

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 12, 2026

SNPAAMapper

RRID:SCR_002012

Type: Tool

Proper Citation

SNPAAMapper (RRID:SCR_002012)

Resource Information

URL: <http://www.ccmb.med.umich.edu/ccdu/SNPAAMapper>

Proper Citation: SNPAAMapper (RRID:SCR_002012)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 19, 2025. A downstream variant annotation program that can effectively classify variants by region (e.g. exon, intron, etc), predict amino acid change type (e.g. synonymous, non-synonymous mutation, etc), and prioritize mutation effects (e.g. CDS versus 5'UTR, etc). Major features: * The pipeline accepts the VCF (Variant Call Format) input file in tab-delimited format and processes the vcf input file containing all cases (G5, lowFreq, and novel) * The variant mapping step has the option of letting users select whether they want to report the bp distance between each identified intron variant and its nearby exon * The pipeline can deal with VCF files called by different SAMTools versions (0.1.18 and older ones) and also offers flexibility in dealing with vcf input files generated using SAMTools with two or three samples * The spreadsheet result file contains full protein sequences for both ref and alt alleles, which makes it easier for downstream protein structure/function analysis tools to take

Abbreviations: SNPAAMapper

Synonyms: SNPAAMapper - A SNP Amino Acid Mapping tool

Resource Type: data processing software, software application, software resource

Defining Citation: [PMID:24250114](#)

Keywords: single nucleotide polymorphism, amino acid, variant, annotation, exon, intron, mutation, next-generation sequencing, perl, downstream analysis, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SNPAAMapper

Resource ID: SCR_002012

Alternate IDs: OMICS_01922, biotools:snpaamapper

Alternate URLs: <https://bio.tools/snpaamapper>

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260912T200053+0000

Ratings and Alerts

No rating or validation information has been found for SNPAAMapper.

No alerts have been found for SNPAAMapper.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.