

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

NextClip

RRID:SCR_005465

Type: Tool

Proper Citation

NextClip (RRID:SCR_005465)

Resource Information

URL: <https://github.com/richardmleggett/nextclip/>

Proper Citation: NextClip (RRID:SCR_005465)

Description: A software tool for analysing reads from Long Mate Pair (LMP) libraries, generating a comprehensive quality report and extracting good quality trimmed and deduplicated reads.

Abbreviations: NextClip

Synonyms: NextClip - Nextera Long Mate Pair analysis and processing tool

Resource Type: software resource

Defining Citation: [PMID:24297520](#)

Resource Name: NextClip

Resource ID: SCR_005465

Alternate IDs: OMICS_01061

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260912T195626+0000

Ratings and Alerts

No rating or validation information has been found for NextClip.

No alerts have been found for NextClip.

Data and Source Information

Usage and Citation Metrics

We found 73 mentions in open access literature.

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

Cadavid S??nchez IC, et al. (2025) Harnessing genetic diversity: The genomic and transcriptomic insights of *Eugenia uniflora* for environmental resilience. *PloS one*, 20(11), e0333437.

Konuma J, et al. (2024) Odd-Paired is Involved in Morphological Divergence of Snail-Feeding Beetles. *Molecular biology and evolution*, 41(6).

Peris D, et al. (2023) Macroevolutionary diversity of traits and genomes in the model yeast genus *Saccharomyces*. *Nature communications*, 14(1), 690.

Henning PM, et al. (2023) Annotation of the *Turnera subulata* (Passifloraceae) Draft Genome Reveals the S-Locus Evolved after the Divergence of *Turneroideae* from *Passifloroideae* in a Stepwise Manner. *Plants (Basel, Switzerland)*, 12(2).

Vilela N, et al. (2023) Integrative omics analyses of the ligninolytic *Rhodospiridium fluviale* LM-2 disclose catabolic pathways for biobased chemical production. *Biotechnology for biofuels and bioproducts*, 16(1), 5.

Jackson HA, et al. (2022) Genomic erosion in a demographically recovered bird species during conservation rescue. *Conservation biology : the journal of the Society for Conservation Biology*, 36(4), e13918.

Reddy B, et al. (2022) Structured Framework and Genome Analysis of *Magnaporthe grisea* Inciting Pearl Millet Blast Disease Reveals Versatile Metabolic Pathways, Protein Families, and Virulence Factors. *Journal of fungi (Basel, Switzerland)*, 8(6).

Thrimawithana AH, et al. (2022) The Genomics and Population Genomics of the Light Brown Apple Moth, *Epiphyas postvittana*, an Invasive Tortricid Pest of Horticulture. *Insects*, 13(3).

Ng CS, et al. (2022) Genome Assembly and Evolutionary Analysis of the Mandarin Duck *Aix galericulata* Reveal Strong Genome Conservation among Ducks. *Genome biology and evolution*, 14(6).

de Figueiredo FL, et al. (2021) Multi-omics analysis provides insights into lignocellulosic biomass degradation by *Laetiporus sulphureus* ATCC 52600. *Biotechnology for biofuels*, 14(1), 96.

Kawato S, et al. (2021) Genome and transcriptome assemblies of the kuruma shrimp, *Marsupenaeus japonicus*. *G3 (Bethesda, Md.)*, 11(11).

Celorio-Mancera MP, et al. (2021) Chromosome Level Assembly of the Comma Butterfly (*Polygonia c-album*). *Genome biology and evolution*, 13(5).

Lichman BR, et al. (2020) The evolutionary origins of the cat attractant nepetalactone in catnip. *Science advances*, 6(20), eaba0721.

Bell L, et al. (2020) The *Eruca sativa* Genome and Transcriptome: A Targeted Analysis of Sulfur Metabolism and Glucosinolate Biosynthesis Pre and Postharvest. *Frontiers in plant science*, 11, 525102.

Imachi H, et al. (2020) Isolation of an archaeon at the prokaryote-eukaryote interface. *Nature*, 577(7791), 519.

Lau KH, et al. (2020) Genome assembly of *Chiococca alba* uncovers key enzymes involved in the biosynthesis of unusual terpenoids. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 27(3).

Beedessee G, et al. (2020) Integrated omics unveil the secondary metabolic landscape of a basal dinoflagellate. *BMC biology*, 18(1), 139.

Dennis AB, et al. (2020) Functional insights from the GC-poor genomes of two aphid parasitoids, *Aphidius ervi* and *Lysiphlebus fabarum*. *BMC genomics*, 21(1), 376.

Kelly LJ, et al. (2020) Convergent molecular evolution among ash species resistant to the emerald ash borer. *Nature ecology & evolution*, 4(8), 1116.

Stephens TG, et al. (2020) Genomes of the dinoflagellate *Polarella glacialis* encode tandemly repeated single-exon genes with adaptive functions. *BMC biology*, 18(1), 56.