

Resource Summary Report

Generated by [NIF](#) on Sep 9, 2026

WASP

RRID:SCR_025497

Type: Tool

Proper Citation

WASP (RRID:SCR_025497)

Resource Information

URL: <https://github.com/bmvdgeijn/WASP/>

Proper Citation: WASP (RRID:SCR_025497)

Description: Software allele-specific pipeline for unbiased read mapping and molecular QTL discovery. Allele-specific software for robust molecular quantitative trait locus discovery.

Resource Type: software resource, software toolkit, source code

Defining Citation: [PMID:26366987](#)

Keywords: molecular QTLs discovery, unbiased allele-specific read mapping and discovery, molecular QTLs, unbiased allele-specific read, mapping and discovery,

Funding: Howard Hughes Medical Institute ;
NHGRI HG006123;
NHGRI HG007036;
NIGMS GM007197;
NIMH MH101825;
NSF

Availability: Free, Available for download, Freely available,

Resource Name: WASP

Resource ID: SCR_025497

License: Apache-2.0

Record Creation Time: 20240718T053247+0000

Record Last Update: 20260905T133500+0000

Ratings and Alerts

No rating or validation information has been found for WASP.

No alerts have been found for WASP.

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 [NIF](#) .

Denault WRP, et al. (2025) fSuSiE enables fine-mapping of QTLs from genome-scale molecular profiles. bioRxiv : the preprint server for biology.

Mansourizadeh H, et al. (2024) Fat-tail allele-specific expression genes may affect fat deposition in tail of sheep. PloS one, 19(12), e0316046.

Widman AJ, et al. (2024) Ultrasensitive plasma-based monitoring of tumor burden using machine-learning-guided signal enrichment. Nature medicine, 30(6), 1655.