

# Resource Summary Report

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## DupRecover

RRID:SCR\_006410

Type: Tool

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### Proper Citation

DupRecover (RRID:SCR\_006410)

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### Resource Information

**URL:** <https://bitbucket.org/wandering/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:** 20260725T190623+0000

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### Ratings and Alerts

No rating or validation information has been found for DupRecover.

No alerts have been found for DupRecover.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.