

Resource Summary Report

Generated by [NIF](#) on Sep 2, 2026

IFTI-Mirage

RRID:SCR_000505

Type: Tool

Proper Citation

IFTI-Mirage (RRID:SCR_000505)

Resource Information

URL: <http://www.ifti.org/>

Proper Citation: IFTI-Mirage (RRID:SCR_000505)

Description: A resource for information pertaining to methodologies, tools and technologies of gene expression. The website offers resources for sequence analysis, database services, and other technologies of gene expression and regulation.

Synonyms: Institute for Transcriptional Informatics-Molecular Informatics Resource for the Analysis of Gene Expression, MIRAGE

Resource Type: data or information resource, database, portal

Keywords: bioinformatics, gene, expression, database, technology, method, tool, sequence, regulation

Availability: Public, Available to the research community

Resource Name: IFTI-Mirage

Resource ID: SCR_000505

Alternate IDs: nlx_19877

Record Creation Time: 20220129T080201+0000

Record Last Update: 20260829T182824+0000

Ratings and Alerts

No rating or validation information has been found for IFTI-Mirage.

No alerts have been found for IFTI-Mirage.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Yang SY, et al. (2017) Replicative genetic association study between functional polymorphisms in AVPR1A and social behavior scales of autism spectrum disorder in the Korean population. Molecular autism, 8, 44.

Zuo J, et al. (2015) An inhibitory role of NEK6 in TGF β /Smad signaling pathway. BMB reports, 48(8), 473.

Hesse RG, et al. (2015) The human ARF tumor suppressor senses blastema activity and suppresses epimorphic tissue regeneration. eLife, 4.

Zhang M, et al. (2013) cAMP responsive element binding protein-1 is a transcription factor of lysosomal-associated protein transmembrane-4 Beta in human breast cancer cells. PloS one, 8(2), e57520.

Wei W, et al. (2007) Comparative analysis of regulatory motif discovery tools for transcription factor binding sites. Genomics, proteomics & bioinformatics, 5(2), 131.