

# Resource Summary Report

Generated by T1D on Aug 2, 2026

## hot scan

RRID:SCR\_002840

Type: Tool

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### Proper Citation

hot scan (RRID:SCR\_002840)

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### Resource Information

**URL:** [https://github.com/itojal/hot\\_scan](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](https://bio.tools/hot_scan)

**License:** GNU General Public License, v2

**Record Creation Time:** 20220129T080215+0000

**Record Last Update:** 20260801T190214+0000

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### Ratings and Alerts

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

No alerts have been found for hot scan.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#).

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.