

# CLASSIFICATION NUMBER OF ORGANISMS USING CLUSTER ANALYSIS OF THE PEPTIDE CHAINS MULTIPLE CHYMOTRYPSIN LACTATE DEHYDROGENASE

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**ABSTRACT :** The current research aims to classify and to build a phylogenetic tree to 19 different organisms based on a series peptide multi-enzyme lactate dehydrogenase using the method of clustering analysis, one of the most important results of this research classify and distinguish organisms into six groups, each group including a number of different organisms are similar in among them. The idea behind of this research paper are building phylogeny tree of chymotrypsin from different species like (turtle, ostrich, dove, bee, koala, walrus, dolphins, whale, camel, monkey, mouse, squirrel, tiger, chicken) then comparing between the groups to get optimal score for which one of the observations or objects in every cluster square measure similar and therefore, the clusters square measure dissimilar to every alternative a result similar to multi chain peptide enzyme lactate dehydrogenase and organism differ in one group from the other groups.

**Key words :** Lactate dehydrogenase, phylogenetic, clustering analysis, NCBI.

## INTRODUCTION

Chymotrypsin and trypsin are serine proteases with similarities in structure and sequence; in the other hand they are different in substrate specificity. And the previous experiments shows us the important role for the two loops that binding outside the pocket however its dominate the 2 enzymes specificity (Wenzhe Ma, 2005).

Chymotrypsin is aromatic residues shape like tyrosine, tryptophan and phenylalanine. When replacing two loops of trypsin L1 and L2 with loops of chymotrypsin and also replaced with mutation D189S, the activity of chymotrypsin increased in new protein around more than 1000- fold against mutant D189S (Chao Tang, 2005).

Chymotrypsin is an enzyme known as protein-digesting the pancreas secreted this enzyme. Play an important role by monitoring patients or people who suffering with pancreatic problem or dysfunction of pancreas. The pancreas is responsible to synthesized of chymotrypsin this process start from biosynthesis protein like a precursor known as chymotrypsinogen that is ambiguously inactive. The two enzymes (chymotrypsin and Trypsin) have high identity in their sequence and also they have high similarity in their tertiary structures (Fig.

1).

The goals behind this research are:

- Building phylogeny tree of chymotrypsin from different groups.
- Comparing between the groups to get optimal score for which one of the observations or objects in each cluster are similar.

## MATERIALS AND METHODS

### Sequences retrieval

The 30 full length amino acid sequences of chymotrypsin was collected (download) from Genebank databases (NCBI). <http://www.ncbi.nlm.nih.gov>

The thirty species are (cattle, buffalo, walrus, dolphins, whale, camel, monkey, mouse, squirrel, tiger, chicken, wolf, zebra, sheep, beetle, cockroach, falcon, mosquito, horse, parrot, turtle, ostrich, dove, bee, koala, octopus, spider, carb, goose and frog).

### Bioinformatics tools and programming

The first step in this research, by using three of different software's and their packages :

1. Multi sequence alignment of individual profiles was