

# Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

## [ALTree](#)

RRID:SCR\_007562

Type: Tool

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### Proper Citation

ALTree (RRID:SCR\_007562)

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### Resource Information

**URL:** <http://claire.bardel.free.fr/software.html>

**Proper Citation:** ALTree (RRID:SCR\_007562)

**Description:** Software package to perform phylogeny based association and localization analysis. Used for association detection and localization of susceptibility sites using haplotype phylogenetic trees. Performs these two phylogeny-based analysis: tests association between candidate gene and disease; pinpoints markers (SNPs) that are putative disease susceptibility loci.

**Synonyms:** ALTREE

**Resource Type:** data processing software, software application, software resource, data analysis software

**Defining Citation:** [PMID:16595555](#), [DOI:10.1093/bioinformatics/btl131](#)

**Keywords:** phylogeny based association, association detection, susceptibility sites, haplotype phylogenetic trees, gene, genetic, genomic

**Availability:** Free, Available for download, Freely available

**Resource Name:** ALTree

**Resource ID:** SCR\_007562

**Alternate IDs:** OMICS\_13032, nlx\_154221

**Alternate URLs:** <https://sources.debian.org/src/altree/>, <https://gitlab.inria.fr/NGS/ALTree>,

**License:** GPL

**Record Creation Time:** 20220129T080242+0000

**Record Last Update:** 20260805T044153+0000

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## Ratings and Alerts

No rating or validation information has been found for ALTree.

No alerts have been found for ALTree.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Zanardo LG, et al. (2021) Experimental evolution of cowpea mild mottle virus reveals recombination-driven reduction in virulence accompanied by increases in diversity and viral fitness. Virus research, 303, 198389.

Blein S, et al. (2015) An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast cancer research : BCR, 17(1), 61.

Dubertret C, et al. (2010) A genetic schizophrenia-susceptibility region located between the ANKK1 and DRD2 genes. Progress in neuro-psychopharmacology & biological psychiatry, 34(3), 492.