

# Resource Summary Report

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## [refgenie](#)

RRID:SCR\_017574

Type: Tool

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### Proper Citation

refgenie (RRID:SCR\_017574)

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### Resource Information

**URL:** <http://refgenie.databio.org>

**Proper Citation:** refgenie (RRID:SCR\_017574)

**Description:** Software tool to organize, retrieve, and share genome analysis resources. Reference genome assembly asset manager. In addition to genome indexes, can manage any files related to reference genomes, including sequences and annotation files. Includes command line interface and server application that provides RESTful API, so it is useful for both tool development and analysis.

**Synonyms:** reference genome manager

**Resource Type:** software resource, software application, service resource, data management software

**Defining Citation:** [DOI:10.1101/698704](https://doi.org/10.1101/698704)

**Keywords:** Organize, retrieve, share, genome, analysis, reference, assembly, asset, manager, sequence, annotation, file, command, line, interface, bio.tools

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

**Resource Name:** refgenie

**Resource ID:** SCR\_017574

**Alternate IDs:** biotools:Refgenie

**Alternate URLs:** <https://bio.tools/Refgenie>

**Record Creation Time:** 20220129T080335+0000

**Record Last Update:** 20260801T190607+0000

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### Ratings and Alerts

No rating or validation information has been found for refgenie.

No alerts have been found for refgenie.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](#) .

Zacharias NM, et al. (2025) Differential Efficacy of Bevacizumab and Erlotinib in Preclinical Models of Renal Medullary Carcinoma and Fumarate Hydratase-Deficient Renal Cell Carcinoma. Molecular cancer therapeutics.

Stolarczyk M, et al. (2021) Identity and compatibility of reference genome resources. NAR genomics and bioinformatics, 3(2), lqab036.

M??lder F, et al. (2021) Sustainable data analysis with Snakemake. F1000Research, 10, 33.

Smith JP, et al. (2021) PEPPRO: quality control and processing of nascent RNA profiling data. Genome biology, 22(1), 155.

Smith JP, et al. (2021) PEPATAC: an optimized pipeline for ATAC-seq data analysis with serial alignments. NAR genomics and bioinformatics, 3(4), lqab101.

Stolarczyk M, et al. (2020) Refgenie: a reference genome resource manager. GigaScience, 9(2).