

Resource Summary Report

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

LS-SNP/PDB

RRID:SCR_010774

Type: Tool

Proper Citation

LS-SNP/PDB (RRID:SCR_010774)

Resource Information

URL: <http://ls-snp.icm.jhu.edu/ls-snp-pdb/>

Proper Citation: LS-SNP/PDB (RRID:SCR_010774)

Description: A web tool for genome-wide annotation of human SNPs.

Abbreviations: LS-SNP/PDB

Resource Type: analysis service resource, service resource, data analysis service, production service resource

Keywords: bio.tools

Resource Name: LS-SNP/PDB

Resource ID: SCR_010774

Alternate IDs: OMICS_00131, biotools:ls-snp

Alternate URLs: <https://bio.tools/ls-snp>

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260728T043350+0000

Ratings and Alerts

No rating or validation information has been found for LS-SNP/PDB.

No alerts have been found for LS-SNP/PDB.

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 [nidm-terms](#) .

Doss CG, et al. (2014) Integrating in silico prediction methods, molecular docking, and molecular dynamics simulation to predict the impact of ALK missense mutations in structural perspective. BioMed research international, 2014, 895831.

Patnala R, et al. (2013) Candidate gene association studies: a comprehensive guide to useful in silico tools. BMC genetics, 14, 39.

Izarzugaza JM, et al. (2012) Interpretation of the consequences of mutations in protein kinases: combined use of bioinformatics and text mining. Frontiers in physiology, 3, 323.