Resource Summary Report

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diARK- a resource for eukaryotic genome resources

RRID:SCR_006900
Type: Tool

Proper Citation

diARK- a resource for eukaryotic genome resources (RRID:SCR_006900)

Resource Information

URL: http://www.diark.org/diark

Proper Citation: diARK- a resource for eukaryotic genome resources (RRID:SCR_006900)

Description: diArk provides access to eukaryotic sequencing projects that have resulted in genome assemblies or cDNA/EST datasets. It gives users a comprehensive search module, as well as detailed options and three different views of the selected data. We have done our best to include all eukaryotic sequencing projects in the world that provide assembled genomic data or a considerable amount of cDNA/EST data.

Synonyms: diArk

Resource Type: data or information resource, database

Keywords: est, eukaryote, eukaryote genome, eukaryotic genome, cdna

Funding:

Resource Name: diARK- a resource for eukaryotic genome resources

Resource ID: SCR_006900

Alternate IDs: nif-0000-02749

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250426T055907+0000

Ratings and Alerts

No rating or validation information has been found for diARK- a resource for eukaryotic genome resources.

No alerts have been found for diARK- a resource for eukaryotic genome resources.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Galperin MY, et al. (2015) The 2015 Nucleic Acids Research Database Issue and molecular biology database collection. Nucleic acids research, 43(Database issue), D1.

Ebersberger I, et al. (2014) The evolution of the ribosome biogenesis pathway from a yeast perspective. Nucleic acids research, 42(3), 1509.

Hatje K, et al. (2012) A phylogenetic analysis of the brassicales clade based on an alignment-free sequence comparison method. Frontiers in plant science, 3, 192.

Hammesfahr B, et al. (2011) diArk 2.0 provides detailed analyses of the ever increasing eukaryotic genome sequencing data. BMC research notes, 4, 338.