

Resource Summary Report

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

CandiSNPer

RRID:SCR_005173

Type: Tool

Proper Citation

CandiSNPer (RRID:SCR_005173)

Resource Information

URL: <http://www2.hu-berlin.de/wikizbnutztier/software/CandiSNPer/>

Proper Citation: CandiSNPer (RRID:SCR_005173)

Description: A webtool which helps in characterizing Single Nucleotide Polymorphisms (SNPs) that are located in the vicinity of an SNP of interest (start SNP). Along with the computation of the maximal Linkage Disequilibrium (LD) region around the start SNP. CandiSNPer provides additional information with respect to the molecular consequences of the SNPs and the genes located in the LD region.

Abbreviations: CandiSNPer

Resource Type: service resource, software resource, source code

Defining Citation: [PMID:20172942](#)

Keywords: single nucleotide polymorphism, gene, plot, linkage disequilibrium, variant, genome-wide association study, genotyping, perl, r

Availability: Free for academic use

Resource Name: CandiSNPer

Resource ID: SCR_005173

Alternate IDs: OMICS_00169

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260905T133128+0000

Ratings and Alerts

No rating or validation information has been found for CandiSNPer.

No alerts have been found for CandiSNPer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.