Resource Summary Report

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SNAP - SNP Annotation and Proxy Search

RRID:SCR_002127
Type: Tool

Proper Citation

SNAP - SNP Annotation and Proxy Search (RRID:SCR_002127)

Resource Information

URL: http://www.broadinstitute.org/mpg/snap/

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Description: A computer program and web-based service for the rapid retrieval of linkage disequilibrium proxy single nucleotide polymorphism (SNP) results given input of one or more query SNPs and based on empirical observations from the International HapMap Project and the 1000 Genomes Project. A series of filters allow users to optionally retrieve results that are limited to specific combinations of genotyping platforms, above specified pairwise r2 thresholds, or up to a maximum distance between query and proxy SNPs. SNAP can also generate linkage disequilibrium plots

Abbreviations: SNAP

Synonyms: SNAP (SNP Annotation and Proxy Search), SNAP 2, SNP Annotation and Proxy Search

Resource Type: data analysis service, analysis service resource, software application, software resource, production service resource, service resource

Defining Citation: PMID:18974171

Keywords: gene, genetic, genomic, r, oracle, single nucleotide polymorphism, linkage disequilibrium, genotypeing array, physical distance, membership, proxy, plot

Funding: NHLBI N01-HC-65226

Resource Name: SNAP - SNP Annotation and Proxy Search

Resource ID: SCR_002127

Alternate IDs: OMICS_01927, nlx_154638

Alternate URLs: http://www.broad.mit.edu/mpg/snap/

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250420T014051+0000

Ratings and Alerts

No rating or validation information has been found for SNAP - SNP Annotation and Proxy Search.

No alerts have been found for SNAP - SNP Annotation and Proxy Search.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 144 mentions in open access literature.

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

Yang S, et al. (2024) Genomic exploration of the endangered oriental stork, Ciconia boyciana, sheds light on migration adaptation and future conservation. GigaScience, 13.

Ibeh N, et al. (2024) De novo transcriptome assembly and genome annotation of the fat-tailed dunnart (Sminthopsis crassicaudata). GigaByte (Hong Kong, China), 2024, gigabyte118.

Kim J, et al. (2023) UBAP2 plays a role in bone homeostasis through the regulation of osteoblastogenesis and osteoclastogenesis. Nature communications, 14(1), 3668.

Barton JC, et al. (2023) Height of non-Hispanic white adults with homeostatic iron regulator HFE genotypes p.C282Y/p.C282Y and wt/wt. Molecular genetics & genomic medicine, 12(1), e2321.

Wang H, et al. (2022) Chromosome-level assembly and annotation of the blue catfish Ictalurus furcatus, an aquaculture species for hybrid catfish reproduction, epigenetics, and heterosis studies. GigaScience, 11.

Wang H, et al. (2022) A Chromosome-level assembly of the Japanese eel genome, insights

into gene duplication and chromosomal reorganization. GigaScience, 11.

He X, et al. (2022) The whole-genome assembly of an endangered Salicaceae species: Chosenia arbutifolia (Pall.) A. Skv. GigaScience, 11.

Liu S, et al. (2022) A high-quality assembly reveals genomic characteristics, phylogenetic status, and causal genes for leucism plumage of Indian peafowl. GigaScience, 11.

Liu P, et al. (2022) The assembled and annotated genome of the masked palm civet (Paguma larvata). GigaScience, 11.

Prado MJ, et al. (2022) Variant predictions in congenital adrenal hyperplasia caused by mutations in CYP21A2. Frontiers in pharmacology, 13, 931089.

Wong KH, et al. (2022) The genome of the mustard hill coral, Porites astreoides. GigaByte (Hong Kong, China), 2022, gigabyte65.

Saenko SV, et al. (2021) The draft genome sequence of the grove snail Cepaea nemoralis. G3 (Bethesda, Md.), 11(2).

Ou M, et al. (2021) Chromosome-level genome assemblies of Channa argusandChanna maculata and comparative analysis of their temperature adaptability. GigaScience, 10(10).

Huang R, et al. (2021) De novo screening of disease-resistant genes from the chromosome-level genome of rare minnow using CRISPR-cas9 random mutation. GigaScience, 10(11).

Li YY, et al. (2021) Association Study of Polymorphisms in Neuronal Nicotinic Acetylcholine Receptor Subunit Genes With Schizophrenia in the Han Chinese Population. Psychiatry investigation, 18(10), 943.

Jae Lee S, et al. (2021) Chromosomal assembly of the Antarctic toothfish (Dissostichus mawsoni) genome using third-generation DNA sequencing and Hi-C technology. Zoological research, 42(1), 124.

Meng F, et al. (2020) Chromosome-level genome assembly of Aldrichina grahami, a forensically important blowfly. GigaScience, 9(3).

Liu C, et al. (2020) Chromosome-level draft genome of a diploid plum (Prunus salicina). GigaScience, 9(12).

Jiang K, et al. (2020) Broadening our understanding of the genetics of Juvenile Idiopathic Arthritis (JIA): Interrogation of three dimensional chromatin structures and genetic regulatory elements within JIA-associated risk loci. PloS one, 15(7), e0235857.

Kang S, et al. (2020) Chromosomal-level assembly of Takifugu obscurus (Abe, 1949) genome using third-generation DNA sequencing and Hi-C analysis. Molecular ecology resources, 20(2), 520.