African Journal of
Biochemistry and Molecular Biology Research

ISSN : 3434-6120

Index: Harvard, Boston, Sydney University, Dimensions, Lens, ResearchGet Scilit, Semantic, Google Scholar, Base etc

https://doi.org/10.58578/AJBMBR.v2i2.5268

Exploring the Dynamics of Enzyme Activity: Environmental and Biological Influences

Muhammad Akram[1], Urooj Rehman[2], Misbah Ahmed[3], Isaac John Umaru[4]
[1]Government College University Faisalabad-Pakistan; [2]Jinnah University for Women, Karachi, Pakistan; [3]Clinical Science Division Hamdard Laboratories Waqf, Pakistan; [4]Federal University Wukari, Taraba State, Nigeria
makram_0451@yahoo.com

Article Info:

Submitted:	Revised:	Accepted:	Published:
Feb 25, 2025	Mar 10, 2025	Mar 22, 2025	Mar 27, 2025

Abstract

The work presents the classification of enzymes and factors that are affecting enzymatic reactions in the living systems. Factors such as temperature, pH, enzyme concentration, substrate concentration, factors of inhibition, factors of activation, and incubation time are important in influencing enzyme reactions, which are responsible for controlling components in living systems. The majority of enzymes are three-dimensional molecules with complex molecular networks and sensitive to various environmental factors.

Keywords: Enzyme reactions, Factors, Biological systems, Classifications, Inhibitors

Introduction

Substances that, when added to an enzyme, change its structure and render it unsuitable for accepting a substrate (Benkovic S et al. 2003). Because of their anti-competitive inhibition, which typically occurs in biological reactions involving two or more substrates or products, these substances are known as uncompetitive inhibitors. Twenty-five percent of the known enzymes show substrate inhibition, according to Michaelis-Menten kinetics. When two or more substrate molecules bind to the enzyme's active site at the same time, an unidentified enzyme-substrate complex is formed. The "primary structure" of an enzyme is composed of a linear chain of amino acids joined by amide bonds. The polypeptide chain is the name given to the chain of amino acids in the fundamental structure. The sequence of an encoded gene's DNA determines the precise arrangement of amino acids. In the enzymatic secondary structure, each amino acid's carboxyl group-containing oxygen and amino group-containing hydrogen are surrounded by a hydrogen bond, indicating that the amino acids in each chain are connected to one another. The chain of routine in protein structure can fold in two different ways, forming secondary structures when it folds on itself. Alpha-helix and beta-helix are the two possible folding patterns for the chain. Enzymes with a three-dimensional structure are said to have a "tertiary structure." According to Murphy JM et al. (2014), the majority of enzymes have a distinct three-dimensional structure that contributes to their selectivity in response.

As both oxidases and reductases, oxidoreductases catalyze a range of oxidation-reduction reactions. This group is commonly referred to as catalase, reductase, and oxidase. Transferases move certain groups from one substrate to another. Acetyltransferase, polymerase, protein kinase, and methylase are common names for this class of enzymes. When water is introduced, a molecule hydrolyzes, breaking up into little pieces. Hydrolases help with this process. For example, protease breaks down protein molecules, while nuclease breaks down nucleic acids. Lyases Cleaving the carbon-carbon, carbon-sulfur, carbon-nitrogen, and carbon-oxygen bonds from a substrate can produce a double bond reaction by removing a group or inducing its opposite process. Aldolase and decarboxylase are members. By assisting in the conversion of optical, isomeric, and geometric isomers, isomerases catalyze the atomic rearrangement within molecules. Examples include Rotamase, Apimase, and Recimase. Ligases: When two molecules unite to form a single entity, they release energy. Examples include RNA ligase, DNA ligase, and peptide

synthase. High molecular weight molecules, such as those with molecular weights between 10,000 and 2,000,000, are found in enzymes.

Their main constituents are chains of amino acids joined by peptides. Next, add an instructive image or picture, for example. Factors Influencing Animal Enzyme Activity The following elements influence how quickly an enzyme reaction occurs: The temperature, the pH, The concentration of the enzyme, The concentration of the substrate, contributing factors, preventing factor. Reaction rate rises as temperature rises, much like the majority of chemical processes in the system. The reaction rate also increases by 50–100% as the temperature rises by 10 degrees. The reaction can fluctuate more when the temperature changes. A temperature difference of one to two degrees causes a ten to twenty percent shift in the pace of response. Temperature increases have a negative impact on several enzymes. Even at mild temperatures, enzymes gradually lose their ability to function. The ideal temperature range for storing enzymes is 5°C or lower. On a freezing, some enzymes lose their activity (Schomburg,et al.,2013). An enzyme's activity will alter when its pH changes. An enzyme becomes more active at a pH that is more conducive to its activity; this is known as the optimal pH. By pursuing extremes, both high and low, certain enzymes completely lose their activity. The pH is also essential for preserving the stability of the enzymes. Additionally, it is required to stabilize the reaction. The pH varies from enzymeto enzyme within the living system (Callahan BP et al., 2007). The relation between the concentration of enzyme and the rate of reaction depends upon the existence of the substrate. The increment of enzymatic concentration must require the presence of substrate in large amounts, and then the reaction rate will speed up in the system. If the amount of substrate is low, then there will be no effect on the reaction rate by increasing the enzymatic concentration. The relation of enzyme concentration and rate demands surplus substrate availabilitymeans reaction should beautonomousof concentration of substrate. Such reactions are known as "zero-order" on the grounds that the rates are autonomous to a concentration of substrate and equivalent to constant K. The arrangement of items continues at a direct rate with time. The more expansion of substrate doesn't help to build more rates of reaction. Within zero-order kinetics, enabling the test to keep running for twofold time brings about twofold the product measurement (Vasella A et al., 2002). The measure of a compound present in a reaction is determined by the action it catalyzes. The relationship between activity and quantity is affected by various factors such as temperature, pH, etc. An enzyme assay must be planned with the goal that the

watched action is corresponding to the measure of chemical present altogether that the compound fixation is the main restricting variable. An enzyme assay must be designed to ensure that the observed activity is proportional to the amount of enzyme present, ensuring that the enzyme concentration is the only limiting factor. This means that the rate of the reaction remains constant and does not depend on the substrate concentration, allowing for accurate measurements of enzyme activity. Therefore, careful control of experimental conditions is essential to maintain this zero-order reaction status throughout the assay. This condition allows for a direct relationship between enzyme concentration and reaction rate, facilitating accurate quantification. Careful selection of substrate concentration and reaction conditions is crucial to maintain this zero-order kinetic regime.

Even while the body uses amylase, lipase, and protease as common synthetic chemicals to process food, other specialized proteins also play a role. The cells lining the processing tracts produce artificial mixtures known as lactase, sucrase, and maltase, which are each designed to convert a particular type of sugar into glucose. Furthermore, your stomach's amazing cells emit two different stimuli: gelatinase and renin. Renin breaks down the proteins in milk into smaller molecules known as peptides, which pepsin then completely prepares. When absorption is completed by pepsin, trypsin, and chymotrypsin, which transport amino acids, gelatinase breaks down collagen and gelatin, two enormous proteins found in meat, into smaller estimated fragments (Aughey GN, et al., 2015).

Substrate Concentration

The substrate concentration in enzymatic reactions has been revealed by the experiment related to maintaining the quantity of enzyme constant and increasing the amount of substrate. The rate of reaction will be increased to the maximum level by increasing the amount of substrate that will have no reaction on the velocity of reaction. It is theoretically proven that when the velocity of the reaction becomes maximum, the enzymes available are converted into an enzyme-substrate complex. Substrate inhibition will occur when there is excessive substrate. When an additional amount of substrate reacted with a given reaction, the rate of reaction will be decreasing. It is thought to be due to the fact that ~~so~~ many substrates compete with each other to fit on the active site and block it and make it unavailable for other substrates. Due to its reaction rate slowing down until enzymes present are not being used (Boyer *et al.*, 2002). In addition to temperature, pH, enzyme

concentration, and substrate concentration, some other factors that also affect the activity of enzymes are ionic strength and physical and chemical parameters. These factors can alter the enzyme's structure and function, ultimately impacting the overall rate of biochemical reactions. Understanding these variables is crucial for optimizing enzyme activity in various applications, from industrial processes to therapeutic interventions.

Inhibitors

An inhibitor is a material that modifies the catalyst or enzyme process and progressively slows down or, in certain situations, stops the reaction. There are three different kinds of inhibitors: uncompetitive, noncompetitive, and competitive. The majority of ideas showed that the enzyme-substrate complex is necessary for inhibition (WarshelA et al. 2006). Competitive inhibition is done when the substrate and substance resembling the substrate are both added to enzymes. The model of the inhibition process was first described in "the lock and key model" and was postulated by Emil Fischer in 1894. Lock and key theory gives the concept of an active site, that one portion or one side of the enzyme surface has a strong affinity for the substrate. The substrate is necessary for making the product and inducing conversion. According to the lock and key model, if an enzyme is considered as a base, then an active site is considered as a lock and substrate as a key. An inserted right key of substrate can open the lock for preceding the reaction. But if a wrong key of substrate is inserted, the lock will not open, and the reaction will not be preceded. In the case of a substrate-resembling substance, inhibitors will win and will be able to open the lock. If a dissimilar substance comes, that will not fit according to the site; the enzyme will reject that substance and will accept the enzyme for a continuing reaction based on the induced fit model that was suggested by Daniel Koshland in 1958 (Cox MM et al., 2013). Substances that, when added to an enzyme, change its structure and render it unsuitable for accepting a substrate (Benkovic S et al. 2003). Because of their anti-competitive inhibition, which typically occurs in biological reactions involving two or more substrates or products, these substances are known as uncompetitive inhibitors. Twenty-five percent of the known enzymes show substrate inhibition, according to Michaelis-Menten kinetics. When two or more substrate molecules bind to the enzyme's active site at the same time, an unidentified enzyme-substrate complex is formed.

Incubation Time

The longer the time consumed for the proceeding reaction, the more will be the formation of the product. Be that as it may, the pace of synthesis of products is definitely not a straightforward direct capacity of the hour of brooding. All proteins suffer denaturation, and henceforth loss of synergist movement, with time. A few compounds, particularly in incompletely purged arrangements, might be recognizably unsteady, losing a lot of action over the time of hatching (Villa al. 2000). In the event that the movement of the catalyst is with the end goal that a significant part of the substrate is spent during the brooding, at that point, regardless of whether the grouping of substrate added was incredible enough to guarantee immersion of the chemical toward the start of the test, it will end up lacking as the hatching continues, and the development of item will diminishes. Catalyst will catalyzedthe responses in a reaction which are reversible. At first, there is practically no item present, and along these lines the response continues just the forward way. In any case, as the response proceeds, ~~so~~ there is a critical aggregation of items, and there is a noteworthy pace of back response. Therefore, the pace of arrangement of item backs off as the brooding continues, and on the off chance that the hatching time is excessively long, at that point the deliberate movement of the compound is dishonestly low(^ *Polgár, L, 2005*). In certain examinations, particularly when exploring the substrate reliance of the pace of response, it is normal to make estimations of the arrangement of item at generally brief time interims (state at regular intervals) for the primary moment or something like that, at that point plot a chart of the measure of item framed against time, and decide the underlying pace of response by attracting the digression to the steepest piece of the rate bend. Notwithstanding, in short brooding periods there can be an extensive blunder of timing; one second is a critical mistake in a short hatching, yet immaterial when the brooding time is a few minutes. Hence, in short hatching periods just a limited quantity of item has been framed, and investigative mistakes are amplified when the measure of item is very little (*RamanathanA,et al., 2014*). Choosing a suitable hatching time relies upon a tradeoff between these different factors. As a general principle, the brooding ought to be long enough to allow a moderate measure of item to be shaped, and long enough that the mistake in timing is immaterial, however not all that long that there is recognizable leveling off of the bend. It should be certain that when you decide the pace of response, in mol of item framed/minute, the protein has been dynamic at a pretty much consistent rate all through your hatching.

Activators Effect

Some enzymes cannot catalyze optimally without additional inorganic metallic cations such as Mg^{2+}, Zn^{2+}, Mn^{2+}, Co^{2+}, Ca^{2+}, Na^{+}, Cu^{2+}, K^{+}, etc., but sparingly anions like chloride ions for amylase (Tsai CJ et al., 2009). These cations often play a crucial role in stabilizing the enzyme's structure or facilitating the binding of substrates, thereby enhancing catalytic efficiency. Understanding the specific requirements of each enzyme can lead to better applications in biotechnology and medicine.

Water

Without water, enzyme activity is drastically decreased, to the point that the enzymes in dried seeds are essentially inactive. Enzyme function requires adequate cellular hydration since water is often one of the reactants and serves as a medium for enzyme reactions.

Accumulation of End-Products

An accumulation of end products slows down enzymatic activity because they crowd the active sites of the enzymes and reduce the likelihood that substrate molecules will interact with them (Changeux JP, 2005).

Some Important Enzymes with Activity

Organs connected to the gastrointestinal tract break down nutrients used for sustenance into tiny particles that are used by organs, tissues, and body cells as a supply of energy and for a few metabolic processes. It takes hours to complete this beautiful process, which yields amino acids, glycerol, unsaturated fatty acids, and clear saccharides. The process is finished by churning nutrients into tiny particles, which is followed by explicit synthetic concoctions synthesis in various gastrum-linked region.

Amylase

Amylase is a gastric-associated enzyme that breaks down starch in food and separates it into smaller sugar iotas. There are two places in the system where the material is synthesized. First, when food is nibbled, amylase, which is produced by the oral glands, isolates starch and converts it to the sugar maltose, stimulating the stomach's mechanism.

Humans will experience a barely sweet taste when maltose is released just as insipid foods like rice or potatoes start to separate in the mouth. Another type of amylase, known as pancreatic amylase, is produced by cells in your pancreas and employs a process to reach the structure connected to your small stomach. A key player in the lytic reaction of starch is salivary amylase. After handling sugar, pancreatic amylase produces glucose, a small molecule that enters your bloodstream and travels throughout your body (Fisher Z, et al., 2005).

Protease

Amino acids and other structural elements of proteins are harmed by protease. The stomach secretes these substances; chymotrypsin, trypsin, and pepsin are the three essential proteases.

When stomach secretions convert pepsinogen, the special cells in the stomach produce an inactive material known as pepsin. Pepsin, on the other hand, breaks the peptide bonds that bind protein molecules together to produce little peptides. The pancreas produces chymotrypsin and trypsin, which are then emptied into the gastrointestinal system by the pancreatic duct. Once the food has been broken down and prepared, it enters the gastrointestinal tract (GIT), where trypsin and chymotrypsin complete the breakdown of proteins by converting them into necessary amino acids.

Lipase

Lipase is an impetus that chemically cuts the fats in humbler iotas known as fatty acids and glycerol. A modest amount of gastric lipase is produced by gastric cells. This protein expressly produces scatters fat in sustenance. The fundamental fountain of lipase in the GIT is the pancreas. In any case, the green-pigmented bile product from the liver moves through the biliary tract to intestinal territory and converts fats into little oil globules. Pancreatic lipase, furthermore called steapsin, follows up on these fat globules, changing them over into unsaturated fats and glycerol, which are pretty much nothing, imperceptible thick particles used by the whole within the system. Unsaturated fats and glycerol travel in blood and lymph vessels to land at all bits of the human body (Noree *et al.*, 2010).

Conclusion

The functioning and upkeep of the many parts of the biological system depend heavily on enzymes. Competitive, non-competitive, and uncompetitive inhibitors that result in unique products can be used to build complex processes. The majority of naturally occurring enzymes are involved in primary metabolism's digestive process, which creates secondary metabolites for biological processes.

References

MurpHy JM, Farhan H, Eyers PA (2017). "Bio-Zombie: the rise of pseudoenzymes in biology". BiochemSoc Trans. 45 (2): 537–544.

MurpHy JM, et al. (2014). "A robust methodology to subclassifypseudokinases based on their nucleotide-binding properties". Biochemical Journal. 457 (2): 323–334.

Schomburg I, Chang A, Placzek S, Söhngen C, Rother M, Lang M, Munaretto C, Ulas S, Stelzer M, Grote A, Scheer M, Schomburg D (January 2013). "BRENDA in 2013: integrated reactions, kinetic data, enzyme function data, improved disease classification: new options and contents in BRENDA". Nucleic Acids Research. 41

Callahan BP, Miller BG (December 2007). "OMP decarboxylase—An enigma persists". Bioorganic Chemistry. 35 (6): 465–9.

Vasella A, Davies GJ, Böhm M (October 2002). "Glycosidase mechanisms".Current Opinion in Chemical Biology. 6 (5): 619–29.

Boyer R (2002). "Chapter 6: Enzymes I, Reactions, Kinetics, and Inhibition". Concepts in Biochemistry (2nd ed.). New York, Chichester, Weinheim, Brisbane, Singapore, Toronto.: John Wiley & Sons, Inc. pp. 137–8.

Warshel A, Sharma PK, Kato M, Xiang Y, Liu H, Olsson MH (August 2006). "Electrostatic basis for enzyme catalysis". Chemical Reviews. 106 (8): 3210–35.

Cox MM, Nelson DL (2013). "Chapter 6.2: How enzymes work". Lehninger Principles of Biochemistry (6th ed.). New York, N.Y.: W.H. Freeman. p. 195.

Benkovic SJ, Hammes-Schiffer S (August 2003). "A perspective on enzyme catalysis".Science. 301 (5637): 1196–202.

Villa J, Strajbl M, Glennon TM, Sham YY, Chu ZT, Warshel A (October 2000). "How important are entropic contributions to enzyme catalysis?".Proceedings of the National Academy of Sciences of the United States of America. 97 (22): 11899–904. .

Polgár, L. (7 July 2005). "The catalytic triad of serine peptidases".Cellular and Molecular Life Sciences. 62 (19–20): 2161–2172.

Ramanathan A, Savol A, Burger V, Chennubhotla CS, Agarwal PK (2014). "Protein conformational populations and functionally relevant substates". Acc. Chem. Res. 47(1): 149–56.

Tsai CJ, Del Sol A, Nussinov R (2009). "Protein allostery, signal transmission and dynamics: a classification scheme of allosteric mechanisms" (PDF). MolBiosyst. 5(3): 207–16.

Changeux JP, Edelstein SJ (June 2005). "Allosteric mechanisms of signal transduction".Science. 308 (5727): 1424–8.

Voet D, Voet J, Pratt C (2016). Fundamentals of Biochemistry. Hoboken, New Jersey: John Wiley & Sons, Inc. p. 336.

Fisher Z, Hernandez Prada JA, Tu C, Duda D, Yoshioka C, An H, Govindasamy L, Silverman DN, McKenna R (February 2005). "Structural and kinetic characterization of active-site histidine as a proton shuttle in catalysis by human carbonic anhydrase II".Biochemistry. 44 (4): 1097–115.

Noree C, Sato BK, Broyer RM, Wilhelm JE (August 2010). "Identification of novel filament-forming proteins in Saccharomyces cerevisiae and DrosopHilamelanogaster".The Journal of Cell Biology. 190 (4): 541–51.

Aughey GN, Liu JL (2015). "Metabolic regulation via enzyme filamentation".Critical Reviews in Biochemistry and Molecular Biology. 51 (4): 282–93.