

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

SNiPer-HD

RRID:SCR_004383

Type: Tool

Proper Citation

SNiPer-HD (RRID:SCR_004383)

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

Ratings and Alerts

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

No alerts have been found for SNiPer-HD.

Data and Source Information

Source: [SciCrunch Registry](#)

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.