

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

HS-TDT

RRID:SCR_009240

Type: Tool

Proper Citation

HS-TDT (RRID:SCR_009240)

Resource Information

URL: <http://www.math.mtu.edu/~shuzhang/software.html>

Proper Citation: HS-TDT (RRID:SCR_009240)

Description: Software application for testing association using tightly linked markers in nuclear pedigrees (entry from Genetic Analysis Software)

Abbreviations: HS-TDT

Synonyms: Haplotype Sharing Transmission Disequilibrium Test

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, unix, ms-windows, bio.tools

Resource Name: HS-TDT

Resource ID: SCR_009240

Alternate IDs: nlx_154401, biotools:hs-tdt

Alternate URLs: <https://bio.tools/hs-tdt>

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260912T200242+0000

Ratings and Alerts

No rating or validation information has been found for HS-TDT.

No alerts have been found for HS-TDT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Lin WY, et al. (2017) Adaptive combination of Bayes factors as a powerful method for the joint analysis of rare and common variants. Scientific reports, 7(1), 13858.

Liang X, et al. (2016) An Adaptive Fisher's Combination Method for Joint Analysis of Multiple Phenotypes in Association Studies. Scientific reports, 6, 34323.

Sha Q, et al. (2016) A Nonparametric Regression Approach to Control for Population Stratification in Rare Variant Association Studies. Scientific reports, 6, 37444.

Wang Z, et al. (2016) Joint Analysis of Multiple Traits Using "Optimal" Maximum Heritability Test. PloS one, 11(3), e0150975.