

Resource Summary Report

Generated by [NIF](#) on Sep 14, 2026

SNAP

RRID:SCR_007936

Type: Tool

Proper Citation

SNAP (RRID:SCR_007936)

Resource Information

URL: <http://snap.genomics.org.cn>

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Description: A sequence analysis tool providing a simple but detailed analysis of human genes and their variations. For each gene, a gene-gene relationship network can be generated based on protein-protein interaction data, metabolic pathway connections and extended through phylogenetic relations. Snap provides tools for designing sequence primers and evaluating RNA splicing effects of single SNPs - known from the databases or defined by you. Primers can be designed for the amplification or sequencing of cDNA, genomic DNA, introns only or exons only., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: SNAP

Synonyms: SNP Annotation Platform

Resource Type: data or information resource, database

Keywords: gene-gene relationship, human gene, human genome, primer design, rna splicing effects, sequence primer design, snp, FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SNAP

Resource ID: SCR_007936

Alternate IDs: nif-0000-03473

Alternate URLs: <http://snap.humgen.au.dk>

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260912T200156+0000

Ratings and Alerts

No rating or validation information has been found for SNAP.

No alerts have been found for SNAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2602 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing Cobitis. *GigaScience*, 15.

Zeng L, et al. (2026) Functional genomics reveals key gene families and molecular pathways for extreme cold survival in the khapra beetle. *BMC biology*, 24(1).

Iqbal MW, et al. (2026) Exploring Deleterious Nonsynonymous SNPs in the ACADM Gene: Insights Into Medium-Chain Acyl-CoA Dehydrogenase Deficiency (MCADD) via In Silico Analysis. *Genetics research*, 2026, 6682668.

Mubarak SMH, et al. (2026) Decoding the impact of nsSNP variants on BCL6 function through integrated computational analysis. *Current research in structural biology*, 11, 100180.

Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin. *GigaScience*, 14.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Ritter EJ, et al. (2025) The assembly and annotation of two teinturier grapevine varieties, Dakapo and Rubired. *GigaByte (Hong Kong, China)*, 2025, gigabyte149.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant *Stylosanthes angustifolia*: insights into genome evolution and drought adaptation. *GigaScience*, 14.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Rathinam M, et al. (2025) A chromosome-scale reference genome assembly of pigeonpea wild relative *Cajanus platycarpus* highlights the evolutionary decline of defence genes in *Cajanus cajan*. *Journal of experimental botany*, 76(20), 6166.

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Zhang G, et al. (2025) Genomic and transcriptomic analyses of *Heteropoda venatoria* reveal the expansion of P450 family for starvation resistance in spiders. *GigaScience*, 14.

Sepic A, et al. (2025) Non-Hospitalized Patients With Post-COVID Condition and Myopathic Electromyography Findings Show no Difference in Symptom Severity and Clinical Manifestations Compared to Those Without Myopathic Findings. *Muscle & nerve*, 71(2), 223.

Philipps J, et al. (2025) Nerve cross-sectional area in vincristine-induced polyneuropathy: A nerve ultrasound pilot study. *Journal of neuroimaging : official journal of the American Society of Neuroimaging*, 35(1), e13255.

Kiernan CK, et al. (2025) Treatments with versus without medication for children with behavioural difficulties in clinical practice: an economic evaluation with observational data. *Journal of child psychology and psychiatry, and allied disciplines*, 66(3), 289.

Helmstetter AJ, et al. (2025) Toward a phylogenomic classification of magnoliids. *American journal of botany*, 112(1), e16451.

Choi S, et al. (2025) Chromosome-level genome assembly of *Salvia sclarea*. *Scientific data*, 12(1), 14.

Chatterjee P, et al. (2025) A computational and structural approach to identify malignant non-synonymous FOXM1 single nucleotide polymorphisms in triple-negative breast cancer. *Scientific reports*, 15(1), 964.

Crespo-Bellido M, et al. (2025) A Systematic Review: The Impact of COVID-19 Policy Flexibilities on SNAP and WIC Programmatic Outcomes. *Advances in nutrition (Bethesda, Md.)*, 16(2), 100361.