

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## TcoF

RRID:SCR\_002158

Type: Tool

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### Proper Citation

TcoF (RRID:SCR\_002158)

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### Resource Information

**URL:** <http://cbrc.kaust.edu.sa/tcof/>

**Proper Citation:** TcoF (RRID:SCR\_002158)

**Description:** Database that facilitates the exploration of proteins involved in the regulation of transcription in humans by binding to regulatory DNA regions (transcription factors) and proteins involved in the regulation of transcription in humans by interacting with transcription factors and not binding to regulatory DNA regions (transcription co-factors).

**Abbreviations:** TcoF

**Synonyms:** Dragon Database for Human Transcription Co-Factors and Transcription Factor Interacting Proteins, TcoF-DB, TcoF - Dragon database of transcription co-factors and transcription factor interacting proteins

**Resource Type:** data or information resource, database

**Defining Citation:** [PMID:20965969](#)

**Keywords:** protein, regulation, transcription, transcription factor, transcription co-factor, bio.tools

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** TcoF

**Resource ID:** SCR\_002158

**Alternate IDs:** biotools:tcof-db, OMICS\_01865

**Alternate URLs:** <https://bio.tools/tcof-db>

**Record Creation Time:** 20220129T080211+0000

**Record Last Update:** 20260801T190913+0000

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## Ratings and Alerts

No rating or validation information has been found for TcoF.

No alerts have been found for TcoF.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Zhang G, et al. (2025) TRAPT: a multi-stage fused deep learning framework for predicting transcriptional regulators based on large-scale epigenomic data. Nature communications, 16(1), 3611.

He ZQ, et al. (2022) Pharmacological Perturbation of Mechanical Contractility Enables Robust Transdifferentiation of Human Fibroblasts into Neurons. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 9(13), e2104682.

Zhang Y, et al. (2022) TcoFBase: a comprehensive database for decoding the regulatory transcription co-factors in human and mouse. Nucleic acids research, 50(D1), D391.

Zhang S, et al. (2019) FisherMP: fully parallel algorithm for detecting combinatorial motifs from large ChIP-seq datasets. DNA research : an international journal for rapid publication of reports on genes and genomes, 26(3), 231.

Huang M, et al. (2018) dbCoRC: a database of core transcriptional regulatory circuitries modeled by H3K27ac ChIP-seq signals. Nucleic acids research, 46(D1), D71.

de Souza MM, et al. (2018) A comprehensive manually-curated compendium of bovine transcription factors. Scientific reports, 8(1), 13747.

Rouchka EC, et al. (2016) Data set for transcriptional response to depletion of the Shoc2 scaffolding protein. Data in brief, 7, 770.

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.

Çelen ?, et al. (2015) Bioinformatics Knowledge Map for Analysis of Beta-Catenin Function in Cancer. PloS one, 10(10), e0141773.

Galperin MY, et al. (2011) The 2011 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. Nucleic acids research, 39(Database issue), D1.