

☞ This is Standalone CD which gives you the complete functional genomic and metabolic pathway information about *E.coli*.

☞ Live boot up CD, independent of computer OS.

☞ Developed by

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# BIOINFORMATICS LAB AU-KBC RESEARCH CENTRE

KNOWLEDGE SOURCE FOR *E-Coli* BIOINFORMATICS

ECOMP

*E.coli* Metabolic Pathway Information

RECDB

Re annotated *E.coli* Database

Project sponsored by DIT, New Delhi

#### Contact

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## RecDB – A Re-annotated Escherichia coli Database

RecDB is a database that contains the completely annotated protein sequence information of the Escherichia coli K-12 substr MG 1655. RecDB database will remain a useful repository with accurate and updated functional information of E. coli K12 substr MG 1655 genome.

### Challenge

Escherichia coli, was one of the favorite model organisms, were initially annotated in 1997. Although, five decades of intense research is being carried out on E.coli genome, still complete and accurate functional information of this organism is not available. Finding relevant gene and protein information of E. coli is a challenging task in the post genomic era.

### Solution

RecDB is a collection of protein information of E. coli K-12 substr MG 1655 easily searchable, that organizes publicly available sequences with up-to-date information derived from expert curation of the scientific biological databases. The complete analysis of E.coli protein sequences were carried out using the advanced computational approaches and develop clues on their biological role. With this being the principal objective, the functional proteomic re-annotation of E.coli K12 substr MG 1655 was carried out. The annotated results were obtained from integration of different functional genomics tools.

Functional re-annotation of E. coli has been carried out using AIM-BLAST, a simple Ajax Interface to EBI BLAST that facilitates multiple sequence analysis at an instance. FGT-(Functional Genomics Tool), well-structured, flexible and a highly systematic functional analysis program were also used to carry out large-scale protein annotation of E coli. Different online functional genomics tools such as BLAST, ScanProsite, ProDom, COG and Pfam which are operating on the diverse computational approaches that have been integrated in FGT tool.

Re-annotation of E. coli helped in postulating featured functions to almost 29% of the protein sequences of which 977 protein functions have been newly predicted. For example, protein sequence ec1915 was previously given a function, reductase. But, re-annotation using the above integrated approach helped us updating this function as Oxidoreductase molybdopterin binding domain. The final list of complete re-annotation data of E. coli protein sequences can be viewed in REC-DB database.

### Features

- ☞ User Friendly
- ☞ Very less time consumable
- ☞ Having complete annotated information of Escherichia coli K-12 substr MG1655
- ☞ Having query search options
- ☞ Contains complete gene information such as gene i.d, gene name, functions, description.

## ECO-MP – Development of Genome-Scale Metabolic Pathway Database for Escherichia coli

ECO-MP is an Escherichia coli metabolic pathway database and it is useful for analysis of biosynthetic pathway of metabolic network. ECO-MP is designed to furnish reconstructed pathways from the inference of the biochemical reactions by association of reaction sets in E.coli by Network Expansion method to form a sub-network

### Challenge

The incomplete pathway information of E.coli is not sufficient for the complete understanding of this model bacterium. Hence, reconstruction of Genome-scale Metabolic Pathway is essential to understand cellular process in Escherichia coli K-12. The study on biochemical pathways in E.coli provides information on reaction catalogues to be modified to obtain maximum yield of industrial products such as hydrogen. ECO-MP, an E.coli metabolic pathway database is meant for analysis of biosynthetic pathway of metabolic network ECO-MP database is created to facilitate user to reconstruct metabolic pathway by various ways in E.coli by utilizing knowledge of subnetworks, alternative pathways and available pathways information represented in it.

### Solution

The ECO-MP database is a valuable resource for metabolic pathways and subnetworks which caters research community to analyze the in-depth knowledge of biological process. The subnetworks generated in ECO-MP by Network Expansion methods are able to give ideas on creating alternative pathways and filling holes, thus can help in finding alternate metabolic pathways involved in important biochemical process. This idea can be extended in altering metabolic pathways to enhance the production of industrial products by metabolic engineering.

From ECO-MP, the alternative path to D-gluconate which converts L-Idonate into 2,5-dihydrodeoxy gluconate is determined. It confirmed that data retrieved from ECO-MP can be used to identify minimal number of reactions that is to be added for further reconstruction work in E. coli. Similarly in Sphingolipid metabolism, 1-(1-Alkenyl)-sn-glycero-3-phosphoethanolamine which is not specified in the formation of Sphingosine which forms a primary part of sphingolipids, with an unsaturated hydrocarbon chain which has potential role in various cellular process.

The data from ECO-MP can also be used for metabolic hole filling. As an example diaminopropanoate is available as a reactant and produce pyruvate as an immediate product but not linked to any pathway in KEGG and this knowledge can be applied in filling metabolic holes.

ECO-MP is created to facilitate user to reconstruct metabolic pathway in E.coli with around 150 subnetworks of which 6 are multistep pathways, and 1050 available Pathways. The subnetworks from ECO-MP can be used to fill metabolic holes or create alternative path by means of Network Expansion method.

### Features

- ☞ User Friendly
- ☞ Having complete metabolic pathway information of Escherichia coli K-12.
- ☞ Facilitated with multiple query options such as GI number, protein sequence and Enzyme name.
- ☞ Contains complete pathway information such as KEGG pathway, KEGG reaction, subnetworks generated by
- ☞ Network Expansion method.