

# Resource Summary Report

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## decontam

RRID:SCR\_028857

Type: Tool

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### Proper Citation

decontam (RRID:SCR\_028857)

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### Resource Information

**URL:** <https://github.com/benjjneb/decontam>

**Proper Citation:** decontam (RRID:SCR\_028857)

**Description:** Software R package for the statistical identification and removal of contaminant sequences in marker-gene (e.g. 16S rRNA) and metagenomics sequencing data. Implements frequency- and prevalence-based contaminant identification methods. Used for simple statistical identification and removal of contaminants in marker-gene and metagenomics sequencing data.

**Resource Type:** software resource, software toolkit, source code

**Defining Citation:** [PMID:30558668](#)

**Keywords:** Statistical identification and removal of contaminants, marker gene, metagenomics, sequencing data,

**Funding:** NIAID R01 AI112401;  
NIDCR R01 DE023113;  
Stanford University

**Availability:** Free, Available for download, Freely available

**Resource Name:** decontam

**Resource ID:** SCR\_028857

**Record Creation Time:** 20260821T194207+0000

**Record Last Update:** 20260912T200601+0000

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### Ratings and Alerts

No rating or validation information has been found for decontam.

No alerts have been found for decontam.

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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.