

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.sci-crunch.org) on May 11, 2025

sweed

RRID:SCR_024357

Type: Tool

Proper Citation

sweed (RRID:SCR_024357)

Resource Information

URL: <https://cme.h-its.org/exelixis/web/software/sweed/>

Proper Citation: sweed (RRID:SCR_024357)

Description: Software tool for likelihood based detection of selective sweeps in thousands of genomes. Software parallel and checkpointable tool that implements composite likelihood ratio test for detecting selective sweeps.

Resource Type: software application, software resource

Defining Citation: [PMID:23777627](https://pubmed.ncbi.nlm.nih.gov/23777627/)

Keywords: likelihood based detection of selective sweeps, parallel and checkpointable tool, composite likelihood ratio test, detecting selective sweeps, genomes,

Funding:

Availability: Free, Available for download, Freely available,

Resource Name: sweed

Resource ID: SCR_024357

Alternate IDs: OMICS_08598

Alternate URLs: <https://sources.debian.org/src/sweed/>

Record Creation Time: 20230830T050217+0000

Record Last Update: 20250508T070203+0000

Ratings and Alerts

No rating or validation information has been found for sweed.

No alerts have been found for sweed.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Durand K, et al. (2022) Incipient speciation between host-plant strains in the fall armyworm. BMC ecology and evolution, 22(1), 52.

Fiteni E, et al. (2022) Host-plant adaptation as a driver of incipient speciation in the fall armyworm (*Spodoptera frugiperda*). BMC ecology and evolution, 22(1), 133.

Niu Q, et al. (2021) Integration of selection signatures and multi-trait GWAS reveals polygenic genetic architecture of carcass traits in beef cattle. Genomics, 113(5), 3325.

Mattle-Greminger MP, et al. (2018) Genomes reveal marked differences in the adaptive evolution between orangutan species. Genome biology, 19(1), 193.