

Resource Summary Report

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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 SERVICE, 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: 20260727T040450+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 [nidm-terms](#).

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.

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.

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.

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.