Resource Summary Report

Generated by NIF on Apr 23, 2025

EC2KEGG

RRID:SCR_012127
Type: Tool

Proper Citation

EC2KEGG (RRID:SCR_012127)

Resource Information

URL: http://sourceforge.net/projects/ec2kegg/

Proper Citation: EC2KEGG (RRID:SCR_012127)

Description: A perl-based package to perform comparative analysis of metabolic pathways between two organisms.

Resource Type: software resource

Defining Citation: PMID:25202338

Keywords: standalone software, perl

Funding:

Resource Name: EC2KEGG

Resource ID: SCR_012127

Alternate IDs: OMICS_05782

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250420T014607+0000

Ratings and Alerts

No rating or validation information has been found for EC2KEGG.

No alerts have been found for EC2KEGG.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Bargiela R, et al. (2023) Evolutionary patterns of archaea predominant in acidic environment. Environmental microbiome, 18(1), 61.

Saha J, et al. (2020) Identification and characterization of differentially expressed genes in the rice root following exogenous application of spermidine during salt stress. Genomics, 112(6), 4125.

Baloni P, et al. (2019) Genome-scale metabolic model of the rat liver predicts effects of diet restriction. Scientific reports, 9(1), 9807.

Sparks ME, et al. (2018) Draft genome sequence of the New Jersey aster yellows strain of 'Candidatus Phytoplasma asteris'. PloS one, 13(2), e0192379.

Bisaga M, et al. (2017) Deep Sequencing of Suppression Subtractive Hybridisation Drought and Recovery Libraries of the Non-model Crop Trifolium repens L. Frontiers in plant science, 8, 213.

Leung E, et al. (2016) Protein Sequence Annotation Tool (PSAT): a centralized web-based meta-server for high-throughput sequence annotations. BMC bioinformatics, 17, 43.

Porollo A, et al. (2014) EC2KEGG: a command line tool for comparison of metabolic pathways. Source code for biology and medicine, 9, 19.

Porollo A, et al. (2014) Comparative genomics of pneumocystis species suggests the absence of genes for myo-inositol synthesis and reliance on inositol transport and metabolism. mBio, 5(6), e01834.