

Resource Summary Report

Generated by [NIF](#) on Aug 31, 2026

RepARK

RRID:SCR_002333

Type: Tool

Proper Citation

RepARK (RRID:SCR_002333)

Resource Information

URL: <https://github.com/PhKoch/RepARK>

Proper Citation: RepARK (RRID:SCR_002333)

Description: Software using a de novo repeat assembly method which avoids potential biases by using abundant k-mers of next-generation sequencing (NGS) whole genome sequencing (WGS) reads without requiring a reference genome.

Synonyms: Repetitive motif detection by Assembly of Repetitive K-mers

Resource Type: software resource

Defining Citation: [PMID:24634442](#)

Keywords: standalone software

Resource Name: RepARK

Resource ID: SCR_002333

Alternate IDs: OMICS_03446

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260829T182103+0000

Ratings and Alerts

No rating or validation information has been found for RepARK.

No alerts have been found for RepARK.

Data and Source Information

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Hartley GA, et al. (2021) Comparative Analyses of Gibbon Centromeres Reveal Dynamic Genus-Specific Shifts in Repeat Composition. *Molecular biology and evolution*, 38(9), 3972.

Mauer KM, et al. (2021) Genomics and transcriptomics of epizoic Seisonidea (Rotifera, syn. Syndermata) reveal strain formation and gradual gene loss with growing ties to the host. *BMC genomics*, 22(1), 604.

Brown EJ, et al. (2020) The Y chromosome may contribute to sex-specific ageing in *Drosophila*. *Nature ecology & evolution*, 4(6), 853.

Brown EJ, et al. (2020) The *Drosophila* Y Chromosome Affects Heterochromatin Integrity Genome-Wide. *Molecular biology and evolution*, 37(10), 2808.

Berthelie J, et al. (2018) A transposable element annotation pipeline and expression analysis reveal potentially active elements in the microalga *Tisochrysis lutea*. *BMC genomics*, 19(1), 378.

Gebre YG, et al. (2016) Identification and characterization of abundant repetitive sequences in *Eragrostis tef* cv. Enatite genome. *BMC plant biology*, 16, 39.

Addisalem AB, et al. (2015) Genomic sequencing and microsatellite marker development for *Boswellia papyrifera*, an economically important but threatened tree native to dry tropical forests. *AoB PLANTS*, 7.