

Resource Summary Report

Generated by [kravitz2](#) on Sep 17, 2026

Samba

RRID:SCR_006557

Type: Tool

Proper Citation

Samba (RRID:SCR_006557)

Resource Information

URL: <http://www.samba.org/>

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Description: Standard Windows interoperability suite of programs for Linux and Unix that provides secure, stable and fast file and print services for all clients using the SMB/CIFS protocol, such as all versions of DOS and Windows, OS/2, Linux and many others. Samba is an important component to seamlessly integrate Linux/Unix Servers and Desktops into Active Directory environments using the winbind daemon.

Abbreviations: Samba

Resource Type: software application, software resource, systems interoperability software

Keywords: interoperability, linux, unix, windows

Availability: GNU General Public License

Resource Name: Samba

Resource ID: SCR_006557

Alternate IDs: nlx_156712

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260912T200236+0000

Ratings and Alerts

No rating or validation information has been found for Samba.

No alerts have been found for Samba.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 133 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Leal K, et al. (2026) Exploration of inactive metabolic pathways in Antarctic *Pseudogymnoascus australis* through elicitation: a genomic and metabolomic approach to investigate its biotechnological potential. *IMA fungus*, 17, e156018.

Totikov AA, et al. (2026) Comparative Genomics and Phylogenomics of the Mustelinae Lineage (Mustelidae, Carnivora). *Genome biology and evolution*, 18(3).

Kosushkin SA, et al. (2026) Genome sequencing uncovers the history of the Russian desman's gradual population decline and contributes to the evolutionary history of *Talpidae*. *BMC ecology and evolution*, 26(1), 12.

Mele S, et al. (2026) A Segment Anything Model-based tool for semi-automated behavioural analysis of *Drosophila* and other model organisms. *Disease models & mechanisms*, 19(2).

Szablińska-Piernik J, et al. (2026) Giant chromosomes of a tiny plant-the complete telomere-to-telomere genome assembly of the simple thalloid liverwort *Apopellia endiviifolia* (Jungermanniopsida, Marchantiophyta). *GigaScience*, 15.

Robino E, et al. (2026) Diversity and varying predation capacities of culturable Amoebozoae against opportunistic vibrios in contrasting Mediterranean coastal environments. *Microbiology spectrum*, 14(3), e0113825.

Neale DB, et al. (2026) A reference genome sequence for the exceptionally long-lived Great Basin bristlecone pine, *Pinus longaeva*. *G3 (Bethesda, Md.)*, 16(6).

Sari E, et al. (2026) Gene duplication, horizontal gene transfer, and trait trade-offs drive evolution of postfire resource acquisition in pyrophilous fungi. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2519152123.

Six C, et al. (2026) Unravelling the molecular diversity of marine cyanobacterial communities in the lagoon of Nouméa (New Caledonia): impact of a cyclonic event. *ISME communications*, 6(1), ycag032.

Naya-Català F, et al. (2026) Dietary rayon microfibers differentially reshape rearing water and host associated microbiomes of farmed European sea bass (*Dicentrarchus labrax*). *Environmental microbiome*, 21(1), 30.

Wen H, et al. (2025) TRFill: synergistic use of HiFi and Hi-C sequencing enables accurate assembly of tandem repeats for population-level analysis. *Genome biology*, 26(1), 227.

Wertz AE, et al. (2025) A semisynthetic, multifactor artificial metalloenzyme retains independent site activity. *Journal of biological inorganic chemistry : JBIC : a publication of the Society of Biological Inorganic Chemistry*, 30(1), 13.

Atkin C, et al. (2025) Provision of medical same day emergency care services within the UK: analysis from the Society for Acute Medicine Benchmarking Audit. *BMJ open*, 15(4), e094580.

Cohen-Rengifo M, et al. (2025) The nasal microbiota of two marine fish species: diversity, community structure, variability, and first insights into the impacts of climate change-related stressors. *FEMS microbiology ecology*, 101(3).

Zhang H, et al. (2025) Spatially resolved C1QC+ macrophage-CD4+ T cell niche in colorectal cancer microenvironment: implications for immunotherapy response. *Cell discovery*, 11(1), 60.

Mansour H, et al. (2025) The Duke Mouse Brain Atlas: MRI and light sheet microscopy stereotaxic atlas of the mouse brain. *Science advances*, 11(18), eadq8089.

Rousseau C, et al. (2025) A Practical Comparison of Short- and Long-Read Metabarcoding Sequencing: Challenges and Solutions for Plastid Read Removal and Microbial Community Exploration of Seaweed Samples. *Molecular ecology resources*, 25(7), e14129.

Bridgford EW, et al. (2025) Network Biomarkers of Alzheimer's Disease Risk Derived from Joint Volume and Texture Covariance Patterns in Mouse Models. *bioRxiv : the preprint server for biology*.

Moon HS, et al. (2025) Smelling the Risk: Early Olfactory Deficits, Brain Networks, and Blood Markers of Alzheimer's Disease Risk in Humanized APOE Mice. *bioRxiv : the preprint server for biology*.

Paulino S, et al. (2025) Drivers of seasonal dynamics in *Ulva* spp. associated microbiota and surface metabolome: The interplay between environment and host physiology. *Current research in microbial sciences*, 9, 100439.