

# Resource Summary Report

Generated by NIF on Aug 19, 2026

## Suite of Nucleotide Analysis Programs

RRID:SCR\_009399

Type: Tool

### Proper Citation

Suite of Nucleotide Analysis Programs (RRID:SCR\_009399)

### Resource Information

**URL:** <https://github.com/gaow/genetic-analysis-software/blob/master/pages/SNAP.md>

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**Description:** THIS RESOURCE IS NO LONGER IN SERVICE, documented May 10, 2017. A pilot effort that has developed a centralized, web-based biospecimen locator that presents biospecimens collected and stored at participating Arizona hospitals and biospecimen banks, which are available for acquisition and use by researchers. Researchers may use this site to browse, search and request biospecimens to use in qualified studies. The development of the ABL was guided by the Arizona Biospecimen Consortium (ABC), a consortium of hospitals and medical centers in the Phoenix area, and is now being piloted by this Consortium under the direction of ABRC. You may browse by type (cells, fluid, molecular, tissue) or disease. Common data elements decided by the ABC Standards Committee, based on data elements on the National Cancer Institute's (NCI's) Common Biorepository Model (CBM), are displayed. These describe the minimum set of data elements that the NCI determined were most important for a researcher to see about a biospecimen. The ABL currently does not display information on whether or not clinical data is available to accompany the biospecimens. However, a requester has the ability to solicit clinical data in the request. Once a request is approved, the biospecimen provider will contact the requester to discuss the request (and the requester's questions) before finalizing the invoice and shipment. The ABL is available to the public to browse. In order to request biospecimens from the ABL, the researcher will be required to submit the requested required information. Upon submission of the information, shipment of the requested biospecimen(s) will be dependent on the scientific and institutional review approval. Account required. Registration is open to everyone., documented September 29, 2016. A workbench tool to make existing population genetic software more accessible and to facilitate the integration of new tools for analyzing patterns of DNA sequence variation, within a phylogenetic context. Collectively, SNAP tools can serve as a bridge between theoretical and applied population genetic analysis. The exploration of DNA sequence variation for making inferences on evolutionary processes in populations requires the coordinated implementation of a Suite of Nucleotide Analysis Programs (SNAP), each bound by specific assumptions and limitations.

**Abbreviations:** SNAP

**Resource Type:** software resource, software application

**Keywords:** gene, genetic, genomic

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Suite of Nucleotide Analysis Programs

**Resource ID:** SCR\_009399

**Alternate IDs:** nlx\_154637

**Old URLs:** <http://www.cals.ncsu.edu/plantpath/people/faculty/carbone/snap.html>

**Record Creation Time:** 20220129T080252+0000

**Record Last Update:** 20260818T043340+0000

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## Ratings and Alerts

No rating or validation information has been found for Suite of Nucleotide Analysis Programs.

No alerts have been found for Suite of Nucleotide Analysis Programs.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 4485 mentions in open access literature.

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

Garc??a DH, et al. (2022) Analysis of Urban Heat Island and Heat Waves Using Sentinel-3 Images: a Study of Andalusian Cities in Spain. Earth systems and environment, 6(1), 199.

Wang J, et al. (2022) Dynamic changes of CSF sPDGFR?? during ageing and AD progression and associations with CSF ATN biomarkers. Molecular neurodegeneration, 17(1), 9.

Helfter C, et al. (2022) Phenology is the dominant control of methane emissions in a tropical non-forested wetland. Nature communications, 13(1), 133.

Shafer PR, et al. (2022) Association of the Implementation of Child Tax Credit Advance Payments With Food Insufficiency in US Households. JAMA network open, 5(1), e2143296.

- Min HK, et al. (2022) Vitronectin-derived bioactive peptide prevents spondyloarthritis by modulating Th17/Treg imbalance in mice with curdlan-induced spondyloarthritis. *PloS one*, 17(1), e0262183.
- Dickinson M, et al. (2022) SNAP, campus food insecurity, and the politics of deservingness. *Agriculture and human values*, 39(2), 605.
- Yang X, et al. (2022) BioNet: a large-scale and heterogeneous biological network model for interaction prediction with graph convolution. *Briefings in bioinformatics*, 23(1).
- Periwal N, et al. (2022) In silico characterization of mutations circulating in SARS-CoV-2 structural proteins. *Journal of biomolecular structure & dynamics*, 40(18), 8216.
- Matthay EC, et al. (2022) What to Do When Everything Happens at Once: Analytic Approaches to Estimate the Health Effects of Co-Occurring Social Policies. *Epidemiologic reviews*, 43(1), 33.
- Higashi RT, et al. (2022) Experiences of increased food insecurity, economic and psychological distress during the COVID-19 pandemic among Supplemental Nutrition Assistance Program-enrolled food pantry clients. *Public health nutrition*, 25(4), 1027.
- Feng X, et al. (2022) A Chromosome-Level Genome Assembly of the Pygmy Mole Cricket *Xya riparia*. *Genome biology and evolution*, 14(1).
- Lohrasbi-Nejad A, et al. (2022) Detection of homologous recombination events in SARS-CoV-2. *Biotechnology letters*, 44(3), 399.
- Parker CW, et al. (2022) Genomic Characterization of *Parengyodontium torokii* sp. nov., a Biofilm-Forming Fungus Isolated from Mars 2020 Assembly Facility. *Journal of fungi* (Basel, Switzerland), 8(1).
- Lin P, et al. (2022) The genome of oil-Camellia and population genomics analysis provide insights into seed oil domestication. *Genome biology*, 23(1), 14.
- Nazario-Toole AE, et al. (2022) Whole-genome Sequencing of SARS-CoV-2: Using Phylogeny and Structural Modeling to Contextualize Local Viral Evolution. *Military medicine*, 187(1-2), e130.
- Khalid Z, et al. (2022) Identification of destabilizing SNPs in SARS-CoV2-ACE2 protein and spike glycoprotein: implications for virus entry mechanisms. *Journal of biomolecular structure & dynamics*, 40(3), 1205.
- Heflin C, et al. (2022) Below the Tip of the Iceberg: Examining Early Childhood Participation in SNAP and TANF from Birth to Age Six. *Population research and policy review*, 41(2), 729.
- Lu W, et al. (2022) Lead contamination of public drinking water and academic achievements among children in Massachusetts: a panel study. *BMC public health*, 22(1), 107.
- Ventura AK, et al. (2022) WIC Participants' Perceptions of COVID-19-Related Changes to WIC Recertification and Service Delivery. *Journal of community health*, 47(2), 184.

Komisarenko V, et al. (2022) Exploiting time series of Sentinel-1 and Sentinel-2 to detect grassland mowing events using deep learning with reject region. Scientific reports, 12(1), 983.