Resource Summary Report

Generated by RRID on Aug 5, 2026

HELIXTREE

RRID:SCR_009067
Type: Tool

Proper Citation

HELIXTREE (RRID:SCR_009067)

Resource Information

URL: http://www.statistics.com/software-directory/helixtree

Proper Citation: HELIXTREE (RRID:SCR_009067)

Description: THIS RESOURCE IS NO LONGER IN SERVCE, documented September 22, 2016.

Abbreviations: HELIXTREE

Synonyms: HelixTree Genetic Association Software

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c++, ms-windows, linux, macos x

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: HELIXTREE

Resource ID: SCR_009067

Alternate IDs: nlx_154059

Old URLs: http://www.goldenhelix.com/SNP_Variation/HelixTree

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260805T044216+0000

Ratings and Alerts

No rating or validation information has been found for HELIXTREE.

No alerts have been found for HELIXTREE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Lee JW, et al. (2022) Absolute Neutrophil Count after the First Chemotherapy Cycle as a Surrogate Marker for Treatment Outcomes in Patients with Neuroblastoma. Cancer research and treatment, 54(1), 259.

Kim YW, et al. (2020) Exploring the Novel Susceptibility Gene Variants for Primary Open-Angle Glaucoma in East Asian Cohorts: The GLAU-GENDISK Study. Scientific reports, 10(1), 221.

Bae JS, et al. (2020) Genome-Wide Association Study for the Identification of Novel Genetic Variants Associated with the Risk of Neuroblastoma in Korean Children. Cancer research and treatment, 52(4), 1251.

Pagliai G, et al. (2019) CLOCK gene polymorphisms and quality of aging in a cohort of nonagenarians - The MUGELLO Study. Scientific reports, 9(1), 1472.

Greenblatt R, et al. (2019) Genetic and clinical predictors of CD4 lymphocyte recovery during suppressive antiretroviral therapy: Whole exome sequencing and antiretroviral therapy response phenotypes. PloS one, 14(8), e0219201.

Hsu LA, et al. (2017) Growth Differentiation Factor 15 May Predict Mortality of Peripheral and Coronary Artery Diseases and Correlate with Their Risk Factors. Mediators of inflammation, 2017, 9398401.

Sun Y, et al. (2017) Genetic variants in telomere-maintenance genes are associated with ovarian cancer risk and outcome. Journal of cellular and molecular medicine, 21(3), 510.

Lee BY, et al. (2017) Association Between a Polymorphism in CASP3 and CASP9 Genes and Ischemic Stroke. Annals of rehabilitation medicine, 41(2), 197.

Sampathkumar R, et al. (2017) HIV-1 Subtypes and 5'LTR-Leader Sequence Variants Correlate with Seroconversion Status in Pumwani Sex Worker Cohort. Viruses, 10(1).

Yoo SD, et al. (2016) Polymorphism of Nitric Oxide Synthase 1 Affects the Clinical Phenotypes of Ischemic Stroke in Korean Population. Annals of rehabilitation medicine, 40(1), 102.

Hill-Burns EM, et al. (2016) Identification of genetic modifiers of age-at-onset for familial Parkinson's disease. Human molecular genetics, 25(17), 3849.

Hildebrandt MA, et al. (2015) Genetic variation in the TNF/TRAF2/ASK1/p38 kinase signaling pathway as markers for postoperative pulmonary complications in lung cancer

patients. Scientific reports, 5, 12068.

Zheng W, et al. (2015) Knowledge-based analysis of genetic associations of rheumatoid arthritis to inform studies searching for pleiotropic genes: a literature review and network analysis. Arthritis research & therapy, 17(1), 202.

Oguchi T, et al. (2015) Investigation of susceptibility genes triggering lachrymal/salivary gland lesion complications in Japanese patients with type 1 autoimmune pancreatitis. PloS one, 10(5), e0127078.

Cava C, et al. (2015) Integrating genetics and epigenetics in breast cancer: biological insights, experimental, computational methods and therapeutic potential. BMC systems biology, 9, 62.

von Otter M, et al. (2014) Genetic associations of Nrf2-encoding NFE2L2 variants with Parkinson's disease - a multicenter study. BMC medical genetics, 15, 131.

Wu S, et al. (2014) Circulating YKL-40 level, but not CHI3L1 gene variants, is associated with atherosclerosis-related quantitative traits and the risk of peripheral artery disease. International journal of molecular sciences, 15(12), 22421.

Park HK, et al. (2013) Assessment of two missense polymorphisms (rs4762 and rs699) of the angiotensinogen gene and stroke. Experimental and therapeutic medicine, 5(1), 343.

Kim KT, et al. (2013) Assessment of NMDA receptor genes (GRIN2A, GRIN2B and GRIN2C) as candidate genes in the development of degenerative lumbar scoliosis. Experimental and therapeutic medicine, 5(3), 977.

McCann B, et al. (2012) Associations between pro- and anti-inflammatory cytokine genes and breast pain in women prior to breast cancer surgery. The journal of pain, 13(5), 425.