

Resource Summary Report

Generated by [RRID](#) on Aug 6, 2026

[speciateIT](#)

RRID:SCR_014615

Type: Tool

Proper Citation

speciateIT (RRID:SCR_014615)

Resource Information

URL: <https://sourceforge.net/projects/speciateit/>

Proper Citation: speciateIT (RRID:SCR_014615)

Description: A software package for speciation of 16S sequence data.

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

Keywords: microbiome, 16s, 16s sequence, speciation

Availability: Available for download

Resource Name: speciateIT

Resource ID: SCR_014615

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260806T054609+0000

Ratings and Alerts

No rating or validation information has been found for speciateIT.

No alerts have been found for speciateIT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Prodger J, et al. (2025) The Futility of Nugent Scoring as a Diagnostic Tool for Neovaginal Bacterial Dysbiosis in Transfeminine People. Research square.

Williams A, et al. (2025) Temporal dynamics of the vaginal microbiome and host immune markers before, during, and after metronidazole treatment for bacterial vaginosis. mSystems, 10(7), e0038025.

Jeong S, et al. (2025) Cervicovaginal microbial features predict Chlamydia trachomatis spread to the upper genital tract of infected women. Infection and immunity, 93(9), e0005725.

Kawasaki R, et al. (2025) Distinct cervical microbiome and metabolite profiles before and after menopause: implications for cervical cancer progression. Frontiers in cellular and infection microbiology, 15, 1589277.

Rojas-Vargas J, et al. (2025) The neovaginal microbiota, symptoms, and local immune correlates in transfeminine individuals with penile inversion vaginoplasty. Cell reports, 44(12), 116546.

Holm JB, et al. (2024) SpeciateIT and vSpeciateDB: Novel, fast and accurate per sequence 16S rRNA gene taxonomic classification of vaginal microbiota. bioRxiv : the preprint server for biology.

Nishio E, et al. (2024) Metabolomic and microbiome analysis of cervicovaginal mucus in in vitro fertilization-embryo transfer: Toward predicting pregnancy success. Reproductive medicine and biology, 23(1), e12568.

Robbins SJ, et al. (2024) Uterine fibroids and longitudinal profiles of the vaginal microbiota in a cohort presenting for transvaginal ultrasound. PloS one, 19(2), e0296346.

Tuddenham S, et al. (2023) Lactobacillus-dominance and rapid stabilization of vaginal microbiota in combined oral contraceptive pill users examined through a longitudinal cohort study with frequent vaginal sampling over two years. EBioMedicine, 87, 104407.

Tsamir-Rimon M, et al. (2023) A manifold-based framework for studying the dynamics of the vaginal microbiome. NPJ biofilms and microbiomes, 9(1), 102.

Haddad LB, et al. (2023) Influence of Hormonal Contraceptive Use and HIV on Cervicovaginal Cytokines and Microbiota in Malawi. mSphere, 8(1), e0058522.

Tsamir-Rimon M, et al. (2023) A Manifold-Based Framework for Studying the Dynamics of the Vaginal Microbiome. bioRxiv : the preprint server for biology.

Sakabe Y, et al. (2022) Longitudinal study of the vaginal microbiome in pregnancies involving preterm labor. Fujita medical journal, 8(3), 96.

Mazibuko-Motau N, et al. (2022) Vaginal microbial shifts are unaffected by oral pre-exposure prophylaxis in South African women. Scientific reports, 12(1), 16187.

Kawahara R, et al. (2021) Changes to the cervicovaginal microbiota and cervical cytokine profile following surgery for cervical intraepithelial neoplasia. *Scientific reports*, 11(1), 2156.

Merenstein D, et al. (2021) *Bifidobacterium animalis* subsp. *lactis* BB-12 Protects against Antibiotic-Induced Functional and Compositional Changes in Human Fecal Microbiome. *Nutrients*, 13(8).

Mtshali A, et al. (2021) Temporal Changes in Vaginal Microbiota and Genital Tract Cytokines Among South African Women Treated for Bacterial Vaginosis. *Frontiers in immunology*, 12, 730986.

Jašarević E, et al. (2021) The composition of human vaginal microbiota transferred at birth affects offspring health in a mouse model. *Nature communications*, 12(1), 6289.

Tamarelle J, et al. (2020) Nonoptimal Vaginal Microbiota After Azithromycin Treatment for *Chlamydia trachomatis* Infection. *The Journal of infectious diseases*, 221(4), 627.

Koirala R, et al. (2020) Effect of oral consumption of capsules containing *Lactobacillus paracasei* LPC-S01 on the vaginal microbiota of healthy adult women: a randomized, placebo-controlled, double-blind crossover study. *FEMS microbiology ecology*, 96(6).