



**Enzyme Handbook: Volume 15: First Supplement
Part 1 Class 3: Hydrolases (Enzyme Handbook
(See S794))**

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Today, as the large international genome sequence projects are gaining a great amount of public attention and huge sequence data bases are created it becomes more and more obvious that we are very limited in our ability to access functional data for the gene products - the proteins, in particular for enzymes. Those data are inherently very difficult to collect, interpret and standardize as they are highly distributed among journals from different fields and are often subject to experimental conditions. Nevertheless a systematic collection is essential for our interpretation of the genome information and more so for possible applications of this knowledge in the fields of medicine, agriculture, etc .. Recent progress on enzyme immobilization, enzyme production, enzyme inhibition, coenzyme regeneration and enzyme engineering has opened up fascinating new fields for the potential application of enzymes in a large range of different areas. It is the functional profile of an enzyme that enables a biologist or physician to analyse a metabolic pathway and its disturbance; it is the substrate specificity of an enzyme which tells an analytical biochemist how to design an assay; it is the stability, specificity and efficiency of an enzyme which determines its usefulness in the biotechnical transformation of a molecule. And the sum of all these data will have to be considered when the designer of artificial biocatalysts has to choose the optimum prototype to start with.

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