Resource Summary Report

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ProOpDB

RRID:SCR_006111
Type: Tool

Proper Citation

ProOpDB (RRID:SCR_006111)

Resource Information

URL: http://operons.ibt.unam.mx/OperonPredictor/

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Description: The Prokaryotic Operon DataBase (ProOpDB) constitutes one of the most precise and complete repository of operon predictions in our days. Using our novel and highly accurate operon algorithm, we have predicted the operon structures of more than 1,200 prokaryotic genomes. ProOpDB offers diverse alternatives by which a set of operon predictions can be retrieved including: i) organism name, ii) metabolic pathways, as defined by the KEGG database, iii) gene orthology, as defined by the COG database, iv) conserved protein motifs, as defined by the Pfam database, v) reference gene, vi) reference operon, among others. In order to limit the operon output to non-redundant organisms, ProOpDB offers an efficient protocol to select the more representative organisms based on a precompiled phylogenetic distances matrix. In addition, the ProOpDB operon predictions are used directly as the input data of our Gene Context Tool (GeConT) to visualize their genomic context and retrieve the sequence of their corresponding 5?? regulatory regions, as well as the nucleotide or amino acid sequences of their genes. The prediction algorithm The algorithm is a multilayer perceptron neural network (MLP) classifier, that used as input the intergenic distances of contiguous genes and the functional relationship scores of the STRING database between the different groups of orthologous proteins, as defined in the COG database. Nevertheless, the operon prediction of our method is not restricted to only those genes with a COG assignation, since we successfully defined new groups of orthologous genes and obtained, by extrapolation, a set of equivalent STRING-like scores based on conserved gene pairs on different genomes. Since the STRING functional relationships scores are determined in an un-bias manner and efficiently integrates a large amount of information coming from different sources and kind of evidences, the prediction made by our MLP are considerably less influenced by the bias imposed in the training procedure using one specific organism.

Abbreviations: ProOpDB

Synonyms: Prokaryotic Operon DataBase (ProOpDB), Prokaryotic Operon DataBase

Resource Type: database, data or information resource

Defining Citation: PMID:20385580

Keywords: genome, operon, gene pair, gene, operon prediction, metabolic pathway, gene orthology, conserved protein motif, protein motif, reference gene, reference operon, visualization, regulatory region, nucleotide, amino acid, sequence, phylogeny, FASEB list

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Resource Name: ProOpDB

Resource ID: SCR_006111

Alternate IDs: nlx_151585

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250412T055025+0000

Ratings and Alerts

No rating or validation information has been found for ProOpDB.

No alerts have been found for ProOpDB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 35 mentions in open access literature.

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

Gupta N, et al. (2022) A comprehensive approach to discover Toxin-Antitoxin systems from human pathogen Helicobacter pylori: A poison and its antidote encapsulated in the genome. Life sciences, 288, 120149.

Pipatthana M, et al. (2021) The repertoire of ABC proteins in Clostridioides difficile. Computational and structural biotechnology journal, 19, 2905.

Assaf R, et al. (2021) Detecting operons in bacterial genomes via visual representation learning. Scientific reports, 11(1), 2124.

Guyet U, et al. (2020) Synergic Effects of Temperature and Irradiance on the Physiology of the Marine Synechococcus Strain WH7803. Frontiers in microbiology, 11, 1707.

Xie R, et al. (2020) Integrated Co-functional Network Analysis on the Resistance and Virulence Features in Acinetobacter baumannii. Frontiers in microbiology, 11, 598380.

Shell Cox J, et al. (2020) General and Genomic DNA-Binding Specificity for the Thermus thermophilus HB8 Transcription Factor TTHB023. Biomolecules, 10(1).

Yuan C, et al. (2019) Myo-inositol utilization by Citrobacter koseri promotes brain infection. Biochemical and biophysical research communications, 517(3), 427.

Alkhalili RN, et al. (2019) Towards Exploring Toxin-Antitoxin Systems in Geobacillus: A Screen for Type II Toxin-Antitoxin System Families in a Thermophilic Genus. International journal of molecular sciences, 20(23).

Cox JS, et al. (2019) Identification and Characterization of Preferred DNA-Binding Sites for the Thermus thermophilus HB8 Transcriptional Regulator TTHA0973. International journal of molecular sciences, 20(13).

Méheust R, et al. (2018) Formation of chimeric genes with essential functions at the origin of eukaryotes. BMC biology, 16(1), 30.

He J, et al. (2018) Functional Characterization of c-di-GMP Signaling-Related Genes in the Probiotic Lactobacillus acidophilus. Frontiers in microbiology, 9, 1935.

Kandari D, et al. (2018) Identification, Functional Characterization, and Regulon Prediction of the Zinc Uptake Regulator (zur) of Bacillus anthracis - An Insight Into the Zinc Homeostasis of the Pathogen. Frontiers in microbiology, 9, 3314.

Yu Y, et al. (2018) Infection and adaption-based proteomic changes of Streptococcus suis serotype 2 in a pig model. Journal of proteomics, 180, 41.

Ooka H, et al. (2018) Design Strategy of Multi-electron Transfer Catalysts Based on a Bioinformatic Analysis of Oxygen Evolution and Reduction Enzymes. Molecular informatics, 37(8), e1700139.

Chowdhury-Paul S, et al. (2018) Proteomic analysis revealed proteins induced upon Azotobacter vinelandii encystment. Journal of proteomics, 181, 47.

Goyal A, et al. (2018) Metabolic adaptations underlying genome flexibility in prokaryotes. PLoS genetics, 14(10), e1007763.

Virtanen JP, et al. (2018) Changes in Transcriptome of Yersinia pseudotuberculosis IP32953 Grown at 3 and 28°C Detected by RNA Sequencing Shed Light on Cold Adaptation. Frontiers in cellular and infection microbiology, 8, 416.

Clerissi C, et al. (2018) Parallels between experimental and natural evolution of legume symbionts. Nature communications, 9(1), 2264.

Pannier L, et al. (2017) Effect of genomic distance on coexpression of coregulated genes in E. coli. PloS one, 12(4), e0174887.

Ahlstrand T, et al. (2017) A novel intrinsically disordered outer membrane lipoprotein of Aggregatibacter actinomycetemcomitans binds various cytokines and plays a role in biofilm response to interleukin-1? and interleukin-8. Virulence, 8(2), 115.