



**HAL**  
open science

**The ESTHER Database (ESTerases and  
alpha/beta-Hydrolase Enzymes and Relatives) is  
dedicated to the analysis of proteins belonging to the  
superfamily of alpha/beta-hydrolases**

Arnaud Chatonnet

► **To cite this version:**

Arnaud Chatonnet. The ESTHER Database (ESTerases and alpha/beta-Hydrolase Enzymes and Relatives) is dedicated to the analysis of proteins belonging to the superfamily of alpha/beta-hydrolases. Protein Bioinformatics Community Resources Retreat / Wellcome Trust Conference Center, Aug 2014, Cambridge, United Kingdom. hal-01837604

**HAL Id: hal-01837604**

**<https://hal.science/hal-01837604>**

Submitted on 5 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

The ESTHER Database (ESTerases and alpha/beta-Hydrolase Enzymes and Relatives) is dedicated to the analysis of proteins belonging to the superfamily of alpha/beta-hydrolases ([bioweb.supagro.inra.fr/esther/](http://bioweb.supagro.inra.fr/esther/))

Alpha/beta hydrolases constitute one of the largest and most diverse protein superfamily, with so far more than 800 000 sequences (of which 42000 non-redundant) grouped in 175 subfamilies (Lenfant et al. 2013). They play fundamental roles in virtually all physiological processes and are targeted by drugs aimed at treating diseases such as diabetes, obesity, and neurodegenerative disorders (24 genes have been found mutated in 22 genetic diseases). Yet, for most of the 120+ predicted mammalian alpha/beta hydrolases we lack biological understanding. Also, despite what their generic name would suggest, many of these proteins are not enzymes (some have lost all residues necessary to constitute an active site) (Marchot and Chatonnet 2012). The functions of few representatives of this latest group are known: intracellular receptors of small molecules, endo cellular membrane trafficking agents, inter-actors with partners at cell-cell interface, hormone precursors. The database was launched in 1994 as a Gopher server and quickly moved to WWW. The underlying system of the database is the venerable ACeDB system. AceDB is a genome database system developed since 1989 primarily by Jean Thierry-Mieg (CNRS, Montpellier) and Richard Durbin (Sanger Institute) originally developed for the *C.elegans* genome project and is still the kernel of the wormbase database and server.

One of the advantages of the system is that the structure of the database (models of relationship between objects) can be retrieved as simple text. All the data can be retrieved as text or xml files. The initial interface to the web is based on CGI scripts AcePerl developed by Lincoln Stein. As a database engine ACeDB compares favorably with Mysql or even commercial database systems. Complex queries can be easily built. Many are used to generate on the fly the different chapters of the server but many examples are also given which can be customized by users. Examples of dedicated searches have been published for example to analyse the mutations of cholinesterases or carboxylesterases responsible for insecticide resistance