Resource Summary Report

Generated by T1D on Aug 1, 2026

HTR

RRID:SCR_009241
Type: Tool

Proper Citation

HTR (RRID:SCR_009241)

Resource Information

URL: http://statgen.ncsu.edu/zaykin/htr.html

Proper Citation: HTR (RRID:SCR_009241)

Description: Software application for haplotype association mapping using unrelated individuals; fixed and sliding window analysis; overall tests and tests for individual haplotype effects (entry from Genetic Analysis Software)

Abbreviations: HTR

Synonyms: Haplotype Trend Regression

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c++, bash shell, ms-windows, unix, solaris, bio.tools

Resource Name: HTR

Resource ID: SCR_009241

Alternate IDs: nlx_154402, biotools:htr

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

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260731T042816+0000

Ratings and Alerts

No rating or validation information has been found for HTR.

No alerts have been found for HTR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Kato H, et al. (2006) Association of single-nucleotide polymorphisms in the suppressor of cytokine signaling 2 (SOCS2) gene with type 2 diabetes in the Japanese. Genomics, 87(4), 446.