

Resource Summary Report

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STAMP

RRID:SCR_018887

Type: Tool

Proper Citation

STAMP (RRID:SCR_018887)

Resource Information

URL: <https://beikolab.cs.dal.ca/software/STAMP>

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Description: Open source software package for analyzing taxonomic or metabolic profiles that promotes best practices in choosing appropriate statistical techniques and reporting results. Graphical software package that provides statistical hypothesis tests and exploratory plots for analyzing taxonomic and functional profiles. Supports tests for comparing pairs of samples or samples organized into two or more treatment groups.

Synonyms: STAMP v2.1.3, statistical analysis of taxonomic and functional profiles

Resource Type: data analysis software, data processing software, data visualization software, software application, software resource, software toolkit

Defining Citation: [PMID:25061070](#)

Keywords: Statistical analysis, taxonomic profile, functional profile, metabolic profile, statistical hypothesis test, plot, sample, sample group, sample pair comparison, bio.tools

Funding: Australian Research Council ;
Canada Foundation for Innovation ;
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Dalhousie Centre for Comparative Genomics and Evolutionary Bioinformatics ;
Dalhousie Faculty of Computer Science ;
Genome Atlantic ;
Natural Sciences and Engineering Research Council of Canada ;
Tula Foundation Killam Trust

Availability: Free, Freely available

Resource Name: STAMP

Resource ID: SCR_018887

Alternate IDs: biotools:stamp-metagenomic

Alternate URLs: <https://github.com/dparks1134/STAMP>,
<https://github.com/dparks1134/STAMP/releases>, <https://bio.tools/stamp-metagenomic>

License: GNU GPL v3.0

Record Creation Time: 20220129T080342+0000

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Ratings and Alerts

No rating or validation information has been found for STAMP.

No alerts have been found for STAMP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 588 mentions in open access literature.

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

Sugiyama N, et al. (2026) Association of low progesterone levels and periodontal disease with threatened preterm labor. Scientific reports, 16(1), 5686.

Virginio Júnior GF, et al. (2026) Fecal microbiota succession in dairy calves is driven by age and modestly influenced by colostrum source. Scientific reports, 16(1).

Huang S, et al. (2026) Sleep deprivation disrupts lacrimal gland homeostasis via hypothalamic-pituitary-adrenal axis and gut dysbiosis in mice. Communications biology, 9(1).

Ling Z, et al. (2026) Gut dysbiosis and systemic inflammation in elderly hypertensive patients with amnesic mild cognitive impairment. Frontiers in immunology, 17, 1871446.

He Z, et al. (2026) Intestinal microbiota-host crosstalk reveals mechanisms regulating residual feed intake in egg-type ducks. BMC genomics, 27(1).

Huang J, et al. (2026) Emulsified essential oil-organic acid mixtures in drinking water reduce Salmonella Typhimurium infection and improve intestinal health in broilers. Poultry science, 105(1), 106138.

Zhang G, et al. (2026) Integrating 16S rRNA gene sequencing and transcriptomics to investigate the hepatoprotective effects of compound Ilicis Rotundae Cortex against

lipopolysaccharide / enrofloxacin-induced liver injury in chicks. *Poultry science*, 105(10), 107036.

Chen K, et al. (2026) Efficacy of *Bifidobacterium lactis* BLa80 in preventing early childhood eczema and respiratory infections via gut microbiome and immune modulation. *Frontiers in nutrition*, 13, 1727191.

Karubakee S, et al. (2026) Unveiling rhizobacterial diversity in rice-maize systems in response to penoxsulam-pendimethalin application. *BMC plant biology*, 26(1).

Wu CE, et al. (2026) Effects of *Ligilactobacillus salivarius* on the control of pullorum disease and cecal microbiota in red-feathered native chickens. *Poultry science*, 105(3), 106384.

Wagner VM, et al. (2026) Real-world benchmarking and validation of foundation model transformers for endometrial cancer subtyping from histopathology. *NPJ precision oncology*, 10(1).

Cha J, et al. (2026) Comparative metagenomic analysis of gut microbiomes in Yunnan ponies and Dutch warmblood horses. *Frontiers in microbiology*, 17, 1807081.

Deng Y, et al. (2026) Dual beneficial activities of *Paenibacillus ottowii* NPDY10: glyphosate degradation, modulation of soil microbial communities, and antagonism against phytopathogenic fungi. *Microbial cell factories*, 25(1).

Laakso H, et al. (2026) Impact of chronic low-dose external gamma- and internal tritium beta-irradiation on the gut microbiome in the context of intestinal tumorigenesis in *ApcMin/+* mice. *mSystems*, 11(4), e0115625.

Shi K, et al. (2026) Systemic remodeling of the multi-organ virome following *Echinococcus* infection in mice. *BMC microbiology*, 26(1).

Kaiyue P, et al. (2026) Fermentation quality and microbial communities of mixed silage from *Pennisetum glaucum* × *purpureum* and *Rosa roxburghii* residue. *BMC microbiology*, 26(1).

Schwarzmann L, et al. (2026) AI-assisted histomorphological stratification of endometrial cancer: real-world validation of foundation models for molecular subtyping. *NPJ precision oncology*, 10(1).

Su WH, et al. (2026) Gut microbiota and metabolomic alterations in newborns of mothers with gestational diabetes mellitus. *Clinical and experimental pediatrics*, 69(1), 26.

Liu Q, et al. (2026) Biocontrol efficiency and mechanism of novel *Streptomyces luomodiensis* SCA4-21 against banana *Fusarium* wilt. *Microbiology spectrum*, 14(1), e0296824.

Shahid MAH, et al. (2026) Changes in the gut microbiome, metabolic pathways, and intestinal gene expression during the peak, mid, and decline egg production phases in laying hens. *Poultry science*, 105(3), 106372.