ural owl, *Strix uralensis* Pallas, 1771. *The Journal of heredity*.

Burns JA, et al. (2024) An in situ digital synthesis strategy for the discovery and description of ocean life. *Science advances*, 10(3), eadj4960.

Scholpp AC, et al. (2024) Differential gene expression in leaves and roots of *Hydrangea serrata* treated with aluminium chloride. *Frontiers in plant science*, 15, 1412189.

Park S, et al. (2024) Dynamic changes in the plastid and mitochondrial genomes of the angiosperm *Corydalis pauciovulata* (Papaveraceae). *BMC plant biology*, 24(1), 303.

Boman J, et al. (2024) Regulatory and evolutionary impact of DNA methylation in two songbird species and their naturally occurring F1 hybrids. *BMC biology*, 22(1), 124.

Park S, et al. (2024) Complete organelle genomes of Korean fir, *Abies koreana* and phylogenomics of the gymnosperm genus *Abies* using nuclear and cytoplasmic DNA sequence data. *Scientific reports*, 14(1), 7636.

Kambara K, et al. (2023) Construction of a de novo assembly pipeline using multiple transcriptome data sets from *Cypripedium macranthos* (Orchidaceae). *PloS one*, 18(6), e0286804.