Resource Summary Report

Generated by dkNET on Apr 16, 2025

EGO - Eukaryotic Gene Orthologs

RRID:SCR_000732
Type: Tool

Proper Citation

EGO - Eukaryotic Gene Orthologs (RRID:SCR_000732)

Resource Information

URL: http://compbio.dfci.harvard.edu/tgi/ego/

Proper Citation: EGO - Eukaryotic Gene Orthologs (RRID:SCR_000732)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. EGO is a database of eukaryotic gene orthologs generated by pair-wise comparison between the Tentative Consensus (TC) sequences that comprise the Dana Farber Gene Indices from individual organisms.

Synonyms: EGO

Resource Type: database, data or information resource

Keywords: eukaryotic gene ortholog, dana farber gene indices, tentative consensus sequence

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: EGO - Eukaryotic Gene Orthologs

Resource ID: SCR_000732

Alternate IDs: nif-0000-02790

Record Creation Time: 20220129T080203+0000

Record Last Update: 20250412T054606+0000

Ratings and Alerts

No rating or validation information has been found for EGO - Eukaryotic Gene Orthologs.

No alerts have been found for EGO - Eukaryotic Gene Orthologs.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Hu P, et al. (2012) Microarray meta-analysis identifies acute lung injury biomarkers in donor lungs that predict development of primary graft failure in recipients. PloS one, 7(10), e45506.

Page GP, et al. (2008) Bioinformatic tools for inferring functional information from plant microarray data: tools for the first steps. International journal of plant genomics, 2008, 147563.