Resource Summary Report

Generated by NIF on Aug 12, 2026

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)

Resource Name: KING

Resource ID: SCR_009251

Alternate IDs: nlx_154419

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260813T054957+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 1175 mentions in open access literature.

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

Liu Q, et al. (2026) Structural variation drives praziquantel response and host adaptation in Schistosoma japonicum. iScience, 29(6), 116118.

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.

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

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

Dobrose MM, et al. (2026) Molecular analysis and immunological characterization of a founder mutation causing ARPC1B deficiency. Genes and immunity, 27(1), 69.

Li X, et al. (2026) Genetic diversity and differentiated adaptive strategies for underrepresented populations at the crossroad of Southeast and East Asia. BMC genomics, 27(1), 149.

Zhang WP, et al. (2026) Genomic consequences of residual recombination in a hybrid apomictic hickory complex. Nature communications, 17(1).

Moksnes MR, et al. (2026) The HUNT study identifies host genetic factors reproducibly associated with human gut microbiota composition. Nature genetics, 58(3), 530.

Abolhassani A, et al. (2026) Genetic contribution to severe COVID-19 in adults under 60 years without major comorbidities in the German National Pandemic Cohort Network (NAPKON). Human genomics, 20(1), 23.

Kanchan K, et al. (2026) Genetic Determinants of Peanut-Specific IgG4 Levels in the Context of Sustained Oral Peanut Exposure in the LEAP Study. Immunology, 178(2), 280.

Castellacci M, et al. (2026) Exploring the genetic diversity of Mediterranean fig trees highlights genes associated with fruit traits. Frontiers in plant science, 17, 1750632.

Martinelli E, et al. (2026) Precision Diagnosis in APOL1 Kidney Disease With the p.N264K M1 Protective Variant. JAMA network open, 9(3), e261452.

Pinosio S, et al. (2026) The FORGENIUS Genomic Resources: New Genotyping Tools and Genomic Data for 23 Forest Tree Species and Their Genetic Conservation Units. Molecular ecology resources, 26(3), e70115.

Hegab Souquette A, et al. (2026) Integrated drivers of basal and acute immunity in diverse human populations. Cell reports. Medicine, 7(4), 102690.

Gmelin D, et al. (2026) GWAS on short tandem repeats identifies genetic mechanisms in Alzheimer's disease. Nature communications, 17(1).

Nguyen T, et al. (2026) Empirically determined baseline masking strategies and other considerations for gene-level burden tests. Nature genetics, 58(6), 1226.

Džigurski J, et al. (2026) Prescribed hormonal contraceptive use trends in the Estonian Biobank: A longitudinal observational study. PLoS medicine, 23(5), e1005086.

Mao C, et al. (2026) Genomic insights into the admixture history and adaptive evolution of the Zhuang people. Molecular biology and evolution, 43(5).

Fuhrer J, et al. (2026) Beyond Exons: Linking Noncoding Heritability and Polygenicity across Complex Human Traits and Disorders. bioRxiv : the preprint server for biology.

Brenner D, et al. (2026) A rare missense variant impacting NEK1 kinase function is associated with ALS. Acta neuropathologica communications, 14(1).