

Resource Summary Report

Generated by T1D on Sep 14, 2026

MODENT - A Tool For Reconstructing Gene Regulatory Networks

RRID:SCR_000220

Type: Tool

Proper Citation

MODENT - A Tool For Reconstructing Gene Regulatory Networks (RRID:SCR_000220)

Resource Information

URL: <http://acgt.cs.tau.ac.il/modent/>

Proper Citation: MODENT - A Tool For Reconstructing Gene Regulatory Networks (RRID:SCR_000220)

Description: A computational tool that reconstructs gene regulatory networks from high throughput experimental data.

Abbreviations: ModEnt

Resource Type: software resource

Defining Citation: [PMID:22216865](https://pubmed.ncbi.nlm.nih.gov/22216865/)

Keywords: gene regulatory network, experimental data, computation, computational tool, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: MODENT - A Tool For Reconstructing Gene Regulatory Networks

Resource ID: SCR_000220

Alternate IDs: biotools:modent, OMICS_01685

Alternate URLs: <https://bio.tools/modent>

License: ModEnt is a free software, and may be used and redistributed for all purposes. 2.The creators of ModEnt shall not be liable for any damage, claim, demand, cost or expense of whatsoever kind or nature directly or indirectly arising out of or resulting from or encountered in connection with the use of ModEnt by Licensee or any person receiving it from Licensee.

Record Creation Time: 20220129T080200+0000

Record Last Update: 20260912T195505+0000

Ratings and Alerts

No rating or validation information has been found for MODENT - A Tool For Reconstructing Gene Regulatory Networks.

No alerts have been found for MODENT - A Tool For Reconstructing Gene Regulatory Networks.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Karlebach G, et al. (2012) Constructing logical models of gene regulatory networks by integrating transcription factor-DNA interactions with expression data: an entropy-based approach. Journal of computational biology : a journal of computational molecular cell biology, 19(1), 30.