Resource Summary Report

Generated by RRID on Aug 2, 2026

TOBFAC

RRID:SCR_005423
Type: Tool

Proper Citation

TOBFAC (RRID:SCR_005423)

Resource Information

URL: http://compsysbio.achs.virginia.edu/tobfac/

Proper Citation: TOBFAC (RRID:SCR_005423)

Description: Database of transcription factor sequences from a single plant species (over 2,500 genes). It is possible to search: # 1,159,022 gene-space sequence reads (GSRs) obtained by methylation filtering from the Tobacco Genome Initiative (TGI). # The DFCI Tobacco Gene Index (Release 4.0 July 5, 2008) that contains 163,524 tobacco EST sequences and 2,288 expressed transcripts (ETs). # The complete TOBFAC database of tobacco transcription factors. It is also possible to search multiple libraries in a single search. They have incorporated tools for downloading all of the sequences from the blast results and also a contig tool to assemble any or all of the resulting sequences. They are also improving the TOBFAC sequences by extending the original contigs using a contig extension tool designed by Ryan Thompson. This has allowed them to refine the predicted genes. These will be updated on a gene family basis as the improved data become available.

Abbreviations: TOBFAC

Synonyms: TOBFAC: The database of tobacco transcription factors

Resource Type: data or information resource, database

Defining Citation: PMID:18221524

Keywords: transcription factor

Availability: Free

Resource Name: TOBFAC

Resource ID: SCR_005423

Alternate IDs: OMICS_00564

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260801T190933+0000

Ratings and Alerts

No rating or validation information has been found for TOBFAC.

No alerts have been found for TOBFAC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Subban P, et al. (2020) Shoot Regeneration Is Not a Single Cell Event. Plants (Basel, Switzerland), 10(1).

Li F, et al. (2016) Identification of Topping Responsive Proteins in Tobacco Roots. Frontiers in plant science, 7, 582.

Rabara RC, et al. (2015) Transcriptome profiling of tobacco under water deficit conditions. Genomics data, 5, 61.

Tang S, et al. (2012) Identification of wounding and topping responsive small RNAs in tobacco (Nicotiana tabacum). BMC plant biology, 12, 28.

Velten J, et al. (2010) A spontaneous dominant-negative mutation within a 35S::AtMYB90 transgene inhibits flower pigment production in tobacco. PloS one, 5(3), e9917.

Mochida K, et al. (2010) Genomics and bioinformatics resources for crop improvement. Plant & cell physiology, 51(4), 497.

Ramirez SR, et al. (2009) Comparative analyses of plant transcription factor databases. Current genomics, 10(1), 10.

Rushton PJ, et al. (2008) TOBFAC: the database of tobacco transcription factors. BMC bioinformatics, 9, 53.