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A Critical Study on Enzyme

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Abstract: Enzymes are core elements of biosynthetic pathways employed in the synthesis of numerous bioproducts. Here, we review enzyme promiscuity, enzyme engineering, enzyme immobilization, and cell-free systems as fundamental strategies of bioprocess development. Initially, promiscuous enzymes are the first candidates in the quest for new activities to power new, artificial, or bypass pathways that expand substrate range and catalyze the production of new products. If the activity or regulation of available enzymes is unsuitable for a process, protein engineering can be applied to improve them to the required level. When cell toxicity and low productivity cannot be engineered away, cell-free systems are an attractive option, especially in combination with enzyme immobilization that allows extended enzyme use. Overall, the above methods support powerful platforms for bioprocess development and optimization.

Key Words: Enzyme, synthesis, catalyze, elements

Enzymes are capable of performing highly selective and efficient chemical transformations under aqueous and mild conditions. Their ability to act on complex, unprotected substrates often with high chemo-and stereoselectivity renders them attractive tools for a wide range of applications, including industrial biocatalysis and diagnostic analyte detection. However, the broader implementation of enzymes in non-native and process-relevant environments is often hindered by their limited stability.

Their ability to act on complex, unprotected substrates often with high chemo-and stereoselectivity renders them attractive tools for a wide range of applications, including industrial biocatalysis and diagnostic analyte detection [1][2][3][4]. However, the broader implementation of enzymes in non-native and process-relevant environments is often hindered by their limited stability. Enzymatic instability can manifest at multiple structural levels (i.e., secondary, tertiary and quaternary) posing significant challenges, particularly for enzymes that show a tendency for aggregation or function as complexes.

In the late nineteenth century and early twentieth century, significant advances were made in the extraction, characterization and commercial exploitation of many enzymes, but it was not until the 1920s that enzymes were crystallized, revealing that catalytic activity is associated with protein molecules. For the next 60 years or so it was believed that all enzymes were proteins, but in the 1980s it was found that some ribonucleic acid (RNA) molecules are also able to exert catalytic effects. These RNAS, which are called ribozymes, play an important role in gene expression. In the same decade, biochemists also developed the technology to generate antibodies that possess catalytic properties.

As well as being highly potent catalysts, enzymes also possess remarkable specificity

in that they generally catalyse the conversion of only one type (or at most a range of similar types) of substrate molecule into product molecules. Some enzymes demonstrate group specificity. For example, alkaline phosphatase (an enzyme that is commonly encountered in first-year laboratory sessions on enzyme kinetics) can remove a phosphate group from a variety of substrates.

The enormous catalytic activity of enzymes can perhaps best be expressed by a constant, kcat that is variously referred to as the turnover rate, turnover frequency or turnover number. This constant represents the number of substrate molecules that can be converted to product by a single enzyme molecule per unit time (usually per minute or per second). Examples of turnover rate values are listed in Table 1. For example, a single molecule of carbonic anhydrase can catalyse the conversion of over half a million molecules of its substrates, carbon dioxide (CO2) and water (H2O), into the product, bicarbonate (HCO3), every second a truly remarkable achievement.

Table 1. Turnover rate of some common enzymes showing wide variation.

Enzyme	Turnover rate (mole product s^{-1} mole $enzyme^{-1}$)
Carbonic anhydrase	600 000
Catalase	93 000
β–galactosidase	200
Chymotrypsin	100
Tyrosinase	1

Enzymes are specific catalysts

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Enzyme names and classification

Enzymes typically have common names (often called ‘trivial names’) which refer to the reaction that they catalyse, with the suffix -ase (e.g. oxidase, dehydrogenase, carboxylase), although individual proteolytic enzymes generally have the suffix -in (e.g. trypsin, chymotrypsin, papain). Often the trivial name also indicates the substrate on which the enzyme acts (e.g. glucose oxidase, alcohol dehydrogenase, pyruvate decarboxylase). However, some trivial names (e.g. invertase, diastase and catalase) provide little information about the substrate, the product or the reaction involved.

For the sake of conciseness, this guide has been limited to some of the basic principles of enzymology, together with an overview of the biotechnological applications of enzymes. It is important to understand the relationship between proteins and the nucleic acids (DNA and RNA) that provide the blueprint for the assembly of proteins within the cell. Genetic engineering is thus predominantly concerned with modifying the proteins that a cell contains, and genetic defects (in medicine) generally relate to the abnormalities that occur in the proteins within cells. Much of the molecular age of biochemistry is therefore very much focused on the study of the cell, its enzymes and other proteins, and their functions.

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