

Development of a Proteome Database from a Genome Sequence or ESTs for Protein Identification and in Silico Prediction

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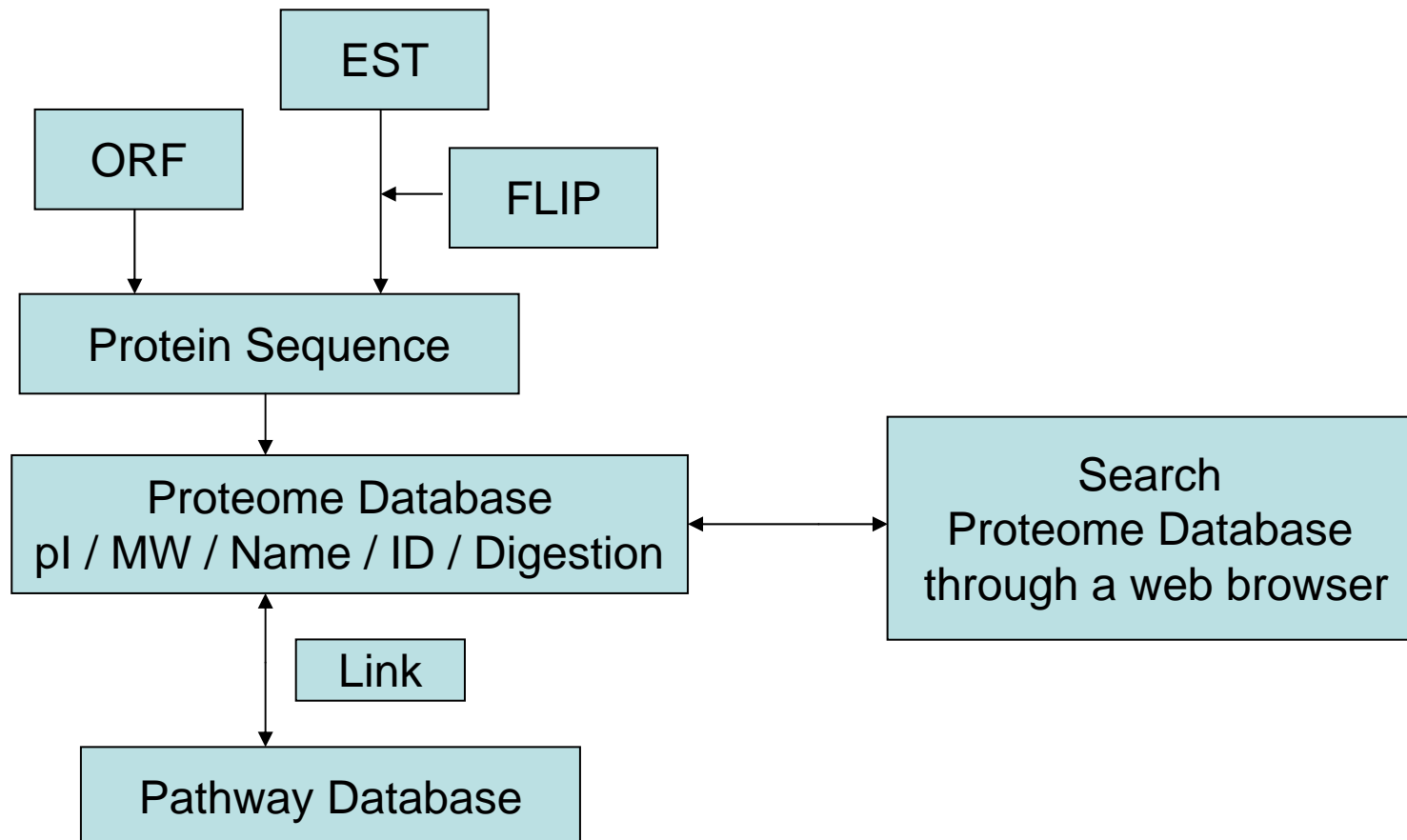


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Create Proteome Database





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Organism	Protein Name	EC	MW	pI	Locus tag	Gene id	Product	Reactions, Pathways
Lb. plantarum WCFS1	NP_784085.1	2.7.7.39	15800.223	7.65	lp_0267	tagD1	glycerol-3-phosphate cytidyltransferase	link
Lb. plantarum WCFS1	NP_784908.1	2.7.7.39	15465.886	7.06	lp_1248	tagD2	glycerol-3-phosphate cytidyltransferase	link



Link to Pathway Database

L. plantarum Gene: [tagD1](#)

[Nucleotide Sequence](#)[Nucleotide Sequence Neighborhood](#)[Protein Sequence](#)

Superclasses: [UNCLASSIFIED](#)

Map Position: [243,093 -> 243,497 \(nucleotides\)](#) [7,348 \(centisomes\)](#) [[click to view in chromosome browser](#)]

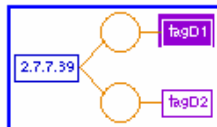
Products: [glycerol-3-phosphate cytidyltransferase](#)

Reactions Catalyzed by Enzymes:

[glycerol-3-phosphate + CTP = CDPglycerol + pyrophosphate](#)

Pathways Involving Enzymes: [glycerol teichoic acid biosynthesis](#)

Gene-Reaction Schematic: [?](#)



Gene Local Context (to scale): [?](#)