Resource Summary Report

Generated by NIF on Apr 21, 2025

KING

RRID:SCR_009251
Type: Tool

Proper Citation

KING (RRID:SCR_009251)

Resource Information

URL: http://people.virginia.edu/~wc9c/KING/

Proper Citation: KING (RRID:SCR_009251)

Description: Software toolset that makes use of high-throughput SNP data typically seen in a genome-wide association study (GWAS) for applications such as family relationship inference and population structure identification (entry from Genetic Analysis Software)

Abbreviations: KING

Synonyms: Kinship-based INference for Gwas

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c++, linux, (64bit), ms-windows, ms-dos, macos, ubuntu, (32bit)

Funding:

Resource Name: KING

Resource ID: SCR_009251

Alternate IDs: nlx_154419

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250421T053723+0000

Ratings and Alerts

No rating or validation information has been found for KING.

No alerts have been found for KING.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 940 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Aizpurua-Iraola J, et al. (2025) A reduction in effective population size has not relaxed purifying selection in the human population of Eivissa (Balearic Islands). Scientific reports, 15(1), 660.

Hossain A, et al. (2025) Palliative care needs and quality of life among adults with advanced chronic illnesses in low-income communities of Bangladesh. BMC palliative care, 24(1), 18.

De Jager P, et al. (2025) GWAS highlights the neuronal contribution to multiple sclerosis susceptibility. Research square.

Tian Y, et al. (2025) Population Genomics Reveals Elevated Inbreeding and Accumulation of Deleterious Mutations in White Raccoon Dogs. Biology, 14(1).

Oetzmann C, et al. (2025) Identifying depression subtypes and investigating their consistency and transitions in a 1-year cohort analysis. PloS one, 20(1), e0314604.

Huang YJ, et al. (2025) A semi-empirical Bayes approach for calibrating weak instrumental bias in sex-specific Mendelian randomization studies. medRxiv : the preprint server for health sciences.

Bellou E, et al. (2025) Benchmarking Alzheimer's disease prediction: personalised risk assessment using polygenic risk scores across various methodologies and genome-wide studies. Alzheimer's research & therapy, 17(1), 6.

Wang L, et al. (2025) Novel loci for triglyceride/HDL-C ratio longitudinal change among subjects without T2D. Journal of lipid research, 66(1), 100702.

Halligan NLN, et al. (2025) Variants in the ?-globin locus are associated with pneumonia in African American children. HGG advances, 6(1), 100374.

Khalkhali-Evrigh R, et al. (2025) Genomic evidence of improved fertility and adaptation in Iranian domestic sheep attributed to introgression from Asiatic Mouflon and urial. Scientific reports, 15(1), 1185.

Jung S, et al. (2025) Rare Variant Analyses in Ancestrally Diverse Cohorts Reveal Novel ADHD Risk Genes. medRxiv : the preprint server for health sciences.

Hovhannisyan A, et al. (2025) Demographic history and genetic variation of the Armenian population. American journal of human genetics, 112(1), 11.

Crouch DJM, et al. (2025) Bayesian Effect Size Ranking to Prioritise Genetic Risk Variants in Common Diseases for Follow-Up Studies. Genetic epidemiology, 49(1), e22608.

Liu T, et al. (2025) Investigating misclassification of type 1 diabetes in a population-based cohort of British Pakistanis and Bangladeshis using polygenic risk scores. Scientific reports, 15(1), 1168.

Gouveia MH, et al. (2025) Subcontinental Genetic Diversity in the All of Us Research Program: Implications for Biomedical Research. bioRxiv : the preprint server for biology.

Malomane DK, et al. (2025) Patterns of population structure and genetic variation within the Saudi Arabian population. bioRxiv : the preprint server for biology.

Bernard AM, et al. (2025) Connections Across Open Water: A Bi-Organelle, Genomics-Scale Assessment of Atlantic-Wide Population Dynamics in a Pelagic, Endangered Apex Predator Shark (Isurus oxyrinchus). Evolutionary applications, 18(1), e70071.

Cristaudo AT, et al. (2025) Mutations of the CEACAM5 Gene PELPK Motif in Patients With Appendiceal or Colorectal Adenocarcinoma. In vivo (Athens, Greece), 39(1), 96.

Dai Y, et al. (2024) Generation of two induced pluripotent stem cell lines from patients with Williams syndrome. Stem cell research, 78, 103460.

Tadaka S, et al. (2024) jMorp: Japanese Multi-Omics Reference Panel update report 2023. Nucleic acids research, 52(D1), D622.