## **Resource Summary Report**

Generated by dkNET on Apr 28, 2025

# **RepARK**

RRID:SCR\_002333

Type: Tool

## **Proper Citation**

RepARK (RRID:SCR\_002333)

#### **Resource Information**

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

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**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

**Funding:** 

Resource Name: RepARK

Resource ID: SCR\_002333

Alternate IDs: OMICS\_03446

**Record Creation Time:** 20220129T080212+0000

**Record Last Update:** 20250420T014100+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

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 7 mentions in open access literature.

**Listed below are recent publications.** The full list is available at dkNET.

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.

Berthelier 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.