

Resource Summary Report

Generated by [RRID](#) on Aug 11, 2026

TreeBeST

RRID:SCR_018173

Type: Tool

Proper Citation

TreeBeST (RRID:SCR_018173)

Resource Information

URL: <http://treesoft.sourceforge.net/treebest.shtml>

Proper Citation: TreeBeST (RRID:SCR_018173)

Description: Software package to build, manipulate and display phylogenetic trees. Designed for building gene trees with known species tree and is highly efficient and accurate.

Synonyms: NJTREE, Tree Building guided by Species Tree

Resource Type: software toolkit, software resource

Keywords: Phylogenetic tree, gene tree, phylogeny

Availability: Free, Available for download, Freely available

Resource Name: TreeBeST

Resource ID: SCR_018173

License: GNU General Public License version 2.0

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260810T040740+0000

Ratings and Alerts

No rating or validation information has been found for TreeBeST.

No alerts have been found for TreeBeST.

Data and Source Information

Usage and Citation Metrics

We found 86 mentions in open access literature.

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

Gao C, et al. (2026) Genomic divergence, introgression and KASP fingerprinting panel development in five cultivar groups of sweet osmanthus. BMC plant biology, 26(1).

Ma Q, et al. (2026) The pan-genome provides insights into evolutionary dynamics and fatty acid metabolism in Aceraceae family. Genome biology, 27(1).

Zhong C, et al. (2026) Genome-Wide Association Study and Whole-Genome Resequencing Reveal Key lincRNA and Candidate Gene for Polled Phenotype in Yak. Animals : an open access journal from MDPI, 16(4).

Yao Y, et al. (2026) Genome-Wide Resequencing Reveals High Connectivity and Localized Adaptive Signals in Manila Clam (*Ruditapes philippinarum*) Populations Along the Southeastern Coast of China. Animals : an open access journal from MDPI, 16(12).

Tulaxi G, et al. (2026) Population Genomics Reveals Genetic Diversity, Introgression, and Genetic Differentiation in Tianshan Mountains Western Honeybees (*Apis mellifera*). Evolutionary applications, 19(5), e70248.

Ding W, et al. (2026) Genome-wide association analysis identifies the genetic basis of body size traits in Tan sheep (*Ovis aries*). BMC genomics, 27(1).

Xue L, et al. (2026) Near telomere-to-telomere diploid genome assembly of *Acrossocheilus wenchowensis*. Scientific data, 13(1).

Chen W, et al. (2025) Whole genome sequencing informs SNP-based breeding strategies to safeguard genetic diversity in captive African lions. Frontiers in veterinary science, 12, 1577726.

Teng Y, et al. (2025) Integrating population genomics and environmental data to predict adaptation to climate change in post-bottleneck Tibetan macaques. Science advances, 11(28), eadw0562.

Guo R, et al. (2025) Genome-wide identification and comparative analysis of strigolactone biosynthetic genes in major solanaceous crops. PloS one, 20(12), e0338033.

Zhan S, et al. (2025) Whole-genome resequencing reveals genetic diversity and selection signatures of Tongjiang and five goat breeds. Frontiers in veterinary science, 12, 1559764.

Gong W, et al. (2025) Genomic analyses identify distinct patterns of selection in game fowl and Nami chicken. Poultry science, 104(12), 106095.

Chen L, et al. (2025) Differential Retention and Loss of a Mycotoxin in Fungal Evolution. Toxins, 17(6).

Luo C, et al. (2025) Genetic diversity and population structure of Kudouzi (*Sophora alopecuroides*) in Northwest China revealed by SNP markers and seed phenotypic traits. *Frontiers in plant science*, 16, 1634581.

Liu S, et al. (2025) Genome of Kumamoto Oyster *Crassostrea sikamea* Provides Insights Into Bivalve Evolution and Environmental Adaptation. *Evolutionary applications*, 18(4), e70100.

Kong X, et al. (2025) Genome-wide association study to dissect the genetic architecture of bolting-related traits in carrot (*Daucus carota*). *Scientific reports*, 15(1), 42864.

Wang G, et al. (2025) *Metarhizium* spp. encode an ochratoxin cluster and a high efficiency ochratoxin-degrading amidohydrolase revealed by genomic analysis. *Journal of advanced research*, 72, 85.

Xia M, et al. (2025) Genetic structure and conservation implications of *Lancea tibetica* (Mazaceae), a traditional Tibetan medicinal plant endemic to the Qinghai- Tibet Plateau. *BMC plant biology*, 25(1), 222.

Li Z, et al. (2024) Intraspecific diploidization of a halophyte root fungus drives heterosis. *Nature communications*, 15(1), 5872.

An K, et al. (2024) Population genetic differentiation and structure of rare plant *Anemone shikokiana* based on genotyping-by-sequencing (GBS). *BMC plant biology*, 24(1), 995.