

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

## SNiPer-HD

RRID:SCR\_004383

Type: Tool

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### Proper Citation

SNiPer-HD (RRID:SCR\_004383)

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### Resource Information

**URL:** <https://www.tgen.org/research/research-divisions/neurogenomics/supplementary-data/sniper-hd-improved-genotype-calling-accuracy.aspx#.UjmeKb5OKM8>

**Proper Citation:** SNiPer-HD (RRID:SCR\_004383)

**Description:** Improved genotype calling accuracy by an expectation-maximization algorithm for high-density SNP arrays.

**Abbreviations:** SNiPer-HD

**Synonyms:** SNiPer-HD: Improved genotype calling accuracy

**Resource Type:** software resource

**Defining Citation:** [PMID:17062589](#)

**Resource Name:** SNiPer-HD

**Resource ID:** SCR\_004383

**Alternate IDs:** OMICS\_00735

**Record Creation Time:** 20220129T080224+0000

**Record Last Update:** 20260725T190549+0000

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### Ratings and Alerts

No rating or validation information has been found for SNiPer-HD.

No alerts have been found for SNiPer-HD.

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### Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Li MX, et al. (2010) A knowledge-based weighting framework to boost the power of genome-wide association studies. PloS one, 5(12), e14480.

Sampson JN, et al. (2009) Genotyping and inflated type I error rate in genome-wide association case/control studies. BMC bioinformatics, 10, 68.