

Resource Summary Report

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

hot scan

RRID:SCR_002840

Type: Tool

Proper Citation

hot scan (RRID:SCR_002840)

Resource Information

URL: https://github.com/itojal/hot_scan

Proper Citation: hot scan (RRID:SCR_002840)

Description: A free software to detect genomic regions unusually rich in translocation breakpoints. More generally, it may be used to detect a region that is unusually rich in a given character of a binary sequence.

Synonyms: hot_scan

Resource Type: software resource

Defining Citation: [PMID:24860160](#)

Keywords: software package, perl, r, bio.tools

Availability: Free, Freely available, Available for download

Resource Name: hot scan

Resource ID: SCR_002840

Alternate IDs: biotools:hot_scan, OMICS_05200

Alternate URLs: https://bio.tools/hot_scan

License: GNU General Public License, v2

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260725T190535+0000

Ratings and Alerts

No rating or validation information has been found for hot scan.

No alerts have been found for hot scan.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Zhang J, et al. (2025) GWAS-based population genetic analysis identifies bZIP29 as a heterotic gene in maize. Plant communications, 6(5), 101289.

You J, et al. (2023) Regulatory controls of duplicated gene expression during fiber development in allotetraploid cotton. Nature genetics, 55(11), 1987.

Zhao T, et al. (2023) Integration of eQTL and machine learning to dissect causal genes with pleiotropic effects in genetic regulation networks of seed cotton yield. Cell reports, 42(9), 113111.

Zhang L, et al. (2020) Genome-wide analysis of expression quantitative trait loci (eQTLs) reveals the regulatory architecture of gene expression variation in the storage roots of sweet potato. Horticulture research, 7(1), 90.

Wang X, et al. (2020) Genome of Solanum pimpinellifolium provides insights into structural variants during tomato breeding. Nature communications, 11(1), 5817.

Shultzaberger RK, et al. (2012) Probing the informational and regulatory plasticity of a transcription factor DNA-binding domain. PLoS genetics, 8(3), e1002614.