Resource Summary Report

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Plant Co-expression Annotation Resource

RRID:SCR_018429
Type: Tool

Proper Citation

Plant Co-expression Annotation Resource (RRID:SCR_018429)

Resource Information

URL: https://www.machado.cnptia.embrapa.br/plantannot

Proper Citation: Plant Co-expression Annotation Resource (RRID:SCR_018429)

Description: Webserver for identifying targets for genetically modified crop breeding pipelines. Used to find proteins that have no annotation or function assigned and could be related to molecular mechanisms regarding abiotic stresses in plants. System aggregates orthology, coexpression networks and genomic data to filter genomes of plants downloaded from Phytozome and NCBI and select candidate proteins in that regard.

Abbreviations: Plantannot

Synonyms: Plantannot v2

Resource Type: data access protocol, service resource, data or information resource, web service, software resource

Defining Citation: DOI:10.1101/2020.05.22.110510

Keywords: Omics, plant, annotation, function, breeding, genetically modified crops, abiotic stress in plant, plant genome, plant genomic data, bio.tools

Funding: Embrapa

Availability: Free, Freely available

Resource Name: Plant Co-expression Annotation Resource

Resource ID: SCR_018429

Alternate IDs: biotools:plantannot

Alternate URLs: https://www.machado.cnptia.embrapa.br/plantannot2, https://bio.tools/plantannot

License: GNU GPL

Record Creation Time: 20220129T080340+0000

Record Last Update: 20250519T204033+0000

Ratings and Alerts

No rating or validation information has been found for Plant Co-expression Annotation Resource.

No alerts have been found for Plant Co-expression Annotation Resource.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

José Andrade Viana M, et al. (2021) Plant Co-expression Annotation Resource: a web server for identifying targets for genetically modified crop breeding pipelines. BMC bioinformatics, 22(1), 46.