

# Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

## kent

RRID:SCR\_026686

Type: Tool

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### Proper Citation

kent (RRID:SCR\_026686)

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### Resource Information

**URL:** <https://github.com/ucscGenomeBrowser/kent>

**Proper Citation:** kent (RRID:SCR\_026686)

**Description:** UCSC Genome Browser source tree. Stable branch: "beta".

**Resource Type:** source code, software resource

**Keywords:** UCSC Genome Browser source tree

**Availability:** Free, Available for download, Freely available

**Resource Name:** kent

**Resource ID:** SCR\_026686

**License:** MIT License

**License URLs:** <https://github.com/ucscGenomeBrowser/kent?tab=License-1-ov-file#readme>

**Record Creation Time:** 20250401T060330+0000

**Record Last Update:** 20260810T040931+0000

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### Ratings and Alerts

No rating or validation information has been found for kent.

No alerts have been found for kent.

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### Data and Source Information

## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Shukla N, et al. (2026) Lift&Add-rapid and robust addition of new species to alignments of conserved non-coding sequences. *Bioinformatics* (Oxford, England), 42(6).

Subramani PG, et al. (2026) DOT1L activity limits transcription elongation velocity and favors RNAPII pausing to facilitate mutagenesis by AID. *Nature communications*, 17(1), 1623.

Holub E, et al. (2026) Effects of thymidylate synthase inhibitors differ in genomic uracilation and mutagenic potential. *Life science alliance*, 9(4).

MacDonald ZG, et al. (2026) Genome assembly for the Sierra Nevada Parnassian (*Parnassius behrii*) and a brief review of butterfly genome sizes. *The Journal of heredity*, 117(4), 888.

Swift SZ, et al. (2026) Integration of Short- and Long-Read RNA Sequencing Enables the Discovery of Circular RNAs. *Cancer research*, 86(5), 1300.

Wooldridge TB, et al. (2025) Chromosome-scale Genomes Show Rapid Diversification and Ancient Gene Flow Among Bear Species. *Genome biology and evolution*, 17(11).

Teyssier E, et al. (2025) A plant Lysin Motif Receptor-Like Kinase plays an ancestral function in mycorrhiza. *Proceedings of the National Academy of Sciences of the United States of America*, 122(24), e2426063122.

Vanhaeren T, et al. (2025) Enhancing R-loop prediction with high-throughput sequencing data. *NAR genomics and bioinformatics*, 7(2), lqaf077.

Zhu WS, et al. (2023) GCLiPP: global crosslinking and protein purification method for constructing high-resolution occupancy maps for RNA binding proteins. *Genome biology*, 24(1), 281.

Penny MK, et al. (2023) Targeting Oncogenic Wnt/??-Catenin Signaling in Adrenocortical Carcinoma Disrupts ECM Expression and Impairs Tumor Growth. *Cancers*, 15(14).

Rele CP, et al. (2022) Manual annotation of Drosophila genes: a Genomics Education Partnership protocol. *F1000Research*, 11, 1579.