

Resource Summary Report

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TAPIR

RRID:SCR_002596

Type: Tool

Proper Citation

TAPIR (RRID:SCR_002596)

Resource Information

URL: <http://www.nitrc.org/projects/tapir/>

Proper Citation: TAPIR (RRID:SCR_002596)

Description: A set of command line tools allowing 2D and 3D image registration, mainly for medical imaging (although also relevant to other image registration problems).

Abbreviations: TAPIR

Synonyms: Tools for Advanced Parameterized Image Registration

Resource Type: data processing software, image analysis software, registration software, software application, software resource

Keywords: magnetic resonance

Availability: Free

Resource Name: TAPIR

Resource ID: SCR_002596

Alternate IDs: nlx_156001

License: Mozilla Public License

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260821T193647+0000

Ratings and Alerts

No rating or validation information has been found for TAPIR.

No alerts have been found for TAPIR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 67 mentions in open access literature.

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

Yu C, et al. (2026) A lightweight TcrLM model predicts T cell receptor and epitope binding specificity. *Cell reports methods*, 6(5), 101378.

Ashraf MA, et al. (2025) An Integrative Computational Approach for Identifying Cotton Host Plant MicroRNAs with Potential to Abate CLCuKoV-Bur Infection. *Viruses*, 17(3).

JanssenDuijghuijsen L, et al. (2025) How to Study the Effects of Dietary Lipids on the Small Intestinal Microbiome? Methodological Design and Evaluation of the Human HealThy fAt, haPpy mIcRobiome (TAPIR) Proof-of-Concept Study. *Current developments in nutrition*, 9(3), 104564.

Marins LMS, et al. (2025) Weekly Text Messages to Support Adherence to Oral Pre-Exposure Prophylaxis (PrEP) Among Gay, Bisexual, and Other Cisgender Men Who Have Sex With Men (MSM) and Transgender Women: Pilot Randomized Controlled Trial Nested in PrEP Brasil Study. *Journal of medical Internet research*, 27, e72360.

Vignale FA, et al. (2025) Yerba mate (*Ilex paraguariensis*) genome provides new insights into convergent evolution of caffeine biosynthesis. *eLife*, 14.

Kong X, et al. (2025) Transcriptional regulation of miR528-PPO module by miR156 targeted SPLs orchestrates chilling response in banana. *Molecular horticulture*, 5(1), 2.

Dechkrong P, et al. (2024) Mutation mapping of a variegated EMS tomato reveals an FtsH-like protein precursor potentially causing patches of four phenotype classes in the leaves with distinctive internal morphology. *BMC plant biology*, 24(1), 265.

Díez-Sainz E, et al. (2024) MicroRNAs from edible plants reach the human gastrointestinal tract and may act as potential regulators of gene expression. *Journal of physiology and biochemistry*, 80(3), 655.

Piombo E, et al. (2024) RNA silencing is a key regulatory mechanism in the biocontrol fungus *Clonostachys rosea*-wheat interactions. *BMC biology*, 22(1), 219.

Wang Y, et al. (2024) Mechanism of zju-miR156c-mediated network in regulating witches' broom symptom of Chinese jujube. *Molecular plant pathology*, 25(11), e70031.

Balhara R, et al. (2024) MYB transcription factors, their regulation and interactions with non-coding RNAs during drought stress in *Brassica juncea*. *BMC plant biology*, 24(1), 999.

Wu JW, et al. (2024) Genome-wide identification, stress- and hormone-responsive expression characteristics, and regulatory pattern analysis of *Scutellaria baicalensis* SbSPLs. *Plant molecular biology*, 114(2), 20.

Enriquez-Felix EE, et al. (2024) Argonaute and Dicer are essential for communication between *Trichoderma atroviride* and fungal hosts during mycoparasitism. *Microbiology spectrum*, 12(4), e0316523.

Díez-Sainz E, et al. (2023) miR482f and miR482c-5p from edible plant-derived foods inhibit the expression of pro-inflammatory genes in human THP-1 macrophages. *Frontiers in nutrition*, 10, 1287312.

Alazem M, et al. (2023) Viral synergism suppresses R gene-mediated resistance by impairing downstream defense mechanisms in soybean. *Plant physiology*, 192(4), 3088.

Lai T, et al. (2023) The Identification and Comparative Analysis of Non-Coding RNAs in Spores and Mycelia of *Penicillium expansum*. *Journal of fungi (Basel, Switzerland)*, 9(10).

Fuller EK, et al. (2023) Concurrent, Convergent, and Discriminant Validity of the DSM-5 Section III Psychopathy Specifier. *Assessment*, 30(6), 1790.

Fu Y, et al. (2023) Integrated microRNA and whole-transcriptome sequencing reveals the involvement of small and long non-coding RNAs in the fiber growth of ramie plant. *BMC genomics*, 24(1), 599.

Fast E, et al. (2023) TAPIR: a T-cell receptor language model for predicting rare and novel targets. *bioRxiv : the preprint server for biology*.

Zhou J, et al. (2022) Genome-Wide Identification and Characterization of the NF-YA Gene Family and Its Expression in Response to Different Nitrogen Forms in *Populus × canescens*. *International journal of molecular sciences*, 23(19).