

Resource Summary Report

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EXOME PICKS

RRID:SCR_009174

Type: Tool

Proper Citation

EXOME PICKS (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: EXOME PICKS

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, bio.tools

Resource Name: EXOME PICKS

Resource ID: SCR_009174

Alternate IDs: nlx_154306, biotools:exomepicks

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

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260905T133245+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 [RRID](#) .

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.