Resource Summary Report

Generated by PRECISE-TBI on Jul 30, 2026

KING

RRID:SCR_009251
Type: Tool

Proper Citation

KING (RRID:SCR_009251)

Resource Information

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

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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 application, software resource

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

Resource Name: KING

Resource ID: SCR_009251

Alternate IDs: nlx_154419

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260727T040447+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 1124 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Liu Y, et al. (2026) Telomere length, aging, and cognitive function in the Midwestern Amish. HGG advances, 7(1), 100533.

Li R, et al. (2026) Whole-genome sequence-based association analysis of African American individuals with bipolar disorder and schizophrenia. HGG advances, 7(1), 100499.

Estand??a A, et al. (2026) The Genetic Consequences of Dispersal and Immigration in a Wild Great Tit Population. Molecular ecology, 35(1), e70206.

Michalek DA, et al. (2026) HLA-focused type 1 diabetes genetic risk prediction in populations of diverse ancestry. Diabetologia, 69(1), 146.

Lange LM, et al. (2025) The LRRK2 p.L1795F variant causes Parkinson's disease in the European population. NPJ Parkinson's disease, 11(1), 58.

Arshad F, et al. (2025) A comprehensive water buffalo pangenome reveals extensive structural variation linked to population-specific signatures of selection. GigaScience, 14.

Xu Z, et al. (2025) PISAD: reference-free intraspecies sample anomalies detection tool based on k-mer counting. GigaScience, 14.

Milo Rasouly H, et al. (2025) Exome analysis links kidney malformations to developmental disorders and reveals causal genes. Nature communications, 16(1), 7290.

Vicente CT, et al. (2025) Methylome analysis of FTLD patients with TDP-43 pathology identifies epigenetic signatures specific to pathological subtypes. Molecular neurodegeneration, 20(1), 80.

Halls D, et al. (2025) Longitudinal study of socio-emotional cognitive processing in individuals with anorexia nervosa and the impact of autistic characteristics on neural processing. Frontiers in psychology, 16, 1583417.

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

Zhang C, et al. (2025) Dysregulation of mTOR signalling is a converging mechanism in lissencephaly. Nature, 638(8049), 172.

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.

Wang X, et al. (2025) Population genomics analyses reveal the role of hybridization in the rapid invasion of fall armyworm. Journal of advanced research, 74, 43.

Dand N, et al. (2025) GWAS meta-analysis of psoriasis identifies new susceptibility alleles impacting disease mechanisms and therapeutic targets. Nature communications, 16(1), 2051.

Chami N, et al. (2025) Genetic subtyping of obesity reveals biological insights into the uncoupling of adiposity from its cardiometabolic comorbidities. medRxiv : the preprint server for health sciences.

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

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.

Xu X, et al. (2025) Transcriptome-wide association study of alternative polyadenylation identifies susceptibility genes in non-small cell lung cancer. Oncogene, 44(26), 2127.

Wang C, et al. (2025) Quantile-specific confounding: correction for subtle population stratification via quantile regression. bioRxiv : the preprint server for biology.