

Resource Summary Report

Generated by [NIF](#) on Sep 1, 2026

HMMvar

RRID:SCR_001177

Type: Tool

Proper Citation

HMMvar (RRID:SCR_001177)

Resource Information

URL: <https://bioinformatics.cs.vt.edu/zhanglab/hmm/>

Proper Citation: HMMvar (RRID:SCR_001177)

Description: Software applying a quantitative prediction method to predict the effect of genetic variation using hidden Markov models.

Abbreviations: HMMvar

Resource Type: software resource

Defining Citation: [PMID:24405700](#)

Keywords: genetic variation, insertion, deletion, indel

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: HMMvar

Resource ID: SCR_001177

Alternate IDs: OMICS_02181

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260829T182045+0000

Ratings and Alerts

No rating or validation information has been found for HMMvar.

No alerts have been found for HMMvar.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.