Resource Summary Report

Generated by NIF on May 19, 2025

Phenotree

RRID:SCR_003591
Type: Tool

Proper Citation

Phenotree (RRID:SCR_003591)

Resource Information

URL: http://bejerano.stanford.edu/phenotree/

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Description: Web server to search for genes involved in given phenotypic difference between mammalian species. The mouse-referenced multiple alignment data files used to perform the forward genomics screen is also available. The webserver implements one strategy of a Forward Genomics approach aiming at matching phenotype to genotype. Forward genomics matches a given pattern of phenotypic differences between species to genomic differences using a genome-wide screen. In the implementation, the divergence of the coding region of genes in mammals is measured. Given an ancestral phenotypic trait that is lost in independent mammalian lineages, it is shown that searching for genes that are more diverged in all trait-loss species can discover genes that are involved in the given phenotype.

Abbreviations: Phenotree

Synonyms: Forward Genomics - Phenotree server, Forward Genomics - Phenotree search

Resource Type: data set, data or information resource, service resource

Defining Citation: PMID:23022484

Keywords: gene, genotype, phenotype, alignment, trait, genome, alignment

Funding:

Availability: Acknowledgement requested, Non-commercial, Free for personal use, Http://stanford.edu/site/terms.html

Resource Name: Phenotree

Resource ID: SCR_003591

Alternate IDs: nlx_157736

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250519T203257+0000

Ratings and Alerts

No rating or validation information has been found for Phenotree.

No alerts have been found for Phenotree.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.