

Resource Summary Report

Generated by [dkNET](#) on Aug 7, 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: sequence analysis software, software resource, data analysis software, data processing software, software application

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: 20260807T042822+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 34 mentions in open access literature.

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

Kamiya T, et al. (2026) Resource landscape shapes the composition and stability of the human vaginal microbiota. *PLoS biology*, 24(2), e3003575.

Parmar R, et al. (2026) The Nugent score is an inappropriate diagnostic tool for neovaginal bacteria in transfeminine people. *Communications medicine*, 6(1).

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.

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

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.

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.

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.

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*.

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.

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.

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.

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.

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.