

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 12, 2026

TFClass

RRID:SCR_012018

Type: Tool

Proper Citation

TFClass (RRID:SCR_012018)

Resource Information

URL: <http://tfclass.bioinf.med.uni-goettingen.de/tfclass>

Proper Citation: TFClass (RRID:SCR_012018)

Description: Database that classifies human transcription factors based on the characteristics of their DNA-binding domains. It comprises six levels (superclasses, classes, families, subfamilies, genera and factor species), two of which are optional (subfamilies and factor species). The full classification can also be obtained as html document and as ontology in obo-format., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: TFClass

Synonyms: Classification of Human Transcription Factors

Resource Type: controlled vocabulary, data or information resource, database, ontology

Defining Citation: [PMID:23180794](#)

Keywords: transcription factor, dna-binding domain, obo

Funding: BMBF ;
European Union FP7 LipidomicNet 202272;
European Union FP7 SysCol 258236;
DFG FKZ0315890B

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: TFClass

Resource ID: SCR_012018

Alternate IDs: OMICS_01864

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260912T195743+0000

Ratings and Alerts

No rating or validation information has been found for TFClass.

No alerts have been found for TFClass.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Paquette A, et al. (2024) A genome scale transcriptional regulatory model of the human placenta. Science advances, 10(26), eadf3411.

Mummey HM, et al. (2024) Single cell multiome profiling of pancreatic islets reveals physiological changes in cell type-specific regulation associated with diabetes risk. bioRxiv : the preprint server for biology.

Zemke NR, et al. (2023) Conserved and divergent gene regulatory programs of the mammalian neocortex. Nature, 624(7991), 390.

Vazquez M, et al. (2022) ExTRI: Extraction of transcription regulation interactions from literature. Biochimica et biophysica acta. Gene regulatory mechanisms, 1865(1), 194778.

Pan Q, et al. (2021) VARAdb: a comprehensive variation annotation database for human. Nucleic acids research, 49(D1), D1431.

Gorkin DU, et al. (2020) An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 583(7818), 744.

Choi J, et al. (2020) Bcl-6 is the nexus transcription factor of T follicular helper cells via repressor-of-repressor circuits. Nature immunology, 21(7), 777.

Wingender E, et al. (2018) TFClass: expanding the classification of human transcription factors to their mammalian orthologs. Nucleic acids research, 46(D1), D343.

Yevshin I, et al. (2017) GTRD: a database of transcription factor binding sites identified by ChIP-seq experiments. Nucleic acids research, 45(D1), D61.

Tripathi S, et al. (2016) Gene regulation knowledge commons: community action takes care of DNA binding transcription factors. Database : the journal of biological databases

and curation, 2016.

Wlochowicz D, et al. (2016) Computational Identification of Key Regulators in Two Different Colorectal Cancer Cell Lines. *Frontiers in genetics*, 7, 42.

Ignatieva EV, et al. (2016) A compendium of human genes regulating feeding behavior and body weight, its functional characterization and identification of GWAS genes involved in brain-specific PPI network. *BMC genetics*, 17(Suppl 3), 158.

Scarpato M, et al. (2015) Novel transcription factor variants through RNA-sequencing: the importance of being "alternative". *International journal of molecular sciences*, 16(1), 1755.