# Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 15, 2025

## 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

**Funding:**

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

**Resource Name:** hot scan

**Resource ID:** SCR_002840

**Alternate IDs:** biotools:hot_scan, OMICS_05200

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

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

**Record Last Update:** 20250410T064927+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 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch.org.

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.

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