Tree and reticulogram REConstruction

RRID:SCR_004497
Type: Tool

Proper Citation

Tree and reticulogram REConstruction (RRID:SCR_004497)

Resource Information

URL: http://www.trex.uqam.ca/

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Description: A web server dedicated to the reconstruction of phylogenetic trees, reticulation networks and to the inference of horizontal gene transfer (HGT) events.

Abbreviations: T-REX

Synonyms: Trex-online

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

Defining Citation: PMID:22675075

Keywords: phylogenetic tree, analysis, visualization, network, bio.tools

Funding:

Resource Name: Tree and reticulogram REConstruction

Resource ID: SCR_004497

Alternate IDs: biotools:t-rex, OMICS_04264

Alternate URLs: https://bio.tools/t-rex

Record Creation Time: 20220129T080224+0000

Record Last Update: 20250412T054912+0000

Ratings and Alerts

No rating or validation information has been found for Tree and reticulogram REConstruction.

No alerts have been found for Tree and reticulogram REConstruction.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

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

Sussmilch FC, et al. (2024) Gaining or cutting SLAC: the evolution of plant guard cell signalling pathways. The New phytologist, 244(6), 2295.

Nath BK, et al. (2023) Lesions and viral loads in racing pigeons naturally coinfected with pigeon circovirus and columbid alphaherpesvirus 1 in Australia. Journal of veterinary diagnostic investigation : official publication of the American Association of Veterinary Laboratory Diagnosticians, Inc, 35(3), 278.

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

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

Lamm MS, et al. (2022) Characterization and distribution of kisspeptins, kisspeptin receptors, GnIH, and GnRH1 in the brain of the protogynous bluehead wrasse (Thalassoma bifasciatum). Journal of chemical neuroanatomy, 121, 102087.

Papadopoulos AO, et al. (2021) Characterisation of a putative M23-domain containing protein in Mycobacterium tuberculosis. PloS one, 16(11), e0259181.

LaLone CA, et al. (2021) International Consortium to Advance Cross-Species Extrapolation of the Effects of Chemicals in Regulatory Toxicology. Environmental toxicology and chemistry, 40(12), 3226.

Hassan MM, et al. (2020) NeoCoV Is Closer to MERS-CoV than SARS-CoV. Infectious diseases, 13, 1178633720930711.

Ara KZG, et al. (2020) Characterization and diversity of the complete set of GH family 3 enzymes from Rhodothermus marinus DSM 4253. Scientific reports, 10(1), 1329.

Mena EL, et al. (2020) Structural basis for dimerization quality control. Nature, 586(7829), 452.

Todisco V, et al. (2020) Next generation sequencing-aided comprehensive geographic coverage sheds light on the status of rare and extinct populations of Aporia butterflies (Lepidoptera: Pieridae). Scientific reports, 10(1), 13970.

Gabriško M, et al. (2020) The in silico characterization of neutral alpha-glucosidase C (GANC) and its evolution from GANAB. Gene, 726, 144192.

Månberger A, et al. (2020) Taxogenomic assessment and genomic characterisation of Weissella cibaria strain 92 able to metabolise oligosaccharides derived from dietary fibres. Scientific reports, 10(1), 5853.

Sloutsky R, et al. (2019) ASPEN, a methodology for reconstructing protein evolution with improved accuracy using ensemble models. eLife, 8.

Johnson-Mackinnon JC, et al. (2019) Multilocus Sequence Typing (MLST) and Random Polymorphic DNA (RAPD) Comparisons of Geographic Isolates of Neoparamoeba perurans, the Causative Agent of Amoebic Gill Disease. Pathogens (Basel, Switzerland), 8(4).

Kumar R, et al. (2019) Intrinsic dynamic behavior of enzyme:substrate complexes govern the catalytic action of ?-galactosidases across clan GH-A. Scientific reports, 9(1), 10346.

Gmiter D, et al. (2019) Draft Genome Sequences of Proteus mirabilis K1609 and K670: A Model Strains for Territoriality Examination. Current microbiology, 76(2), 144.

Pers D, et al. (2018) Ankyrin domain encoding genes from an ancient horizontal transfer are functionally integrated into Nasonia developmental gene regulatory networks. Genome biology, 19(1), 148.

de Farias ST, et al. (2017) Origin and Evolution of RNA-Dependent RNA Polymerase. Frontiers in genetics, 8, 125.