

# Resource Summary Report

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## T-REX

RRID:SCR\_010715

Type: Tool

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### Proper Citation

T-REX (RRID:SCR\_010715)

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### Resource Information

**URL:** <http://trex.biohpc.org/>

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**Description:** T-REX is a free, platform-independent online tool that allows for an integrated, rapid, and more robust analysis of T-RFLP data. Despite increasing popularity and improvements in terminal restriction fragment length polymorphism (T-RFLP) and other microbial community fingerprinting techniques, there are still numerous obstacles that hamper the analysis of these datasets. Many steps are required to process raw data into a format ready for analysis and interpretation. These steps can be time-intensive, error-prone, and can introduce unwanted variability into the analysis. Accordingly, we developed T-REX, free, online software for the processing and analysis of T-RFLP data. Analysis of T-RFLP data generated from a multiple-factorial study was performed with T-REX. With this software, we were able to i) label raw data with attributes related to the experimental design of the samples, ii) determine a baseline threshold for identification of true peaks over noise, iii) align terminal restriction fragments (T-RFs) in all samples (i.e., bin T-RFs), iv) construct a two-way data matrix from labeled data and process the matrix in a variety of ways, v) produce several measures of data matrix complexity, including the distribution of variance between main and interaction effects and sample heterogeneity, and vi) analyze a data matrix with the additive main effects and multiplicative interaction (AMMI) model.

**Abbreviations:** T-REX

**Synonyms:** T-REX (T-RFLP analysis EXpedited), T-REX: Software for the processing and analysis of T-RFLP data, T-RFLP analysis EXpedited

**Resource Type:** data analysis service, service resource, analysis service resource, production service resource

**Defining Citation:** [PMID:19500385](#)

**Funding:** Microsoft Corporation ;  
NSF DGE 0221658

**Resource Name:** T-REX

**Resource ID:** SCR\_010715

**Alternate IDs:** nlx\_89468

**Record Creation Time:** 20220129T080300+0000

**Record Last Update:** 20260810T040537+0000

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## Ratings and Alerts

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

No alerts have been found for T-REX.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 122 mentions in open access literature.

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

Aleidi SM, et al. (2026) Untargeted metabolomics profiling of childhood asthma: linking metabolic pattern to disease severity. *Molecular and cellular pediatrics*, 13(1), 6.

Thomson RES, et al. (2026) Thermostable ancestors enabled evolutionary diversification of promiscuous chemical defence enzymes. *The EMBO journal*, 45(9), 2938.

Seif M, et al. (2026) Anti-inflammatory activity and metabolite profiling of myo-inositol in LPS-stimulated macrophages. *PloS one*, 21(2), e0341193.

Motiwalla T, et al. (2025) Molecular dynamic simulations to assess the structural variability of ClpV from *Enterobacter cloacae*. *Frontiers in bioinformatics*, 5, 1498916.

Hagyouf YA, et al. (2025) Molecular signatures of xenograft colorectal cancer in mice treated with topotecan: A mass spectrometry-based study. *Toxicology reports*, 14, 102045.

Bryant N, et al. (2025) Rhinovirus as a driver of airway T cell dynamics in children with treatment-refractory recurrent wheeze. *JCI insight*, 10(9).

Wu Z, et al. (2025) Human autoimmunity at single cell resolution in aplastic anemia before and after effective immunotherapy. *Nature communications*, 16(1), 5048.

Thirman HL, et al. (2025) Connecting chemical structure to single cell signaling profiles. *Communications biology*, 8(1), 1137.

Belmonte-Reche E, et al. (2025) Insight into the epigenetic regulation of gene expression in the bloodstream and procyclic forms of *Trypanosoma brucei* through the involvement of G-quadruplexes. *NAR genomics and bioinformatics*, 7(3), lqaf100.

Aryal S, et al. (2025) Antimicrobial potential of actinomycetes from high altitude Nepalese soils. *Scientific reports*, 15(1), 33915.

Choi JH, et al. (2025) No evidence that human GIGYF2 interacts with GRB10: implications for human disease. *Life science alliance*, 8(9).

Alqudah MAY, et al. (2025) Metabolomic Analysis, Antiproliferative, Anti-Migratory, and Anti-Invasive Potential of Amlodipine in Lung Cancer Cells. *Drug design, development and therapy*, 19, 1215.

Marshall JP, et al. (2024) Circadian regulation of locomotion, respiration, and arousability in adult blacklegged ticks (*Ixodes scapularis*). *Scientific reports*, 14(1), 14804.

Sterzi L, et al. (2024) Genetic barriers more than environmental associations explain *Serratia marcescens* population structure. *Communications biology*, 7(1), 468.

Thirman HL, et al. (2024) Single Cell Profiling Distinguishes Leukemia-Selective Chemotypes. *bioRxiv : the preprint server for biology*.

Chen W, et al. (2024) Phylogenomics analysis of velvet regulators in the fungal kingdom. *Microbiology spectrum*, 12(2), e0371723.

Febra C, et al. (2024) Acute venous thromboembolism plasma and red blood cell metabolomic profiling reveals potential new early diagnostic biomarkers: observational clinical study. *Journal of translational medicine*, 22(1), 200.

Arsyadi A, et al. (2023) A Nitrate-Transforming Bacterial Community Dominates in the *Miscanthus* Rhizosphere on Nitrogen-Deficient Volcanic Deposits of Miyake-jima. *Microorganisms*, 11(2).

Miranda RP, et al. (2023) Genome Organization of Four Brazilian *Xanthomonas albilineans* Strains Does Not Correlate with Aggressiveness. *Microbiology spectrum*, 11(3), e0280222.

Zenati RA, et al. (2023) Evaluation of Two Simultaneous Metabolomic and Proteomic Extraction Protocols Assessed by Ultra-High-Performance Liquid Chromatography Tandem Mass Spectrometry. *International journal of molecular sciences*, 24(2).