

Resource Summary Report

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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

Resource Name: T-REKS

Resource ID: SCR_010768

Alternate IDs: OMICS_00116

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260801T190417+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

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

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).

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).

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

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-Perez 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.