

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

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

Resource Name: EC2KEGG

Resource ID: SCR_012127

Alternate IDs: OMICS_05782

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260905T132721+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 [PRECISE-TBI](#) .

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.