

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

[freelbis](#)

RRID:SCR_001241

Type: Tool

Proper Citation

freelbis (RRID:SCR_001241)

Resource Information

URL: <https://github.com/grenaud/freelbis>

Proper Citation: freelbis (RRID:SCR_001241)

Description: A software basecaller for Illumina sequencers with calibrated quality scores.

Abbreviations: freelbis

Synonyms: freelbis - Improved Base Identification System

Resource Type: software resource

Defining Citation: [PMID:23471300](#)

Keywords: illumina, basecaller, sequencer

Availability: Free, Freely available

Resource Name: freelbis

Resource ID: SCR_001241

Alternate IDs: OMICS_02217

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260808T185727+0000

Ratings and Alerts

No rating or validation information has been found for freelbis.

No alerts have been found for freelbis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Sontowski R, et al. (2020) Infection Patterns and Fitness Effects of Rickettsia and Sodalis Symbionts in the Green Lacewing Chrysoperla carnea. Insects, 11(12).

Helm C, et al. (2018) Convergent evolution of the ladder-like ventral nerve cord in Annelida. Frontiers in zoology, 15, 36.

Glocke I, et al. (2017) Extending the spectrum of DNA sequences retrieved from ancient bones and teeth. Genome research, 27(7), 1230.

Slon V, et al. (2017) A fourth Denisovan individual. Science advances, 3(7), e1700186.

Richter S, et al. (2017) Comparative analyses of glycerotoxin expression unveil a novel structural organization of the bloodworm venom system. BMC evolutionary biology, 17(1), 64.

Aguado MT, et al. (2016) Characterization of the complete mitochondrial genomes from Polycladida (Platyhelminthes) using next-generation sequencing. Gene, 575(2 Pt 1), 199.

Aguado MT, et al. (2016) Syllidae mitochondrial gene order is unusually variable for Annelida. Gene, 594(1), 89.

Ni S, et al. (2016) Improvement in detection of minor alleles in next generation sequencing by base quality recalibration. BMC genomics, 17, 139.

Mora-Bermudez F, et al. (2016) Differences and similarities between human and chimpanzee neural progenitors during cerebral cortex development. eLife, 5.

Stiller M, et al. (2016) Single-strand DNA library preparation improves sequencing of formalin-fixed and paraffin-embedded (FFPE) cancer DNA. Oncotarget, 7(37), 59115.

Richter S, et al. (2015) The Utility of Genome Skimming for Phylogenomic Analyses as Demonstrated for Glycerid Relationships (Annelida, Glyceridae). Genome biology and evolution, 7(12), 3443.

Aguado MT, et al. (2015) The making of a branching annelid: an analysis of complete mitochondrial genome and ribosomal data of Ramisyllis multicaudata. Scientific reports, 5, 12072.