## **Resource Summary Report**

Generated by dkNET on May 10, 2025

# **DupRecover**

RRID:SCR\_006410

Type: Tool

### **Proper Citation**

DupRecover (RRID:SCR\_006410)

#### **Resource Information**

URL: https://bitbucket.org/wanding/duprecover/overview

**Proper Citation:** DupRecover (RRID:SCR\_006410)

Description: Software that facilitates accurate estimation for sampling-induced read

duplication in deep sequencing experiments.

Abbreviations: DupRecover

Resource Type: software resource

**Defining Citation: PMID:24389657** 

**Keywords:** python, overcorrection, variant, allele fraction, copy number variation

Funding: MD Anderson Odyssey recruitment fellowship;

The MD Anderson Cancer Center Sheikh Khalifa Ben Zayed Al Nahyan Institute of

Personalized Cancer Therapy;

NCI R01CA172652-01; NCI P30CA016672

Availability: Free, Public

Resource Name: DupRecover

Resource ID: SCR 006410

Alternate IDs: OMICS\_02201

**Record Creation Time:** 20220129T080236+0000

**Record Last Update:** 20250420T014326+0000

### Ratings and Alerts

No rating or validation information has been found for DupRecover.

No alerts have been found for DupRecover.

### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We have not found any literature mentions for this resource.