Resource Summary Report

Generated by kravitz2 on Jul 31, 2026

EXOMEPICKS

RRID:SCR_009174
Type: Tool

Proper Citation

EXOMEPICKS (RRID:SCR_009174)

Resource Information

URL: http://genome.sph.umich.edu/wiki/ExomePicks

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Description: Software application that suggests individuals to be sequenced in a large pedigree. ExomePicks assumes that a genotyping chip or another cost effective means will be used to determine IBD sharing in the pedigree and that, subsequently, one would like to sequence a minimal number of individuals and use their sequences together with IBD information to deduce the sequence of other individuals in the pedigree. We are currently using it in the context of whole exome and whole genome sequencing studies to pick individuals to be sequenced from large family collections. (entry from Genetic Analysis Software)

Abbreviations: EXOMEPICKS

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, bio.tools

Resource Name: EXOMEPICKS

Resource ID: SCR_009174

Alternate IDs: nlx_154306, biotools:exomepicks

Alternate URLs: https://bio.tools/exomepicks

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260731T042809+0000

Ratings and Alerts

No rating or validation information has been found for EXOMEPICKS.

No alerts have been found for EXOMEPICKS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Sul JH, et al. (2020) Contribution of common and rare variants to bipolar disorder susceptibility in extended pedigrees from population isolates. Translational psychiatry, 10(1), 74.

Ullah E, et al. (2019) Comparison and assessment of family- and population-based genotype imputation methods in large pedigrees. Genome research, 29(1), 125.

Toma C, et al. (2018) An examination of multiple classes of rare variants in extended families with bipolar disorder. Translational psychiatry, 8(1), 65.

Farlow JL, et al. (2015) Lessons learned from whole exome sequencing in multiplex families affected by a complex genetic disorder, intracranial aneurysm. PloS one, 10(3), e0121104.

Sidore C, et al. (2015) Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. Nature genetics, 47(11), 1272.

Almasy L, et al. (2014) Data for Genetic Analysis Workshop 18: human whole genome sequence, blood pressure, and simulated phenotypes in extended pedigrees. BMC proceedings, 8(Suppl 1), S2.