

Resource Summary Report

Generated by [RRID](#) on Sep 11, 2026

ShotGun

RRID:SCR_002529

Type: Tool

Proper Citation

ShotGun (RRID:SCR_002529)

Resource Information

URL: <http://www.unc.edu/~yunmli/shotgun.html>

Proper Citation: ShotGun (RRID:SCR_002529)

Description: Software for short read simulating in order to facilitate sequencing-based study designs.

Synonyms: ShotGun: a Flexible Short Read Simulator to Facilitate Sequencing-based Study Designs

Resource Type: data analysis software, data processing software, sequence analysis software, simulation software, software application, software resource

Defining Citation: [PMID:23357921](#)

Keywords: sequence based study design, short read stimulation, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: ShotGun

Resource ID: SCR_002529

Alternate IDs: biotools:abcd, OMICS_00255

Alternate URLs: <https://bio.tools/abcd>

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260905T132449+0000

Ratings and Alerts

No rating or validation information has been found for ShotGun.

No alerts have been found for ShotGun.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 35 mentions in open access literature.

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

Sorokin DY, et al. (2026) Physiology, functional genomics, and proteomics of *Verruconatronum alginivorum* gen. nov., sp. nov., the first isolated haloalkaliphile within Verrucomicrobiota, representing a new family, Verruconatronumaceae fam. nov. Applied and environmental microbiology, 92(6), e0047526.

de Medeiros Azevedo T, et al. (2026) Unlocking the microbiome of an extremophile plant: metagenomic insights into *Calotropis procera*'s endo-rhizosphere communities. World journal of microbiology & biotechnology, 42(4).

Frey B, et al. (2026) Metagenomic insights into viral and microbial genes of Russian High-Arctic soil microbiomes. Communications biology, 9(1).

Shih J, et al. (2025) StrainFacts accurately quantifies both endogenous and live biotherapeutic product strain abundances in simulated and clinical vaginal microbiota samples. bioRxiv : the preprint server for biology.

Brockway MM, et al. (2025) Comparing Impacts of Donor Human Milk to Formula Supplementation on the Gut Microbiome of Full-Term Infants Born Via Cesarean Section: Protocol for a Pilot Randomized Controlled Trial. Journal of human lactation : official journal of International Lactation Consultant Association, 41(4), 575.

Banerjee G, et al. (2025) Deep sequencing-derived Metagenome Assembled Genomes from the gut microbiome of liver transplant patients. Scientific data, 12(1), 39.

Watt K, et al. (2025) Epigenetic alterations facilitate transcriptional and translational programs in hypoxia. Nature cell biology, 27(11), 1965.

Yang Y, et al. (2025) Structural elucidation and characterization of GH29A α -L-fucosidases and the effect of pH on their transglycosylation. The FEBS journal, 292(3), 653.

Rubalskii E, et al. (2025) Characterization and genome analysis of the novel virulent Burkholderia phage Bm1, which is active against pan-drug-resistant Burkholderia multivorans. Archives of virology, 170(5), 106.

- Edwin NR, et al. (2025) Consistent microbial insights across sequencing methods in soil studies: the role of reference taxonomies. *mSystems*, 10(7), e0105924.
- Pang Y, et al. (2024) Predicting adherence to gamified cognitive training using early phase game performance data: Towards a just-in-time adherence promotion strategy. *PloS one*, 19(10), e0311279.
- Sirirungruang S, et al. (2024) Structural and biochemical basis for regiospecificity of the flavonoid glycosyltransferase UGT95A1. *The Journal of biological chemistry*, 300(9), 107602.
- Feng M, et al. (2024) Microbial genetic potential differs among cryospheric habitats of the Damma glacier. *Microbial genomics*, 10(10).
- Cowie AE, et al. (2024) The crystal structure of *Grindelia robusta* 7,13-copalyl diphosphate synthase reveals active site features controlling catalytic specificity. *The Journal of biological chemistry*, 300(12), 107921.
- Debeljak P, et al. (2023) Seasonal patterns in microbial carbon and iron transporter expression in the Southern Ocean. *Microbiome*, 11(1), 187.
- Avelar-Barragan J, et al. (2023) Characterizing the microbiome of patients with myeloproliferative neoplasms during a Mediterranean diet intervention. *mBio*, 14(6), e0230823.
- Pietrzak B, et al. (2022) A Clinical Outcome of the Anti-PD-1 Therapy of Melanoma in Polish Patients Is Mediated by Population-Specific Gut Microbiome Composition. *Cancers*, 14(21).
- Ghosh TS, et al. (2022) Toward an improved definition of a healthy microbiome for healthy aging. *Nature aging*, 2(11), 1054.
- Bloom SM, et al. (2022) Cysteine dependence of *Lactobacillus iners* is a potential therapeutic target for vaginal microbiota modulation. *Nature microbiology*, 7(3), 434.
- Demarchi B, et al. (2022) Ancient proteins resolve controversy over the identity of *Genyornis* eggshell. *Proceedings of the National Academy of Sciences of the United States of America*, 119(43), e2109326119.