

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

T-PIC

RRID:SCR_010867

Type: Tool

Proper Citation

T-PIC (RRID:SCR_010867)

Resource Information

URL: <http://www.math.miami.edu/~vhower/tpic.html>

Proper Citation: T-PIC (RRID:SCR_010867)

Description: A software for determining DNA/protein binding sites from a ChIP-Seq experiment.

Abbreviations: T-PIC

Resource Type: software resource

Resource Name: T-PIC

Resource ID: SCR_010867

Alternate IDs: OMICS_00464

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260903T235044+0000

Ratings and Alerts

No rating or validation information has been found for T-PIC.

No alerts have been found for T-PIC.

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 [kravitz2](#) .

Kindrick JD, et al. (2026) Hypoxic regulation of chromatin and gene transcription. Communications biology, 9(1).

Lafleur VN, et al. (2023) Multi-level interaction between HIF and AHR transcriptional pathways in kidney carcinoma. Life science alliance, 6(4).

Lombardi O, et al. (2022) Pan-cancer analysis of tissue and single-cell HIF-pathway activation using a conserved gene signature. Cell reports, 41(7), 111652.

Vergara Z, et al. (2017) Retrotransposons are specified as DNA replication origins in the gene-poor regions of Arabidopsis heterochromatin. Nucleic acids research, 45(14), 8358.

Salama R, et al. (2015) Heterogeneous Effects of Direct Hypoxia Pathway Activation in Kidney Cancer. PloS one, 10(8), e0134645.

Tran NT, et al. (2014) A survey of motif finding Web tools for detecting binding site motifs in ChIP-Seq data. Biology direct, 9, 4.

Osmanbeyoglu HU, et al. (2012) Improving ChIP-seq peak-calling for functional co-regulator binding by integrating multiple sources of biological information. BMC genomics, 13 Suppl 1(Suppl 1), S1.

Devaraj SG, et al. (2007) Regulation of IRF-3-dependent innate immunity by the papain-like protease domain of the severe acute respiratory syndrome coronavirus. The Journal of biological chemistry, 282(44), 32208.