

Resource Summary Report

Generated by [dkNET](#) on Aug 7, 2026

Stampy

RRID:SCR_005504

Type: Tool

Proper Citation

Stampy (RRID:SCR_005504)

Resource Information

URL: <http://www.well.ox.ac.uk/project-stampy>

Proper Citation: Stampy (RRID:SCR_005504)

Description: A software package for the mapping of short reads from illumina sequencing machines onto a reference genome. It's recommended for most workflows, including those for genomic resequencing, RNA-Seq and Chip-seq. Stampy excels in the mapping of reads containing that contain sequence variation relative to the reference, in particular for those containing insertions or deletions. It can map reads from a highly divergent species to a reference genome for instance. Stampy achieves high sensitivity and speed by using a fast hashing algorithm and a detailed statistical model. Stampy has the following features: * Maps single, paired-end and mate pair Illumina reads to a reference genome * Fast: about 20 Gbase per hour in hybrid mode (using BWA) * Low memory footprint: 2.7 Gb shared memory for a 3Gbase genome * High sensitivity for indels and divergent reads, up to 10-15% * Low mapping bias for reads with SNPs * Well calibrated mapping quality scores * Input: Fastq and Fasta; gzipped or plain * Output: SAM, Maq's map file * Optionally calculates per-base alignment posteriors * Optionally processes part of the input * Handles reads of up to 4500 bases

Abbreviations: Stampy

Resource Type: software resource

Defining Citation: [PMID:20980556](#)

Keywords: bio.tools

Resource Name: Stampy

Resource ID: SCR_005504

Alternate IDs: OMICS_00691, biotools:stampy

Alternate URLs: <https://bio.tools/stampy>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260801T190259+0000

Ratings and Alerts

No rating or validation information has been found for Stampy.

No alerts have been found for Stampy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 184 mentions in open access literature.

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

Xu Z, et al. (2026) The nucleoid-associated protein subunit HupA positively regulates the Pqs system and pyocyanin production in *Pseudomonas aeruginosa*. *Applied and environmental microbiology*, 92(4), e0242525.

Kang M, et al. (2026) NGSMHC: a simple bioinformatics tool for comprehensively typing major histocompatibility complex genes in non-human species using next-generation sequencing data. *Animal bioscience*, 39(2), 250468.

Wang X, et al. (2025) An antibiotic-responsive regulator orchestrates chronic-to-acute virulence switch in *Pseudomonas aeruginosa*. *Nucleic acids research*, 53(10).

Llopart A, et al. (2025) A high-resolution crossover landscape in *Drosophila santomea* reveals rapid and concerted evolution of multiple properties of crossing over control. *PLoS genetics*, 21(10), e1011885.

Gagnon S, et al. (2025) TBpore cluster: A novel phylogenetic pipeline for tuberculosis transmission studies using nanopore next-generation sequencing data. *PloS one*, 20(6), e0325914.

Garc  a-Berro A, et al. (2025) A north-south hemispheric migratory divide in the butterfly *Vanessa cardui*. *Nature communications*, 16(1), 11341.

Shahreen N, et al. (2025) Minimal gene signatures enable high-accuracy prediction of antibiotic resistance in *Pseudomonas aeruginosa*. *NPJ systems biology and applications*, 11(1), 108.

Cornetti L, et al. (2024) Long-term balancing selection for pathogen resistance maintains trans-species polymorphisms in a planktonic crustacean. *Nature communications*, 15(1),

Officer K, et al. (2024) Genomic insights into anthroponotic tuberculosis in captive sun bears (*Helarctos malayanus*) and an Asiatic black bear (*Ursus thibetanus*) in Cambodia. *Scientific reports*, 14(1), 7343.

Edwards SV, et al. (2024) A nuclear genome assembly of an extinct flightless bird, the little bush moa. *Science advances*, 10(21), eadj6823.

Liu X, et al. (2024) A genome-wide association study reveals the relationship between human genetic variation and the nasal microbiome. *Communications biology*, 7(1), 139.

Kingsley EP, et al. (2024) Adaptive tail-length evolution in deer mice is associated with differential *Hoxd13* expression in early development. *Nature ecology & evolution*, 8(4), 791.

Tapanes E, et al. (2024) The genetic basis of divergent melanistic pigmentation in benthic and limnetic threespine stickleback. *Heredity*, 133(4), 207.

Miyazaki S, et al. (2023) *Zfp296* knockout enhances chromatin accessibility and induces a unique state of pluripotency in embryonic stem cells. *Communications biology*, 6(1), 771.

Durak MR, et al. (2023) Genome-Wide Discovery of Structural Variants Reveals Distinct Variant Dynamics for Two Closely Related *Monilinia* Species. *Genome biology and evolution*, 15(6).

Li X, et al. (2023) Comparing genomic variant identification protocols for *Candida auris*. *Microbial genomics*, 9(4).

Lee CK, et al. (2023) Successful Confirmation of Dual Genital Herpes Co-Infection with Herpes Simplex Virus 1 and Herpes Simplex Virus 2 Using Unbiased Metagenomic Next-Generation Sequencing. *Viruses*, 15(9).

Lange JD, et al. (2022) A Population Genomic Assessment of Three Decades of Evolution in a Natural *Drosophila* Population. *Molecular biology and evolution*, 39(2).

Pan B, et al. (2022) Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. *Genome biology*, 23(1), 2.

Freitas S, et al. (2022) Parthenogenesis in *Darevskia* lizards: A rare outcome of common hybridization, not a common outcome of rare hybridization. *Evolution; international journal of organic evolution*, 76(5), 899.