

Resource Summary Report

Generated by [nidm-terms](#) on Aug 10, 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, simulation software, data processing software, software application, sequence analysis software, 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: 20260810T040330+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 [nidm-terms](#) .

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.

Edwin NR, et al. (2025) Consistent microbial insights across sequencing methods in soil studies: the role of reference taxonomies. mSystems, 10(7), e0105924.

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.

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.

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

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.