

# Resource Summary Report

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## iTOL

RRID:SCR\_018174

Type: Tool

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### Proper Citation

iTOL (RRID:SCR\_018174)

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### Resource Information

**URL:** <https://itol.embl.de/>

**Proper Citation:** iTOL (RRID:SCR\_018174)

**Description:** Web tool for display, annotation and management of phylogenetic trees.  
Accessible with any modern web browser.

**Synonyms:** interactive Tree Of Life

**Resource Type:** software resource, service resource, web service, data access protocol

**Defining Citation:** [PMID:30931475](#)

**Keywords:** Phylogenetic tree, phylogeny, data visualization, data annotation, data management, dataset, bio.tools

**Funding:** German Federal Ministry of Education and Research ;  
European Research Council ;  
European Molecular Biology Laboratory

**Availability:** Free, Freely available

**Resource Name:** iTOL

**Resource ID:** SCR\_018174

**Alternate IDs:** biotools:itol

**Alternate URLs:** <https://bio.tools/itol>

**Record Creation Time:** 20220129T080339+0000

**Record Last Update:** 20260821T043034+0000

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### Ratings and Alerts

No rating or validation information has been found for iTOL.

No alerts have been found for iTOL.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 5217 mentions in open access literature.

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

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Huang KK, et al. (2026) Mutational Signatures and Clonal Hematopoiesis in Intestinal Metaplasia across Countries with Varying Stomach Cancer Incidence. *Cancer discovery*, 16(3), 497.

Nickles GR, et al. (2026) Tracing the origins of crmA megasynthase through lichen genomes. *Current biology : CB*, 36(13), 3354.

Delgado-Suarez EJ, et al. (2026) Emergence of multidrug-resistant blaCTX-M-65/gyrA\_D87Y clones among the circulating *Salmonella* *Infantis* population in Mexico. *Microbial genomics*, 12(2).

Withatanung P, et al. (2026) Phage-based diagnostic assay for melioidosis using multiplex PCR targeting *Burkholderia* phage terminase genes. *iScience*, 29(3), 114831.

Chen L, et al. (2026) Mycobacterial metallophosphatase MmpE acts as a nucleomodulin to regulate host gene expression and promote intracellular survival. *eLife*, 14.

Zeng L, et al. (2026) Functional genomics reveals key gene families and molecular pathways for extreme cold survival in the khapra beetle. *BMC biology*, 24(1).

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. *PLoS biology*, 24(6), e3003855.

Tang B, et al. (2026) Acquired antimicrobial resistance genes in *Bordetella* Species: a global genomic analysis. *The Journal of antimicrobial chemotherapy*, 81(1).

Cheng X, et al. (2026) Engineering seed-specific gossypol-free cotton for human-safe consumption by harnessing the dominant-negative effect of the Gl2e mutation. *Plant communications*, 7(2), 101628.

Farias FM, et al. (2026) Streptocyclin BTW is a novel member of a diverse family of circular bacteriocins in the genus *Streptococcus*. *Molecular nutrition & food research*, 70(1), e70290.

Dong S, et al. (2026) Metabolomic and Single-Cell Transcriptomic Analyses Shed Light on Secondary Metabolite Profiling and Potential Developmental Dynamics of Glandular Trichomes in *Artemisia argyi*. *Plant biotechnology journal*, 24(3), 1064.

Shie SS, et al. (2026) Clinical and genomic insights into persistent carbapenem-resistant *Klebsiella pneumoniae* bacteremia: risk factors, resistance mechanisms, and treatment challenges. *Biomedical journal*, 49(2), 100905.

Tachibana K, et al. (2026) Identification and intracellular functional characterization of myosin XI and VIII in the lycophyte *Selaginella moellendorffii*. *Planta*, 263(3), 66.

Han X, et al. (2026) Two kinds of novel reassortment H3 subtypes of avian influenza viruses: similar genetic composition, different mammalian transmission capabilities. *Poultry science*, 105(4), 106564.

Song X, et al. (2026) Identification of the IDA peptide family in tomato and function of SIIDA8 in salt stress. *BMC plant biology*, 26(1), 300.

Tao J, et al. (2026) Clinical and molecular characterization of NDM-9 and NDM-13 producing multidrug-resistant *Escherichia coli* strains in China. *BMC microbiology*, 26(1), 113.

Dos Santos LDR, et al. (2026) Environmental occurrence of *optrA*-mediated linezolid resistance in *Enterococcus* isolates and genomic insights into *Enterococcus faecium* ST54 co-harboring *optrA*, *poxA*, and *cfr(D)* genes. *World journal of microbiology & biotechnology*, 42(2), 70.

Zhao D, et al. (2026) Tomato antiviral ubiquitin-proteasome system recognizes viral 59 kDa protein to confer tomato chlorosis virus resistance. *Nature communications*, 17(1).

Yu C, et al. (2026) Graph pan-genome advances genetic discoveries and the improvement of eggplant. *Horticulture research*, 13(1), uhaf248.