## **Resource Summary Report**

Generated by <u>NIF</u> on May 20, 2025

# T-REX

RRID:SCR\_010715 Type: Tool

## **Proper Citation**

T-REX (RRID:SCR\_010715)

## **Resource Information**

URL: http://trex.biohpc.org/

#### Proper Citation: T-REX (RRID:SCR\_010715)

**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:** production service resource, data analysis service, service resource, analysis 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: 20250519T204807+0000

### **Ratings and Alerts**

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

No alerts have been found for T-REX.

Data and Source Information

Source: <u>SciCrunch Registry</u>

## **Usage and Citation Metrics**

We found 110 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

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.

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

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

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.

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).

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

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).

Nsele NN, et al. (2023) Pezizomycetes Genomes Reveal Diverse P450 Complements Characteristic of Saprotrophic and Ectomycorrhizal Lifestyles. Journal of fungi (Basel, Switzerland), 9(8).

Alkner S, et al. (2023) Protocol for the T-REX-trial: tailored regional external beam radiotherapy in clinically node-negative breast cancer patients with 1-2 sentinel node macrometastases - an open, multicentre, randomised non-inferiority phase 3 trial. BMJ open, 13(9), e075543.

Bunma C, et al. (2023) Burkholderia pseudomallei biofilm resists Acanthamoeba sp. grazing and produces 8-O-4'-diferulic acid, a superoxide scavenging metabolite after passage through the amoeba. Scientific reports, 13(1), 16578.

Han R, et al. (2023) The antihelminth drug rafoxanide reverses chromosomal-mediated colistin-resistance in Klebsiella pneumoniae. mSphere, 8(5), e0023423.

Aghila Rani KG, et al. (2023) Effects of medwakh smoking on salivary metabolomics and its association with altered oral redox homeostasis among youth. Scientific reports, 13(1), 1870.

Guardalupi F, et al. (2023) A pro-inflammatory environment in bone marrow of Treg transplanted patients matches with graft-versus-leukemia effect. Leukemia, 37(7), 1572.

Mora-Sala B, et al. (2022) New Reports of Phytophthora Species in Plant Nurseries in Spain. Pathogens (Basel, Switzerland), 11(8).

Dahabiyeh LA, et al. (2022) Molecular and metabolic alterations of 2,3-dihydroquinazolin-4(1H)-one derivatives in prostate cancer cell lines. Scientific reports, 12(1), 21599.

Abushawish KYI, et al. (2022) Multi-Omics Analysis Revealed a Significant Alteration of Critical Metabolic Pathways Due to Sorafenib-Resistance in Hep3B Cell Lines. International journal of molecular sciences, 23(19).

Saheb Sharif-Askari N, et al. (2022) Saliva metabolomic profile of COVID-19 patients

associates with disease severity. Metabolomics : Official journal of the Metabolomic Society, 18(11), 81.

Alsoud LO, et al. (2022) Identification of Insulin Resistance Biomarkers in Metabolic Syndrome Detected by UHPLC-ESI-QTOF-MS. Metabolites, 12(6).

Lan Y, et al. (2022) Endosymbiont population genomics sheds light on transmission mode, partner specificity, and stability of the scaly-foot snail holobiont. The ISME journal, 16(9), 2132.