

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## SNIPPEEP

RRID:SCR\_013309

Type: Tool

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### Proper Citation

SNIPPEEP (RRID:SCR\_013309)

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### Resource Information

**URL:** <http://snippeep.sourceforge.net/>

**Proper Citation:** SNIPPEEP (RRID:SCR\_013309)

**Description:** Software application that is an interactive graphic interface to visualise results from whole genome genotyping. It allows one to visualise single subjects and groups of subjects, and provides a direct connection with the UCSC Genome Browser. (entry from Genetic Analysis Software)

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

**Keywords:** gene, genetic, genomic, c

**Resource Name:** SNIPPEEP

**Resource ID:** SCR\_013309

**Alternate IDs:** nlx\_154019

**Record Creation Time:** 20220129T080315+0000

**Record Last Update:** 20260905T133255+0000

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### Ratings and Alerts

No rating or validation information has been found for SNIPPEEP.

No alerts have been found for SNIPPEEP.

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### Data and Source Information

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

## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Leblond CS, et al. (2019) Both rare and common genetic variants contribute to autism in the Faroe Islands. NPJ genomic medicine, 4, 1.

Leblond CS, et al. (2014) Meta-analysis of SHANK Mutations in Autism Spectrum Disorders: a gradient of severity in cognitive impairments. PLoS genetics, 10(9), e1004580.

Leblond CS, et al. (2012) Genetic and functional analyses of SHANK2 mutations suggest a multiple hit model of autism spectrum disorders. PLoS genetics, 8(2), e1002521.