

# Resource Summary Report

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## BEERS2

RRID:SCR\_027287

Type: Tool

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### Proper Citation

BEERS2 (RRID:SCR\_027287)

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### Resource Information

**URL:** <https://github.com/itmat/BEERS2>

**Proper Citation:** BEERS2 (RRID:SCR\_027287)

**Description:** Software for simulation of RNA-seq reads. Combines flexible and highly configurable design with detailed simulation of entire library preparation and sequencing pipeline and is designed to include effects of polyA selection and RiboZero for ribosomal depletion, hexamer priming sequence biases, GC-content biases in polymerase chain reaction (PCR) amplification, barcode read errors and errors during PCR amplification.

**Resource Type:** source code, software resource, simulation software, software application

**Defining Citation:** [PMID:38605641](#)

**Keywords:** RNA-seq reads, simulation of RNA-seq reads,

**Funding:** NCATS 5UL1TR000003;  
NHLBI R01HL155934;  
NHLBI R01HL147472;  
NIGMS DP2GM146251

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

**Resource Name:** BEERS2

**Resource ID:** SCR\_027287

**License:** GNU GPL v3

**Record Creation Time:** 20250811T213301+0000

**Record Last Update:** 20260818T043826+0000

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### Ratings and Alerts

No rating or validation information has been found for BEERS2.

No alerts have been found for BEERS2.

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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.