Resource Summary Report

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TrED

RRID:SCR_005869
Type: Tool

Proper Citation

TrED (RRID:SCR_005869)

Resource Information

URL: http://www.mgc.ac.cn/TrED/

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Description: TrED is a database of Trichophyton rubrum, a fungus. The database contains strains, cDNA libraries, pathways, and microarray data as well as a directed set of literature. Trichophyton rubrum is the most common dermatophyte species and the most frequent cause of fungal skin infections in humans worldwide. It""s a major concern because feet and nail infections caused by this organism is extremely difficult to cure. A large set of expression data including expressed sequence tags (ESTs) and transcriptional profiles of this important fungal pathogen are now available. Careful analysis of these data can give valuable information about potential virulence factors, antigens and novel metabolic pathways. We intend to create an integrated database TrED to facilitate the study of dermatophytes, and enhance the development of effective diagnostic and treatment strategies. All publicly available ESTs and expression profiles of T. rubrum during conidial germination in time-course experiments and challenged with antifungal agents are deposited in the database. In addition, comparative genomics hybridization results of 22 dermatophytic fungi strains from three genera, Trichophyton, Microsporum and Epidermophyton, are also included. ESTs are clustered and assembled to elongate the sequence length and abate redundancy. TrED provides functional analysis based on GenBank, Pfam, and KOG databases, along with KEGG pathway and GO vocabulary. It is integrated with a suite of custom web-based tools that facilitate querying and retrieving various EST properties, visualization and comparison of transcriptional profiles, and sequence-similarity searching by BLAST. TrED is built upon a relational database, with a web interface offering analytic functions, to provide integrated access to various expression data of T. rubrum and comparative results of dermatophytes. It is devoted to be a comprehensive resource and platform to assist functional genomic studies in dermatophytes.

Abbreviations: TrED

Synonyms: TrED - T. rubrum Expression Database, Trichophyton rubrum Expression Database, Trichophyton rubrum Expression Database (TrED)

Resource Type: data processing software, database, software application, data analysis software, software resource, data or information resource

Defining Citation: PMID:17650345

Keywords: expressed sequence tag, transcriptional profile, fungal pathogen, bmu01672, chuv862.00, mya-3108, cdna, pathway, microarray, classification, blast, unisequence, peptide, annotation

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Resource Name: TrED

Resource ID: SCR_005869

Alternate IDs: nlx_149408

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250418T055116+0000

Ratings and Alerts

No rating or validation information has been found for TrED.

No alerts have been found for TrED.

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.

Xing D, et al. (2023) A Comparative Study on Heavy Metal Removal from CCA-Treated Wood Waste by Yarrowia lipolytica: Effects of Metal Stress. Journal of fungi (Basel, Switzerland), 9(4).

Liu T, et al. (2014) Analysis of gene expression changes in Trichophyton rubrum after skin interaction. Journal of medical microbiology, 63(Pt 5), 642.

Schaper E, et al. (2012) Repeat or not repeat?--Statistical validation of tandem repeat prediction in genomic sequences. Nucleic acids research, 40(20), 10005.

Peres NT, et al. (2010) Transcriptional profiling reveals the expression of novel genes in response to various stimuli in the human dermatophyte Trichophyton rubrum. BMC microbiology, 10, 39.

Silveira HC, et al. (2010) Transcriptional profiling reveals genes in the human pathogen Trichophyton rubrum that are expressed in response to pH signaling. Microbial pathogenesis, 48(2), 91.