Resource Summary Report

Generated by dkNET on Apr 16, 2025

SOLAR

RRID:SCR_000850
Type: Tool

Proper Citation

SOLAR (RRID:SCR_000850)

Resource Information

URL: http://solar-eclipse-genetics.org

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Description: A flexible and extensive software package for genetic variance components analysis, including linkage analysis, quantitative genetic analysis, and covariate screening. Operations are included for calculation of marker-specific or multipoint identity-by-descent (IBD) matrices in pedigrees of arbitrary size and complexity, and for linkage analysis of quantitative traits which may involve multiple loci (oligogenic analysis), dominance effects, and epistasis. (entry from Genetic Analysis Software)

Abbreviations: SOLAR

Synonyms: Sequential Oligogenic Linkage Analysis Routines

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, fortran, c, c++, tcl, unix, (solaris 7-10/solaris x86 8-9/digital unix 4.0e/sg irix), linux, macos, ms-windows

Funding:

Resource Name: SOLAR

Resource ID: SCR_000850

Alternate IDs: nlx_154653

Old URLs: http://www.sfbr.org/Departments/genetics_detail.aspx?p=37

Record Creation Time: 20220129T080203+0000

Record Last Update: 20250416T063228+0000

Ratings and Alerts

No rating or validation information has been found for SOLAR.

No alerts have been found for SOLAR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Peng Y, et al. (2021) Chromosome-level genome assembly of the Arctic fox (Vulpes lagopus) using PacBio sequencing and Hi-C technology. Molecular ecology resources, 21(6), 2093.

Yang P, et al. (2019) Genome sequence of the Chinese white wax scale insect Ericerus pela: the first draft genome for the Coccidae family of scale insects. GigaScience, 8(9).

Wu YM, et al. (2018) Draft genomes of two blister beetles Hycleus cichorii and Hycleus phaleratus. GigaScience, 7(3), 1.

Workalemahu T, et al. (2018) Genetic and Environmental Influences on Fetal Growth Vary during Sensitive Periods in Pregnancy. Scientific reports, 8(1), 7274.

Chen JA, et al. (2018) Neurodegenerative disease biomarkers A?1-40, A?1-42, tau, and p-tau181 in the vervet monkey cerebrospinal fluid: Relation to normal aging, genetic influences, and cerebral amyloid angiopathy. Brain and behavior, 8(2), e00903.

Li S, et al. (2017) Twin birth changes DNA methylation of subsequent siblings. Scientific reports, 7(1), 8463.

Winbo A, et al. (2017) Sex is a moderator of the association between NOS1AP sequence variants and QTc in two long QT syndrome founder populations: a pedigree-based measured genotype association analysis. BMC medical genetics, 18(1), 74.

Thomson PA, et al. (2016) Balanced translocation linked to psychiatric disorder, glutamate, and cortical structure/function. NPJ schizophrenia, 2, 16024.

Silva CT, et al. (2015) Heritabilities, proportions of heritabilities explained by GWAS findings, and implications of cross-phenotype effects on PR interval. Human genetics, 134(11-12), 1211.

Spieker EA, et al. (2015) Shared genetic variance between obesity and white matter integrity in Mexican Americans. Frontiers in genetics, 6, 26.

Ruggiero D, et al. (2015) Genetic variants modulating CRIPTO serum levels identified by genome-wide association study in Cilento isolates. PLoS genetics, 11(1), e1004976.

Liu AY, et al. (2014) Genome-wide linkage and regional association study of obesity-related phenotypes: the GenSalt study. Obesity (Silver Spring, Md.), 22(2), 545.

Franceschini N, et al. (2014) Mapping of a blood pressure QTL on chromosome 17 in American Indians of the strong heart family study. BMC cardiovascular disorders, 14, 158.

Santos DM, et al. (2014) Genotype by sex and genotype by age interactions with sedentary behavior: the Portuguese Healthy Family Study. PloS one, 9(10), e110025.

Fairweather-Tait SJ, et al. (2013) The contribution of diet and genotype to iron status in women: a classical twin study. PloS one, 8(12), e83047.

Nikpay M, et al. (2012) Genetic mapping of habitual substance use, obesity-related traits, responses to mental and physical stress, and heart rate and blood pressure measurements reveals shared genes that are overrepresented in the neural synapse. Hypertension research : official journal of the Japanese Society of Hypertension, 35(6), 585.

Rexroad CE, et al. (2012) QTL affecting stress response to crowding in a rainbow trout broodstock population. BMC genetics, 13, 97.

Cannon DS, et al. (2010) Genome-wide linkage analyses of two repetitive behavior phenotypes in Utah pedigrees with autism spectrum disorders. Molecular autism, 1(1), 3.

Schuur M, et al. (2010) Insulin-resistance and metabolic syndrome are related to executive function in women in a large family-based study. European journal of epidemiology, 25(8), 561.

Johansson A, et al. (2009) Extended haplotypes in the growth hormone releasing hormone receptor gene (GHRHR) are associated with normal variation in height. PloS one, 4(2), e4464.