Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 21, 2025

T-REKS

RRID:SCR_010768
Type: Tool

Proper Citation

T-REKS (RRID:SCR_010768)

Resource Information

URL: http://bioinfo.montp.cnrs.fr/?r=t-reks/

Proper Citation: T-REKS (RRID:SCR_010768)

Description: An algorithm for de novo detection and alignment of repeats in sequences based on K-means algorithm.

Abbreviations: T-REKS

Resource Type: software resource

Defining Citation: PMID:19671691

Keywords: matlab

Funding:

Resource Name: T-REKS

Resource ID: SCR_010768

Alternate IDs: OMICS_00116

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250420T014508+0000

Ratings and Alerts

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

No alerts have been found for T-REKS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Schultz CJ, et al. (2022) A targeted bioinformatics approach identifies highly variable cell surface proteins that are unique to Glomeromycotina. Mycorrhiza, 32(1), 45.

Monzon V, et al. (2022) Large-Scale Discovery of Microbial Fibrillar Adhesins and Identification of Novel Members of Adhesive Domain Families. Journal of bacteriology, 204(6), e0010722.

Osmanli Z, et al. (2022) The Difference in Structural States between Canonical Proteins and Their Isoforms Established by Proteome-Wide Bioinformatics Analysis. Biomolecules, 12(11).

Jarnot P, et al. (2022) Insights from analyses of low complexity regions with canonical methods for protein sequence comparison. Briefings in bioinformatics, 23(5).

Monzon V, et al. (2021) Discovery of fibrillar adhesins across bacterial species. BMC genomics, 22(1), 550.

Whelan F, et al. (2021) Periscope Proteins are variable-length regulators of bacterial cell surface interactions. Proceedings of the National Academy of Sciences of the United States of America, 118(23).

Lombardi L, et al. (2019) Characterization of the Candida orthopsilosis agglutinin-like sequence (ALS) genes. PloS one, 14(4), e0215912.

Herlitze I, et al. (2018) Molecular modularity and asymmetry of the molluscan mantle revealed by a gene expression atlas. GigaScience, 7(6).

Moreno-Pérez DA, et al. (2017) Characterising PvRBSA: an exclusive protein from Plasmodium species infecting reticulocytes. Parasites & vectors, 10(1), 243.

Verma S, et al. (2016) Draft genome sequencing and secretome analysis of fungal phytopathogen Ascochyta rabiei provides insight into the necrotrophic effector repertoire. Scientific reports, 6, 24638.

Sharma M, et al. (2015) Expansion and Function of Repeat Domain Proteins During Stress and Development in Plants. Frontiers in plant science, 6, 1218.

Guy AJ, et al. (2015) Insights into the Immunological Properties of Intrinsically Disordered Malaria Proteins Using Proteome Scale Predictions. PloS one, 10(10), e0141729.

Schaper E, et al. (2014) Deep conservation of human protein tandem repeats within the eukaryotes. Molecular biology and evolution, 31(5), 1132.

Cantu D, et al. (2013) Genome analyses of the wheat yellow (stripe) rust pathogen Puccinia striiformis f. sp. tritici reveal polymorphic and haustorial expressed secreted proteins as candidate effectors. BMC genomics, 14, 270.

Saunders DG, et al. (2012) Using hierarchical clustering of secreted protein families to classify and rank candidate effectors of rust fungi. PloS one, 7(1), e29847.

Albornos L, et al. (2012) ST proteins, a new family of plant tandem repeat proteins with a DUF2775 domain mainly found in Fabaceae and Asteraceae. BMC plant biology, 12, 207.

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