

Resource Summary Report

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Guppy basecaller

RRID:SCR_023196

Type: Tool

Proper Citation

Guppy basecaller (RRID:SCR_023196)

Resource Information

URL: https://community.nanoporetech.com/docs/prepare/library_prep_protocols/Guppy-protocol/v/gpb_2003_v1_revao_14dec2018

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Description: Software toolkit that enables real-time basecalling and several post-processing features that works on Oxford Nanopore Technologies sequencing platforms. Data processing toolkit that contains Oxford Nanopore Technologies basecalling algorithms, and several bioinformatic post-processing features. Provided as binaries to run on Windows, OS X and Linux platforms, as well as being integrated with MinkNOW, Oxford Nanopore device control software.

Resource Type: software toolkit, software resource

Keywords: Oxford Nanopore Technologies, sequencing platform, basecalling algorithm,

Availability: Restricted

Resource Name: Guppy basecaller

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Alternate URLs:

https://media.tghn.org/medialibrary/2021/10/ONT_bioinformatics_pipeline_-_basecalling_to_alignment_V1.1.pdf

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Ratings and Alerts

No rating or validation information has been found for Guppy basecaller.

No alerts have been found for Guppy basecaller.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. *Genome biology*, 27(1).

Pradhan B, et al. (2026) Dynamic and Ongoing De Novo L1 Retrotransposition Contributes to Genome Plasticity and Intrapatient Heterogeneity in Ovarian Cancer. *Cancer research*, 86(4), 1073.

Dor?? G, et al. (2026) First draft genome of the decaploid species, *Ludwigia grandiflora* subsp. *hexapetala*, validated through gene expression. *GigaByte (Hong Kong, China)*, 2026, gigabyte176.

Lee M, et al. (2026) LINE-1 Locus Transcription Nucleates Oncogenic Chromatin Architecture. *Cancer discovery*, 16(4), 800.

Pigeault R, et al. (2026) Within-Host Environmental Heterogeneity Is Associated With Phenotypic but Not Genomic Diversity in *Wolbachia* Endosymbionts. *Environmental microbiology reports*, 18(1), e70286.

Mortazavi M, et al. (2026) Long-read genome sequencing improves detection and functional interpretation of structural and repeat variants in autism. *Cell genomics*, 6(5), 101186.

Bjornson S, et al. (2026) Stepwise evolutionary transitions in *Cladophorales* plastid genomes reveal origins of hairpin chromosomes. *Current biology : CB*, 36(7), 1659.

Ritter EJ, et al. (2025) The assembly and annotation of two teinturier grapevine varieties, Dakapo and Rubired. *GigaByte (Hong Kong, China)*, 2025, gigabyte149.

Ahn A, et al. (2025) Impact of Acute Endurance Exercise on Alternative Splicing in Skeletal Muscle. *bioRxiv : the preprint server for biology*.

Ahn A, et al. (2025) Impact of Acute Endurance Exercise on Alternative Splicing in Skeletal Muscle. *FASEB bioAdvances*, 7(8), e70024.

Ye F, et al. (2025) Characteristics and filtering of low-frequency artificial short deletion variations based on nanopore sequencing. *GigaScience*, 14.

Lee GY, et al. (2025) Rifampin mediated decapsulation and enhanced bacterial clearance: a new mechanism of rifamycins. *EBioMedicine*, 117, 105787.

Mehta I, et al. (2025) Control of pili synthesis and putrescine homeostasis in *Escherichia coli*. *eLife*, 13.

De Thier O, et al. (2025) First chromosome-level genome assembly of the colonial chordate model *Botryllus schlosseri* (Tunicata). *GigaScience*, 14.

Higginson LA, et al. (2025) The RNA exosome maintains cellular RNA homeostasis by controlling transcript abundance in the brain. *Cell reports*, 45(1), 116729.

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. *bioRxiv* : the preprint server for biology.

Dar SA, et al. (2024) Full-length direct RNA sequencing uncovers stress granule-dependent RNA decay upon cellular stress. *eLife*, 13.

McCormick CA, et al. (2024) Multicellular, IVT-derived, unmodified human transcriptome for nanopore-direct RNA analysis. *GigaByte* (Hong Kong, China), 2024, gigabyte129.

Salindeho RA, et al. (2024) Re-sequencing of the complete chloroplast genome of *Cinnamomum burmanni* (Nees & T.Nees) Blume (Lauraceae) from Indonesia using MinION Oxford Nanopore Technologies. *F1000Research*, 13, 127.

Manzulli V, et al. (2024) *Psychrobacter raelei* sp. nov., isolated from a dog with peritonitis. *International journal of systematic and evolutionary microbiology*, 74(4).