

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

kent

RRID:SCR_026686

Type: Tool

Proper Citation

kent (RRID:SCR_026686)

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: software resource, source code

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: 20260912T200509+0000

Ratings and Alerts

No rating or validation information has been found for kent.

No alerts have been found for kent.

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 [SPARC SAWG](#) .

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.

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).

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.