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Enzymatic hydrolysis in food processing: biotechnological advancements, applications, and future perspectives

Dinara Akimova, Aitbek Kakimov, Anuarbek Suychinov, Zhumatay Urazbayev, Yerlan Zharykbasov, Nadir Ibragimov, Aigul Bauyrzhanova, Assiya Utegenova

ABSTRACT

In food processing, enzymatic hydrolysis has become a revolutionary biotechnological instrument that provides consistency and sustainability that are unmatched by traditional techniques. This work thoroughly analyzes current developments in enzymatic hydrolysis and examines its uses in various food processing contexts. The biotechnological aspects—such as substrate specificity, enzyme engineering, and sustainable process optimization—are the main focus. The historical background and development of enzymatic hydrolysis in food processing are explored at the study's outset, highlighting the process's transformation from a specialized use to a critical component of contemporary biotechnological food production. A thorough literature review underscores the specificity of enzymes in dissolving various dietary components, offering insights into the biotechnological nuances controlling substrate-enzyme interactions. A careful examination of the many enzymes used in enzymatic hydrolysis and a full assessment of their uses and specificities are provided. Enzymatic hydrolysis selection criteria are outlined, taking regulatory compliance, thermostability, pH sensitivity, and substrate specificity into account. The integration of enzymatic hydrolysis into workflows for food processing is also covered, focusing on compatibility with current infrastructure and processing parameters. The case studies that demonstrate the effective use of enzymatic hydrolysis in various food production situations are the core of the research. These examples illustrate the adaptability and effectiveness of enzymatic processes in improving food quality, from developing gluten-free products to optimizing fermentation in baked goods. In its futuristic conclusion, the article imagines how enzymatic hydrolysis will continue to influence food processing in the years to come. The biotechnological viewpoint strongly emphasizes current research directions, such as integrating enzymatic processes into sustainable food production techniques and engineering enzymes for increased specificity. This biotechnological investigation highlights how enzymatic hydrolysis may completely change the food processing industry by providing accuracy, sustainability, and creativity in pursuing wholesome, nutrient-dense, and aesthetically pleasing food items.

Keywords: enzymatic hydrolysis, food processing, biotechnology, protein hydrolysis, carbohydrate hydrolysis

INTRODUCTION

Using enzymes to convert complex compounds into simpler ones is a process known as enzymatic hydrolysis, and it has a long history and a big influence on the food business. With the discovery of enzymes as biocatalysts with the ability to change particular chemical bonds selectively, the regulated use of enzymatic hydrolysis gained importance in the middle of the 20th century. As a result, important enzymes, including lipases, amylases, and proteases, were systematically included in food processing, changing the sensory and functional characteristics of different food items. Many materials have been subjected to enzymatic hydrolysis, including starch and

hemicellulose. For example, research on the kinetics of hemicellulose hydrolysis has been done, which is crucial for comprehending the process of hemicellulose pyrolysis and expanding its applications. With starch saccharifying enzymes like α-amylase and glucoamylase, enzymatic hydrolysis has also been investigated as a starch hydrolysis alternative to acid hydrolysis. Moreover, enzymatic hydrolysis influences outside of the food sector. Medical applications such as the enzymatic hydrolysis of biodegradable polymers like poly(L-lactide) (PLLA), which is employed in tissue engineering, have also been researched concerning it. The enzymatic hydrolysis rate of polylactic acid (PLLA) is contingent upon its chemical and physical characteristics, with crystallinity being a major determinant of its breakdown trajectory **[1]**, **[2]**, **[3]**, **[4]**.

The development of computational biology and enzyme engineering fueled the customization of enzymes, enabling previously unheard-of control over reaction pathways and specificity. In the late 20th and early 21st centuries, enzymatic hydrolysis gained popularity for meeting new consumer demands, such as those for gluten-free and protein-enriched products. Additional information on particular uses for enzymatic hydrolysis can be found in the search results. For example, ultrasonication has been utilized extensively as a low-temperature, environmentally friendly, non-thermal processing method to support enzymatic hydrolysis, resulting in a notable increase in enzyme hydrolysis efficiency and an increase in the biological activity of substrates **[5]**, **[6]**, **[7]**, **[8]**.

Enzymatic hydrolysis is a vital food processing technique involving enzymes to change the molecular structures of raw food ingredients. Enzymes' specificity makes it possible to regulate and alter proteins, carbohydrates, lipids, and othe vital nutritional ingredients precisely. With its origins in the study of natural enzymatic processes and the subsequent application of these principles in food processing, this procedure has a long history. It has gained special notoriety with the development of contemporary biotechnology. Enzymatic hydrolysis has changed throughout time, going from being a common technology in food formulation to being employed in traditional food operations like dairy production and brewing. A revolution in food production occurred in the middle of the 20th century when scientists started methodically introducing enzymatic hydrolysis, which increased productivity and improved the quality of the final product. Research on the potential of enzymatic hydrolysis to customize food items to particular customer tastes exploded in the following decades, setting the groundwork for its adoption as a common practice. Enzymatic hydrolysis is now an essential part of food processing, demonstrating a dedication to accuracy, sustainability, and satisfying customers' ever-evolving demands for innovative and superior culinary experiences. The search results shed light on several enzymatic hydrolysis-related applications and studies, such as the use of enzymes to get around the challenges of fat biotransformation in the anaerobic digestion of fatty wastes from the food processing industry, the impact of processing decisions and enzymatic hydrolysis on the functionality of pulse proteins, and the in silico enzymatic hydrolysis of soy sauce cake glycinin G4 to reveal bioactive peptides as possible food ingredients **[5-9]**. Figure 1 depicts the enzymes used in food processing and some industrial applications.

Because they can precisely accelerate biological reactions as biocatalysts, enzymes are essential to the biotechnological processes used in food production. They support the development of higher yields, softer processing conditions, and functional ingredients. Because they are extremely focused catalysts, enzymes allow for the precise alteration of raw materials to produce finished goods with desired textures, tastes, and nutritional profiles. Compared to conventional approaches, their catalytic activity enables the tuning of processes, resulting in improved product yields. Furthermore, enzymes function well at lower temperatures and moderate pH levels, which is consistent with the increasing need for food processing that is both sustainable and energy-efficient. Agro-industrial food waste may produce industrially significant enzymes, which provide cost-effective options for commercializing compounds with added value. Microbial enzymes contribute to the sustainable use of agro-industrial food and crop waste by providing cleaner, more environmentally friendly ways to generate fine chemicals and compounds. The production of customized enzymes by genetically modified microorganisms (GEMs) provides special food processing skills. To assure the safety of GEM-produced food components and enzymes, regulatory bodies assess the safety of GEMs and the resultant food substances. This encourages a more coordinated approach to these products' safety evaluation and regulatory control. Scientific guidelines have been created specifically for food enzymes to help applicants prepare applications for food enzyme authorization. This guideline defines the scientific information that should be included in applications for the licensing of food enzymes and addresses the characterization of microorganisms employed as production organisms. Bacteriophage endolysins are lytic enzymes encoded by bacteriophages that are being researched for their potential to replace or enhance antibiotics in clinical and food production settings. This is in addition to their involvement in food production. By breaking down bacterial cell walls, these endolysins have demonstrated promise as antibiotic substitutes and may be developed through bioengineering **[10]**, **[11]**, **[12]**, **[13]**, **[14]**.

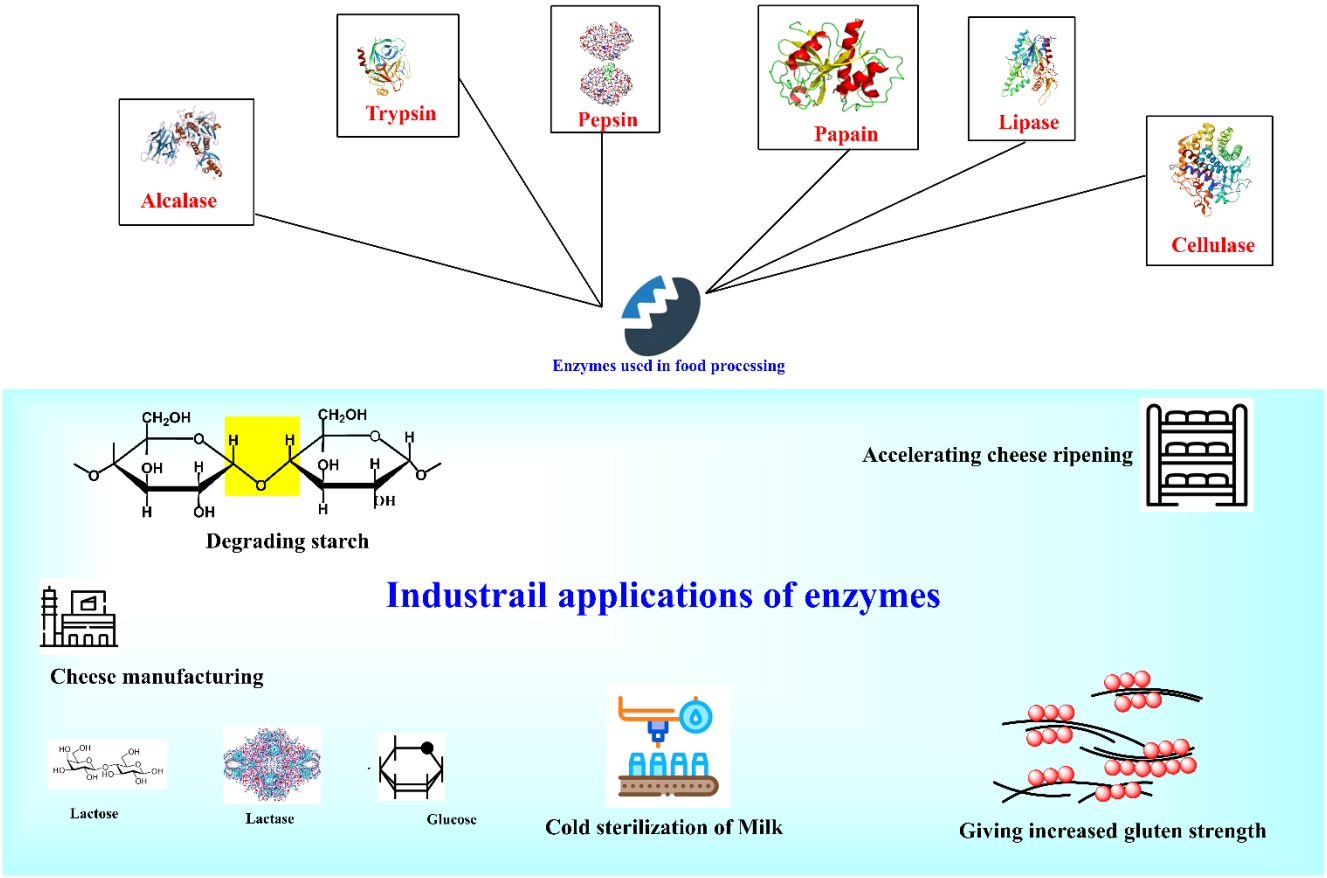

Figure 1 Scheme of industrial applications of enzymes in food processing.

Masterful Precision in Proteolysis: Unveiling the Specificity of Proteases

Proteinases, another name for proteases, are enzymes that cleave peptide links inside proteins with amazing specificity. This specificity, dictated by the protease's affinity for certain amino acid sequences, is the outcome of a molecular conversation between the enzyme and the protein, which serves as its substrate. Protease specificity is not random; it is the outcome of evolutionary adaptation and fine-tuning to match the enzyme's activity with biological requirements. Recent studies have shown that proteases may be reprogrammed to break novel sequences of our choice, opening up new medicinal and biotechnological possibilities. An effective method for producing proteases with custom specificities was established by research that detailed the development of botulinum neurotoxin proteases with reprogrammed specificity. Another work described a method for producing proteases with modified specificities to cleave. An effective method for producing proteases with custom specificities was established by research that detailed the development of botulinum neurotoxin proteases with reprogrammed specificity. Different research described a method for producing proteases with modified specificities to cleave a desired target protein. Protease substrate specificity is a tightly controlled mechanism essential to maintaining cellular homeostasis. Enzymes that deubiquitinate proteins and Ubl-specific proteases (ULPs) are two types of proteases that can identify and extract ubiquitin and proteins that resemble ubiquitin from their substrates. It is yet unclear how precisely these proteases differentiate between various modifiers or between these modifiers' polymeric forms **[15]**, **[16]**, **[17]**.

Chymotrypsin: Precision in Proteolysis

Protease chymotrypsin breaks peptide bonds next to aromatic amino acids, including phenylalanine and tyrosine. The enzyme's evolved molecular structure, which has been fine-tuned by natural selection, is the cause of its targeted specificity. The preference of chymotrypsin for aromatic amino acids is especially important in proteins where these residues are arranged in a certain way, helping to break down the protein under control and produce targeted peptide fragments. Recent studies have demonstrated the unique application of proteases like α-lytic protease for bottom-up proteomics by using orthogonal-specificity proteases to enhance proteome coverage. These alternative proteases improve proteome coverage through cleavage at sequences complementary to trypsin, thereby increasing proteome coverage by 101% relative to trypsin digestion alone. Furthermore, studies have been conducted to characterize the substrate specificity of other proteases, such as metacaspases, which prefer cleaving peptide bonds after arginine or lysine residues at specific sites. Understanding the substrate specificity of these

proteases is relevant for determining the types of proteins they cleave in vivo. Additionally, research has been conducted on the phage-assisted continuous evolution of proteases with altered substrate specificity, establishing a strategy for generating proteases with altered specificities to cleave a target protein of interest **[16]**, **[18]**, **[19]**.

Pepsin

Within the stomach's acidic environment, the protease pepsin demonstrates extraordinary selectivity and versatility in its enzymatic action. Pepsin plays a critical function in the early stages of protein digestion by selectively cleaving peptide bonds in proteins, helping to break down complex protein structures into smaller peptides partially. This adaptability is carefully tailored to the acidic environment. The use of pepsin in scientific and industrial situations has also been studied. One research, for example, highlighted the specialized uses of pepsin that need acidic conditions by optimizing an existing peptic digest process to investigate membrane proteins using bacteriorhodopsin from purple membranes as a reference. Another study utilized pepsin for the limited proteolysis of human growth hormone under acidic solvent conditions. It demonstrated the enzyme's activity at low pH and its role in selective cleavage of peptide bonds. Additionally, the adaptability of pepsin to acidic conditions has been leveraged in industrial processes, such as in the development of an acidic endo-beta-1,4-glucanase with high protease resistance for potential use as a pig feed additive. In summary, pepsin's adaptability to acidic conditions and specificity in cleaving peptide bonds play a pivotal role in the stomach's initial stages of protein digestion. Furthermore, research has demonstrated the diverse applications of pepsin's behavior in acidic environments, ranging from membrane protein analysis to industrial processes **[20]**, **[21]**, **[22]**.

Amylases: Maestros of Carbohydrate Metamorphosis

Amylases are enzymes that break down complex carbohydrates, particularly starches, and glycogen, into simpler sugars. They exhibit a remarkable ability to catalyze the hydrolysis of specific glycosidic bonds, precisely directing the controlled deconstruction of polysaccharides into sugars. There are different classes of amylases, including α-amylase and glucoamylase, widely distributed in bacteria, actinomycetes, and fungi. Microbial α-amylases are the most popular source of industrial α-amylase due to their cost-effectiveness and suitability for industrial demands. The specificity of amylases is a testament to their nuanced enzymatic capabilities. For example, the maltooligosaccharide-forming amylase (MFAse) from *Bacillus stearothermophilus* has been engineered to enhance its specificity for producing maltohexaose from starch, demonstrating the potential for modifying amylases to achieve desired product specificity. The α-amylase is an enzyme with a broad substrate preference and product specificity and is the main representative of family GH13. Still, it is also present in other glycoside hydrolase families such as GH57 and GH119. The α-amylase specificity is present in several subfamilies within family GH13, and these enzymes employ a reaction mechanism giving retention of configuration **[24-26]**.

The precision of α-amylases in cleaving internal α-1,4-glycosidic bonds within starch molecules is a testament to their enzymatic virtuosity. This targeted approach ensures a strategic disassembly of the starch polymer, revealing shorter oligosaccharides as the outcome. The liberation of maltose and maltotriose, resulting from the enzymatic action of α-amylases, marks the initial steps in the breakdown of starch, as these shorter oligosaccharides become the building blocks for subsequent enzymatic actions. The strategic breaking of internal bonds by α-amylases sets the stage for a cascade of molecular transformations, with the liberated maltose and maltotriose molecules becoming substrates for further enzymatic processes. This cascade of transformations acts as a molecular domino effect, with each cleavage event paving the way for subsequent modifications in the carbohydrate landscape. The specificity of α-amylases in cleaving internal bonds results from their remarkable ability to catalyze the hydrolysis of specific glycosidic bonds, precisely directing the controlled deconstruction of polysaccharides into sugars. This specificity is the molecular compass that guides α-amylases to their designated targets within the carbohydrate structures. The engineering of maltooligosaccharide-forming amylases (MFAs) to enhance their specificity for producing specific sugar fragments, such as maltohexaose, demonstrates the potential for tailoring these enzymes for specific industrial applications **[25]**.

The strategic positioning of β-Amylases in enzymatic hydrolysis plays a crucial role in the controlled liberation of maltose molecules from the non-reducing end of starch, contributing to the sequential breakdown of starch into simpler sugars. β-Amylases exhibit focused catalytic action by directing their enzymatic prowess to the non-reducing end of starch. This ensures meticulous control and systematic liberation of maltose molecules, which become integral building blocks in the carbohydrate metamorphosis journey. The specificity of β-Amylases acting on the non-reducing end is pivotal in orchestrating a controlled release of maltose units, unlike indiscriminate cleavage, ensuring a stepwise breakdown of starch into manageable fragments. Each liberated maltose unit becomes a molecular currency, ready to participate in further carbohydrate metamorphosis. The study of the impact of different amylases on the utilization of cornstarch in broiler chickens fed a corn-based diet showed that

the type and concentration of amylase supplementation can affect the digestibility of energy, feed conversion rate, and other physiological parameters in broiler chickens **[27]**, **[28]**.

Lipase

The specificity of lipases, such as pancreatic lipase, plays a crucial role in the hydrolysis of triglycerides, leading to the liberation of essential fatty acids and glycerol. Lipases, including pancreatic lipase, demonstrate distinctive action at the water-lipid interface, allowing them to effectively engage with lipid substrates, illustrating their prowess in molecular domains where hydrophobic and hydrophilic forces coalesce. Lipases' specificity and affinity for triglycerides make them essential in the culinary field, contributing to texture modification and sensory enhancement in lipid-containing foods. Research has also shown the optimization of enzymatic hydrolysis of oils, such as *Moringa oleifera* Lam oil, using lipase-catalyzed hydrolysis, demonstrating the specific affinity of lipases for fatty acids. Additionally, studies have investigated the synergistic effects of combi-lipases in the efficient hydrolysis of soybean oil, highlighting the importance of lipase specificity in the hydrolysis process **[29]**, **[30]**, **[31]**.

The primary dietary fat, triglycerides, are highly specific to pancreatic lipase and essential for hydrolyzing them. Studies have indicated that pancreatic lipase's selectivity for triglycerides stems from its capacity to hydrolyze ester bonds at particular locations along the glycerol backbone. This results in the regulated release of fatty acids and glycerol. This specificity is necessary for the controlled hydrolysis of triglycerides, which releases vital components and aids in the body's absorption of nutrients and energy metabolism. Research has further indicated that the pancreatic lipase's β5-loop and lid domains play a role in its substrate selectivity, underscoring the complex interplay between the structure and function of the enzyme **[32]**, **[33]**, **[34]**. **[35]**, **[36]**.

Cellulase

The ability of cellulases to specifically target cellulose, the primary constituent of plant cell walls, enables the controlled hydrolysis of cellulose into glucose units, with significant ecological and industrial applications. Cellulases, such as endoglucanases, exoglucanases, and β-glucosidases, have a remarkable affinity for cellulose, which allows them to act on the ends of cellulose chains, hydrolyze cellobiose into individual glucose units, and break internal β-1,4-glycosidic linkages. This selectivity is crucial in the regulated breakdown of cellulose chains, which release glucose units. This metabolic unit gives microorganisms a direct source of energy and aids in the synthesis of biofuel. methods used by fungi to access and break down cellulose. Furthermore, studies have demonstrated that the effectiveness of biological deconstruction of polymer materials is enhanced by the spatiotemporally coordinated action of cellulases that have a synergistic function in polymer chain depolymerization. Thus, the cellulose-specificity of cellulases reveals a metabolic symphony with revolutionary potential for many businesses, including the manufacture of biofuel and the environmentally friendly uses of immobilized cellulases **[36]**, **[37]**, **[38]**.

Endoglucanases & Exoglucanases

One of the most distinctive features of endoglucanases' enzymatic activity is their specialization in cleaving internal β-1,4-glycosidic linkages inside the cellulose structure, which starts the regulated disintegration of cellulose chains and produces shorter cellulose fragments. The release of glucose units is the final result of the operations of β-glucosidases and exoglucanases, which are set in motion by this regulated fragmentation. As demonstrated by research, the efficiency of biological deconstruction of polymer materials is enhanced by the spatiotemporally coordinated action of enzymes with synergistic function in polymer chain depolymerization. This emphasizes the significance of endoglucanases' cooperative role with other cellulases in the cellulolytic orchestra. Further research is required to better understand the catalytic mechanisms of endoglucanases and their importance in cellulose deconstruction. Studies have also shown that endoglucanases, especially those from glycoside hydrolase family 48 (GH48), are essential components of natural lignocellulose-degrading systems and greatly synergize with complementary endocellulases in free cellulase systems or cellulosome systems. Thus, endoglucanases' internal accuracy in cleaving β-1,4-glycosidic linkages is crucial for optimizing cellulose accessibility and maximizing the effectiveness of the cellulolytic ensemble, emphasizing the grace of enzymatic processes in nature's grand bio-fabrication **[37]**, **[39]**, **[40]**.

As virtuosos in the cellulolytic ensemble, exoglucanases exhibit dexterity at the extremities of cellulose chains, systematically releasing cellobiose units and aiding in the cellulose polymer's methodical unravelling. Their tailored activities guarantee harmonic development in the cellulolytic orchestra by preparing the released cellobiose units as substrates for the last enzymatic acts in the cellulolytic symphony. Studies have demonstrated that the efficient biological breakdown of polymer materials is enhanced by the spatiotemporally coordinated action of enzymes with synergistic roles in polymer chain depolymerization. This highlights the significance of exoglucanases' cooperative role with other cellulases in the cellulolytic orchestra. Furthermore, research has

demonstrated the vital function of exoglucanases in the orderly disintegration of the cellulose polymer and the production of cellobiose units for the latter phases of cellulose hydrolysis, highlighting the grace and effectiveness of nature's enzymatic artistry. Thus, exoglucanases, under their accuracy at the ends of cellulose chains, are essential for the systematic disintegration of the cellulose polymer, which enhances the effectiveness of cellulose deconstruction and readys cellobiose units for the last phases of cellulose hydrolysis **[37]**, **[39]**, **[40]**.

Enzymes known as β-glucosidases are essential for the last phase of cellulose breakdown. Their area of expertise is the breakdown of cellobiose, a disaccharide produced by previous enzymatic procedures. This process breaks down cellobiose into separate glucose units, signifying the successful completion of cellulose breakdown. The many uses of glucose in energy metabolism, the synthesis of biofuels, and other metabolic pathways make the release of glucose by β-glucosidases important. According to research, β-glucosidases, like the cellulolytic component C1 of Trichoderma koningii, function as beta-1,4-glucan cellobiohydrolases. They release terminal cellobiose units from cellulose and work closely with cellobiase to prolong cellulose hydrolysis and release glucose. Studies on the real-time monitoring of cellobiose and glucose synthesis during enzymatic biomass hydrolysis have also been carried out, underscoring the need to precisely measure these products to optimize the industrial degradation process.

Additionally, the hydrolysis process of cellobiose to glucose by β-glucosidase has been tested using computational fluid dynamics (CFD) simulations, showing the possibility of immobilizing β-glucosidase on an appropriate substrate to enhance its catalytic activity. The release of glucose by β-glucosidases is vital because glucose is a treasure trove of energy and a crucial building block for the synthesis of biofuels. It has been demonstrated that immobilizing β-glucosidases on appropriate substrates enhances their catalytic activity, which may have consequences for a range of industrial uses, such as the generation of biofuel **[41]**, **[42]**, **[43]**.

Metabolic Symphony Unveiled by Cellulases

The term "metabolic symphony" describes cellulose's sequential and well-coordinated breakdown into glucose by many cellulase types. This technique is compared to a well-balanced composition significantly affecting several sectors and the natural world. How endoglucanases, exoglucanases, and β-glucosidases work together to cleave cellulose into glucose units demonstrates the specificity of cellulases. Cellulases play a subtle symphony of sequential cleavage in the biochemical orchestra that is nature. They are like virtuosos in the orchestra. This orchestration results from several cellulases working together, each having a specific function in converting cellulose to glucose. In the metabolic symphony of cellulases, endoglucanases initiate the process by cleaving internal bonds, and exoglucanases control the process in a choreographed manner. The last note of cellulose hydrolysis is played by β-glucosidases, which break down cellobiose into individual glucose units. The release of glucose, the primary component of nature's biochemical repertory, has profound effects on the metabolism of energy, the synthesis of biofuels, and other vital biological functions. Within the industrial domain, the metabolic symphony facilitated by cellulases presents both transformational possibilities and long-term fixes. It creates opportunities for the production of biofuel, sustainable bioprocessing, and the development of biotechnology. The ability of cellulases to be particular serves as a light in sustainable bioprocessing, providing practical and eco-friendly methods for turning biomass into valuable products. Unlocking the energy held in cellulose and opening the door for sustainable practices, the "metabolic symphony" of cellulases echoes across the complexities of nature as well as the opportunities inside industrial environments **[43]**, **[44]**.

Glucose as Metabolic Currency

The most common polymer on Earth, cellulose is vital in maintaining soil nutrients and renewable energy sources. The enzymes known as cellulases, which are generated by various microbes, are essential in the breakdown of cellulose into glucose units, which can then be directly used as an energy source by bacteria and creatures that break down cellulose. Turning cellulose into glucose demonstrates how valuable and versatile glucose is. The manufacture of biofuels has excellent potential because of cellulases' ability to break down cellulose into glucose units under regulated conditions. The released glucose transforms from the inflexible walls of plant cells into tanks of sustainable biofuels, serving as a crucial precursor for bioethanol synthesis. The precise enzymatic activities of cellulases provide an ecologically favorable substitute for conventional fossil fuels and contribute to sustainable energy solutions. Cellulases, including β-glucosidases, endoglucanases, and exoglucanases, turn cellulose into a metabolic symphony that demonstrates the complex biochemical processes that support life and have the power to revolutionize several sectors. Microorganisms such as *Bacillus licheniformis* can produce cellulase, including glucosidase and endo-glucanase, which are crucial for the breakdown of cellulose **[45]**, **[46]**.

Pectinase

Pectinases are crucial enzymatic artisans who are vital to the processing of fruits and vegetables. They include pectin esterases, polygalacturonases, and pectin lyases. During processing, these enzymes precisely control texture, modifying the physical characteristics of fruits and vegetables. By altering the structural characteristics of pectin, they also support efforts to extend processed foods' shelf life by preserving their quality and freshness for longer. Furthermore, food processors can customize products to suit a wide range of preferences thanks to the specificity of pectinases, which ensures that every innovation reflects a keen understanding of the changing tastes and expectations of the modern consumer **[47]**, **[48]**, **[49]**, **[50]**. A class of enzymes known as pectinases is dedicated to degrading the complex material known as pectin. This group of enzymes includes pectin lyases, polygalacturonases, and esterases specific to different bonds in the pectin molecule. Pectinases are crucial to the food business, especially when processing fruits and vegetables, since their specific activities affect the quality and sensory qualities of the end product. Pectinases' enzymatic actions, such as de-esterification and depolymerization, help processed food items have a different texture, better quality, and longer shelf lives. Pectinases are derived from higher plants and microbes and are widely employed in the food sector, especially in the extraction of fruit juice **[47]**, **[48]**.

Pectin esterase

The enzymes known as pectin esterases are essential to the enzymatic conversion of pectin because they break down ester bonds found in the structure of the protein. This specific activity helps to de-esterify pectin, which modifies its structural characteristics and affects how processed fruits and vegetables feel. Pectin esterases demonstrate catalytic accuracy in hydrolyzing bonds by selectively targeting particular sites and cleaving ester links. Pectin esterase-mediated de-esterification significantly impacts fruit and vegetable texture during processing, changing the extent of esterification and causing differences in the firmness, viscosity, and overall mouthfeel of processed foods. Pectin esterases are essential in cooking because they affect the texture and flavor of processed fruits and vegetables and are becoming increasingly common. Pectin esterases facilitate de-esterification, which improves mouthfeel and consistency in processed fruits and vegetables. This balance in texture control allows for the modification of culinary attributes. Pectin esterases are the master builders of pectin hydrolysis; they meticulously manipulate the structure of ester bonds and the texture of fruits and vegetables to produce finished foods that are not only aesthetically pleasing but also showcase the intricate artistry of enzymatic science **[48]**, **[49]**.

Polygalacturonase

Enzymes known as polygalacturonases are adept at breaking bonds involving galacturonic acid, a crucial part of pectin. Pectin is depolymerized due to this enzymatic cleavage, which affects the quality and consistency of processed fruit and vegetable products. Polygalacturonases target galacturonic acid precisely, resulting in targeted cleavage and thorough dissection of the structural details of pectin. Pectin's molecular structure changes due to the galacturonic acid bond's enzymatical breaking by polygalacturonases, which starts the depolymerization process. Polygalacturonases play a vital role in the depolymerization process, which determines the final culinary creations' quality by affecting the consistency of processed fruit and vegetable products. Polygalacturonases are essential in the culinary arts because they affect the sensory attributes and characteristics of processed fruits and vegetables. They may also be a creative tool for food scientists and processors. The depolymerization of pectin by polygalacturonases is an essential process that shapes the texture of processed fruit and vegetable products. This process enhances the overall quality of processed goods by customising culinary features to suit a wide range of customer tastes. Polygalacturonases play a vital role in the depolymerization process, which determines the final culinary creations' quality by affecting the consistency of processed fruit and vegetable products. Polygalacturonases are essential in the culinary arts because they affect the sensory attributes and characteristics of processed fruits and vegetables. They may also be a creative tool for food scientists and processors. The depolymerization of pectin by polygalacturonases is an essential process that shapes the texture of processed fruit and vegetable products. This process enhances the overall quality of processed goods by enabling the customization of culinary features to suit a wide range of customer tastes **[48]**, **[50]**, **[51]**.

Pectin lyases

Pectin lyases are enzymes that catalyze elimination reactions within the pectin structure, forming unsaturated products. This enzymatic transformation modifies pectin's physical properties, impacting processed fruits and vegetables' texture and shelf life. Pectin lyases exhibit enzymatic precision in catalyzing elimination reactions, selectively cleaving specific bonds within the pectin structure, and creating unsaturated products. The formation of unsaturated products initiates a molecular rearrangement within the pectin structure, impacting its physical

properties. Pectin lyases catalyze an enzymatic change that affects processed fruits and vegetables' texture, hardness, and general structural integrity, affecting how long they last on the shelf. Pectin lyases affect the shelf life of processed goods, change the texture of processed fruits and vegetables, and foster culinary creativity by bringing variety to the sensory characteristics of processed meals **[52]**, **[53]**. During processing, pectinases are essential for maintaining the color and taste of fruits and vegetables. Their focused efforts help to improve the overall quality of food items by preventing undesired changes in texture and appearance.

Furthermore, pectinases influence the structural integrity of pectin, which helps to modulate shelf stability and increase the shelf life of processed goods. This enzymatic alteration helps preserve the quality and freshness of fruits and vegetables throughout time, demonstrating the accuracy and importance of pectinases at the nexus of enzymatic science and culinary artistry. Pectinases' accuracy as enzymatic instruments in the food processing toolset is reflected in their specialization in targeting different bonds within the pectin structure. Pectinases, the builders of pectin hydrolysis, are essential because they bridge the gap between enzymatic science and culinary creativity by enhancing fruit and vegetable products' palatability and aesthetic appeal **[54]**, **[55]**.

The search results may include further details on the significance of pectin degradation in the environment and industry. Pectinases, which comprise pectin esterases, polygalacturonases, and pectin lyases, are essential for breaking down plant cell walls, and pectin is an integral part of building cell walls. Pectinases are used in industry to enhance the quality of fruit juices and can also be employed to break down tea leaves or coffee cherries. These enzymes could also help lessen the negative effects of cotton and paper on the environment. The search results also highlight the importance of comprehending microbial pectin degradation, particularly in species phylogenetically different from Aspergillus and Enterobacteriaceae, as it may decrease the expense and increase the efficiency of plant cell wall breakdown for biofuel or chemical production and help identify novel enzymes with other industrial uses **[56]**.

Pectinases are essential for processing fruits and vegetables because they improve the overall quality of the final product by preserving taste and refining texture. By carefully breaking apart certain bonds in pectin to break down the plant cell wall, these enzymes function as molecular architects, molding the texture and keeping the original tastes of plant-based goods. Pectinases also help improve product quality by prolonging the shelf life of processed foods and preserving the nutritional value of fruits and vegetables over time. Their practical uses in the food processing sectors, such as oil extraction, juice processing, and alcoholic beverage processing, enhance output levels and product quality. Pectinases, including polygalacturonases, are widely utilized in various food processing sectors, including wine clarifying, fruit juice extraction, and jam and jelly manufacturing. Pectinases are, therefore, necessary to convert unprocessed plant materials into the delectable works of art that adorn our dinner tables **[57]**, **[58]**, **[59]**.

Nucleases

As genetic sculptors in enzymatic hydrolysis, nucleases are essential for breaking down nucleic acids like DNA and RNA and for developing tastes in various culinary applications, including the maturation of cheese. Their ability to precisely hydrolyze nucleic acids releases a symphony of tastes, improving food items' overall flavor character. Nucleases play a crucial role in the ripening of cheese for the following reasons:

1. Development of flavor: Nucleases break nucleic acids, which release bound flavors and improve the cheese's overall flavor. 2. Production of aroma: Flavor chemicals like 3-methyl butanol and 1-pentanol, which give the cheese its distinct flavor, can be formed by the hydrolysis of nucleic acids. 3. Smoother and creamier texture: Enzymatic hydrolysis breaks down proteins to give cheese a smoother, creamier texture. 4. Less allergens: Cheese that has had its milk proteins hydrolyzed has fewer allergens, making it better for those with a milk allergy. To get the ideal flavor and texture in cheese, optimizing the parameters for enzymatic hydrolysis, including temperature, enzyme concentration, and hydrolysis duration is essential.

For instance, one study discovered that employing bromelain to hydrolyze cockle meat wash water precipitate produced a product with a nitrogen concentration of 0.6% and a hydrolysis degree of 48%. These circumstances have been demonstrated to result in a hydrolysate containing flavorings in oysters and clams. Nucleases have been used in food in ways other than cheese, such as the hydrolysis of fish bone protein to enhance the taste and antioxidant capacity of the resulting hydrolysates. To recover proteins from fish backbones, steam explosion-assisted extraction has been compared to hot-pressure extraction, and the functional characteristics and IgG/IgE-binding capability of skimmed cow milk have been investigated using enzymatic hydrolysis **[60]**, **[61]**, **[62]**, **[63]**.

Reaction Mechanisms: Navigating the Specificity Terrain

The active sites of enzymes display selectivity, essential for molecule recognition and catalysis in enzymatic hydrolysis activities. The interaction of chemical fingerprints and geometric geometries determines the specificity of active sites, allowing enzymes to identify the substrates they are meant to bind to precisely. Enzymes and

substrates have extraordinary geometric and chemical complementarity, fitting together like a jigsaw. The active site pockets' particular configuration of atoms, charges, and functional groups ensures that substrates locate their binding partners and start the chain reaction of catalysis. Knowing the specificity of active sites reveals the beauty of molecular recognition in enzymatic hydrolysis. It offers insights into the molecular level of reaction orchestration, where specificity and accuracy are paramount **[64]**, **[65]**, **[66]**.

Lock-and-Key vs. Induced Fit Models: A Choreography of Molecular Recognition

Lock-and-Key Model

According to the lock-and-key concept, the substrate (the key) and the enzyme (the lock) must fit precisely. According to this paradigm, the substrate and the active site of the enzyme exhibit predetermined complementarity that enables smooth binding. The active site pockets' particular configuration of atoms, charges, and functional groups ensures that substrates locate their binding partners and start the chain reaction of catalysis. Adding a dynamic aspect to the chemical interaction, the induced fit model adds flexibility to the lock-and-key model's rigidity. According to this hypothesis, conformational changes occur in both the enzyme and the substrate during binding. Because of its flexibility, the active site's shapes may be adjusted to meet the substrate's structure and guarantee a snug fit. The dance between the substrate and the enzyme changes in reaction to their interaction, growing more intimate as they adjust to each other's structural peculiarities. The induced fit model's intrinsic flexibility becomes essential in the complex world of enzymatic hydrolysis. Different substrates pose different structural difficulties, and the dance between the substrate and the enzyme needs to consider this diversity. With its elegant adaptability, the induced fit model enables enzymes to accept substrates of different sizes and shapes, resulting in a flexible and efficient molecular stage performance **[67]**, **[68]**, **[69]**.

In the context of enzymatic hydrolysis, the search results shed light on the catalytic processes of several enzyme types, including proteases and carbohydrate-binding modules (CBMs). The results highlight the wide range of molecular tools that different enzyme classes use, which helps explain why different enzyme classes approach different substrates in enzymatic hydrolysis with customized accuracy. The first two search results provide insight into the lock-and-key and induced fit processes involved in the interaction between an enzyme and its substrate by discussing the selectivity and conformational changes in protease active sites. These findings demonstrate the adaptive usefulness of the lock-and-key mechanism in promoting high efficiency in enzymatic reactions by offering a thorough knowledge of the molecular interactions and conformational changes that influence future reactions with substrates. The function of CBMs in the enzymatic hydrolysis of complex carbohydrates is the subject of the following two findings. They demonstrate how CBMs, which are physically and functionally independent of the catalytic domains they are linked with, contribute to the hydrolysis of certain substrates via unique methods, highlighting the customized accuracy with which enzymes tackle the hydrolysis of complex carbohydrates **[66]**, **[69]**, **[70]**, **[71]**.

Co-factors and Coenzymes: Catalysts' Trusted Allies

In enzymatic hydrolysis, co-factors and coenzymes are crucial partners that are crucial to catalytic mastery. Non-protein molecules called co-factors attach to enzymes to increase their catalytic activity and improve the accuracy and efficiency of enzymatic hydrolysis. They facilitate biological reactions and function as molecular bridges by bridging molecules between enzymes and their substrates. As a subclass of co-factors, coenzymes are organic compounds that improve other enzymes' activity and participate actively in the catalytic dance. They experience reversible chemical changes during catalysis and shuttle back and forth between the enzyme and the substrate, enabling key stages in the reaction pathway. Comprehending the function of these indispensable associates is paramount to precisely crafting enzymatic procedures, as they offer indispensable perspectives into the enzymatic choir, directing enzymes through the complexities of catalysis and exhibiting the musical interaction that underpins the grace of enzymatic processes **[69]**.

Competitive and Non-competitive Inhibition: A Molecular Chessboard

Enzyme inhibition that is not competitive occurs when an inhibitor attaches to the enzyme at a position other than the active site, changing the enzyme's structure and lowering its activity. The substrate concentration cannot be increased to overcome this inhibition. Non-competitive inhibitors are frequently employed in the creation of medicinal treatments for a range of illnesses. For the treatment of neuropathic pain and chronic inflammation, for example, studies on non-competitive inhibition of enzymes like fatty acid amide hydrolase (FAAH) have been carried out **[72]**, **[73]**, **[74]**. **[75]**, **[76]**.

Non-competitive inhibition is based on the molecular mechanism of the inhibitor attaching itself to the complex of enzyme and substrate, hence reducing the enzyme's turnover rate. This kind of inhibition is

distinguished by its capacity to change the enzyme's Vmax and its independence from the concentration of the substrate. It is essential to comprehend the molecular mechanisms of non-competitive inhibition to design therapeutic interventions that work and to understand biological systems better. The listed publications and research articles shed light on the possible biological and therapeutic uses of non-competitive inhibition and its molecular underpinnings. These discoveries enhance the comprehension of enzyme control and the creation of innovative therapy approaches for various ailments.

One study that clarifies the role of non-competitive inhibitors in managing neuropathic pain and chronic inflammation is the molecular basis of the non-competitive inhibition of fatty acid amide hydrolase (FAAH). Furthermore, studies on the supramolecular interaction between β-galactosidase and a molecular cage demonstrate how a non-competitive inhibitor affects enzyme activity and how it may be used for antimicrobial activity. Because of these results, the strategic dynamics of enzyme inhibition and its consequences for many biological and therapeutic contexts are better understood **[72]**, **[76]**.

Inhibitors can contribute to the enzymatic hydrolysis process through competitive and non-competitive inhibition. Non-competitive inhibitors attach to a location different from the enzyme's active site, causing conformational changes, whereas competitive inhibitors imitate the substrate and compete for the active site. It is essential to comprehend these pathways to maximize enzymatic hydrolysis. Research on the enzymatic hydrolysis of proteins in red tilapia viscera revealed that competitive inhibitors, such as lipids, may significantly compete with genuine substrates for the enzyme's active site. Conversely, non-competitive inhibitors, like certain catalysts, might cause the enzyme to alter conformation, which can impact the catalytic process as a whole **[77]**, **[78]**, **[79]**. **[80]**, **[81]**.

Orchestrating Precision: Allosteric Ballet in Enzymatic Hydrolysis

Like a choreographed masterpiece, the complex process of allosteric control in enzymatic hydrolysis introduces a subtle ballet of molecular interactions that extends beyond the boundaries of the active site. Allosteric regulation presents a dance at a separate stage—the allosteric site—in contrast to the direct involvement observed in competitive and non-competitive inhibition. This is where an allosteric effector molecule enters the picture. It binds to a location other than the active site, changing the enzyme's shape and affecting its catalytic activity. The balletic precision required to regulate enzymatic activities precisely is provided by allostery regulation. The allosteric effector regulates the enzyme's activity, which also sets the speed and tempo of the catalytic performance. Enzymatic hydrolysis may be precisely regulated by this subtle control, guaranteeing that it proceeds with the elegance and dexterity of a well-practiced process. Allosteric control brings a symphony of molecular motions to the big spectacle of enzymatic hydrolysis, where the far-off murmurs at the allosteric site reverberate throughout the enzyme. A smooth integration of regulatory cues is produced by the active site and allosteric site's perfect synchronization, reminiscent of a ballet's timed movements. The designers of enzymatic systems must comprehend the fundamentals of allosteric control. Scientists may create choreographies that enable dynamic and responsive enzymatic hydrolysis by carefully arranging molecules that act as allosteric effectors. This ensures that the dance of chemical changes unfolds with grace and accuracy **[82]**, **[83]**.

Awakening the Catalysts: Unveiling the Secrets of Enzyme Activation

Enzyme activation is an essential first step in the complex realm of enzymatic hydrolysis, marking the beginning of the biochemical process. Deciphering the elements that cause an enzyme to activate is like unlocking the latent potential of an old ritual by knowing which cues to use. Among the crucial elements of enzyme activation are:

1. Cofactors as Vitalizing Liquids: Cofactors, organic molecules, or metal ions are frequently needed to activate enzymes. These cofactors give enzymes life and cause them to emerge from dormancy **[84]**, **[85]**.

2. Post-Translational Magic: Enzymes can undergo post-translational modifications, such as phosphorylation, acetylation, or glycosylation, which can change them and set off a series of events that lead to the enzyme's activation **[85]**.

3. Harmony in Activation: Cofactor availability, post-translational modification accuracy, and molecular cue alignment are just a few of the variables that play a subtle role in orchestrating enzyme activation. This harmonic interaction aroused enzymes to a crescendo of catalytic frenzy **[86]**.

4. Harmonizing the Resurrection: Like contemporary magicians, scientists practice precisely controlling the activation of enzymes. They acquire the ability to precisely control enzymes' waking by learning the cofactors' language and the subtleties of post-translational modifications. Thanks to this fine-tuning, enzymatic hydrolysis will proceed with the elegance of a well-rehearsed show **[86]**.

Criteria for Selecting Enzymes in Enzymatic Hydrolysis

Many parameters should be taken into account while choosing enzymes for enzymatic hydrolysis. It is essential to examine the characteristics of the substrate, including proteins, carbohydrates, and fats, to select enzymes that have a natural affinity for the intended substrate. Because enzymes have preferences for particular bonds, knowing the desired transformation helps the selection process so that the selected enzymes coincide with the required bonds. Choosing the proper enzyme turns becomes a calculated move, much like picking the appropriate explorer for a certain area. The functional impact of enzymatic hydrolysis on pulse proteins varies significantly depending on the enzyme, substrate, heat treatment, level of hydrolysis, and pH during processing. Cellulases' substrate specificity was established concerning the fibers of genetically distinct cotton lines **[87]**, **[88]**.

Fine-Tuning the Hydrolytic Symphony: Optimal pH and Temperature Choreography

Temperature and pH levels are critical factors in determining the rhythm and harmony of the catalytic process during enzymatic hydrolysis. Like virtuoso musicians, enzymes resonate at a certain pH, producing a harmonic symphony of catalysis. Enzymes exhibit their highest effectiveness at the sweet spot, which is the ideal pH range. The hydrolytic ballet's beat is set by temperature, an understated yet powerful maestro in the enzymatic ensemble. Enzymes function best and work at their peak in a range of temperatures. The design of enzymatic hydrolysis processes involves strategic considerations such as selecting enzymes that grow best in specific pH and temperature ranges and maintaining these parameters during hydrolysis. Enzymes may show their catalytic virtuosity in an environment where pH and temperature are precisely controlled. This leads to ideal substrate transformation and the production of culinary marvels. The hydrolytic symphony is shaped by temperature and pH, which catalyze the story to a crescendo. The effectiveness of enzymatic hydrolysis is determined by their subtle artistic influence on enzyme activity, which goes beyond plain technical details. Enzymes convert substrates into carefully planned pH sensitivity and temperature responsiveness culinary compositions in this choreographed dance. This demonstrates the intricate interactions between variables that raise enzymatic hydrolysis to the level of a symphony of culinary brilliance **[89]**.

Criteria for Selecting Enzymes in Enzymatic Hydrolysis

The choice of enzymes for enzymatic hydrolysis is an important stage that greatly impacts the procedure's effectiveness and outcome. When selecting enzymes for a particular hydrolysis application, a few important factors are to consider. Some requirements are the ideal pH and temperature ranges, substrate selectivity, enzyme fortitude (chemical stability and thermostability), and thoughtful regulation of pH and temperature. Regarding the kind of substrate and the targeted linkages, enzymes show selectivity. The enzyme selection should align with the target substrate to achieve effective hydrolysis. For example, various substrates are best suited for different specificities of proteases, carbohydrates, and lipases. The temperature and pH levels greatly impact how well enzymes hydrolyze materials. Enzymes function best in particular pH and temperature ranges. To maximize substrate transformation efficiency, the pH and temperature of the enzymatic milieu must align with the selected enzymes' ideal ranges. Choosing the right enzymes for enzymatic hydrolysis requires careful consideration of chemical stability and thermostatability. Enzymes that are thermostatable continue to function in high-temperature environments, which enhances efficiency. Enzyme resistance to denaturation or inactivation caused by different additives, processing aids, and chemicals within the food matrix is ensured by chemical stability **[88]**. When developing gluten-free goods, enzymatic hydrolysis is essential for overcoming difficulties arising from the special characteristics of gluten proteins. In this context, the advantages of enzymatic hydrolysis are clear from several applications. By breaking down gluten proteins into smaller peptides, enzymatic proteolysis uses proteases from bacteria or fungi to provide cohesive and stretchy characteristics. Complex networks are broken down in this process, which lessens the natural stiffness of gluten-free dough and gives it a softer, more malleable feel akin to its conventional gluten-containing counterparts. Because of their capacity to hydrolyze starches, amylases play a major role in enhancing dough handling and water absorption. Amylases in gluten-free flours hydrolyze complex carbohydrates to release simpler sugars that improve the flour's ability to retain water. Thus, the consistency and workability of the dough is improved. Enzymes like amylases and proteases reduce the bitterness in gluten-free recipes. These enzymes work on proteins and starches, respectively, to lessen the bitter flavor of some gluten-free foods. This is achieved by dissolving certain peptide linkages and complex carbohydrates, improving the overall palatability of gluten-free compositions. Enzymes, such as transglutaminases, are essential for improving the texture and structure of fermented foods free of gluten. Transglutaminases catalyze cross-link formation between proteins, improving structural cohesiveness and taste better. The process of enzymatic hydrolysis is useful for increasing the bioavailability of nutrients. Vital minerals are released by identifying and eliminating antinutritional elements like phytates and protease inhibitors found in gluten-free grains, improving overall nutritional value by increasing their availability for absorption in the digestive tract. Proteases and other

pertinent enzymes aid in the enzymatic modification process, which is essential for increasing the amount of gluten-free baked goods. Enhancing the gas retention qualities of gluten-free flours helps create an environment more conducive to gas retention, increasing the amount of baked goods free of gluten. Similarly, enzymatic modification using amylases and proteases changes the structure and content of gluten-free foods to improve the texture and crunchiness of gluten-free snacks. As a consequence, customers get a more pleasurable sensory experience. These uses highlight how adaptable and successful enzymatic hydrolysis addresses obstacles in creating gluten-free products. It is feasible to produce gluten-free goods with the appropriate texture and mouthfeel and a sensory experience that is on par with their conventional, gluten-containing equivalents by carefully using enzymes **[90]**, **[91]**, **[92]**, **[93]**. Enzymatic adjustments are essential for improving the quality of products that are free of gluten. Enzymes such as amylases, transglutaminases, proteases, and others play a role in modifying the structure of gluten-free substitutes to enhance their attributes. Amylases, for example, work on complex starch structures to improve the end product's texture, malleability, and leavening by affecting dough handling, water absorption, and gas retention. Transglutaminases help proteins cross-link, strengthening the protein network, improving gas retention, and improving the texture of baked goods devoid of gluten. Furthermore, to improve the quality of gluten-free goods, enzymes, including phytases, proteases, and hemicellulases, alter non-gluten polysaccharides, lessen bitterness, and improve nutrient accessibility. These enzymatic procedures provide answers to problems relating to gluten-free baking, including managing dough, texture, volume, and sensory qualities. Enzymatic modification research is still ongoing, and it might lead to future improvements in the creation of goods devoid of gluten **[94]**, **[95]**, **[96]**, **[97]**.

CONCLUSION

To sum up, enzymatic hydrolysis has become a revolutionary and adaptable method for creating gluten-free goods, providing creative answers to the problems caused by the lack of gluten. The applications concerning many facets of the production of gluten-free products demonstrate the important influence of enzymatic interventions on texture, flavor, and nutritional value. The crunchiness problem in gluten-free snacks can be solved using enzymatic modification made possible by amylases and proteases. This method alters the structure and makeup of gluten-free components, adding to a more satisfying sensory experience evocative of classic gluten-containing treats. Additionally essential to enhancing nutritional bioavailability in gluten-free goods is enzymatic hydrolysis. Amylases and phytases work in tandem to break down complex carbohydrates and phytic acid, respectively. This increases the amount of energy available during digestion and improves the absorption of vital minerals. Enzymatic hydrolysis is a useful method for reducing the bitterness of gluten-free food. Amylases, lipases, and proteases collaborate to convert bitter molecules into smaller, less noticeable peptides. This tactical move improves the sensory experience, giving customers a more appealing choice. Furthermore, the use of amylases and hemicellulases for enzymatic modification of gluten-free flours is beneficial in customizing rheological characteristics, resolving issues related to water absorption, and enhancing the general consistency of dough. Protease-based enzymatic hydrolysis in gluten-free snacks and convenience meals demonstrates the potential of this process to improve texture and other sensory aspects. These enzymes help produce gluten-free foods with improved crispiness and mouthfeel, satisfying customer expectations for quality by carefully altering protein structures. Essentially, the combined data from various uses highlights the accuracy and versatility of enzymatic hydrolysis in addressing the intrinsic constraints of gluten-free recipes.

REFERENCES

1. Yuan, Q., Liu, S., Ma, M.-G., Ji, X.-X., Choi, S.-E., & Si, C. (2021). The Kinetics Studies on Hydrolysis of Hemicellulose. In Frontiers in Chemistry (Vol. 9). Frontiers Media SA. https://doi.org/10.3389/fchem.2021.781291
2. Arola, S., Malho, J., Laaksonen, P., Lille, M., & Linder, M. B. (2013). The role of hemicellulose in nanofibrillated cellulose networks. In Soft Matter (Vol. 9, Issue 4, pp. 1319–1326). Royal Society of Chemistry (RSC). https://doi.org/10.1039/c2sm26932e
3. Malek, M.I.A., A.S. Azmi, and N.I.M. Puad. Review on applications of sago starch processing effluent. 2016.
4. You, W., Duan, B., Wang, M., & Lam, W. (2011). Isothermal and Non-isothermal Crystallization Kinetics of Poly(L-Lactide)/Carbonated Hydroxyapatite Nanocomposite Microspheres. In Advances in Diverse Industrial Applications of Nanocomposites. InTech. https://doi.org/10.5772/14715
5. Qian, J., Chen, D., Zhang, Y., Gao, X., Xu, L., Guan, G., & Wang, F. (2023). Ultrasound-Assisted Enzymatic Protein Hydrolysis in Food Processing: Mechanism and Parameters. In Foods (Vol. 12, Issue 21, p. 4027). MDPI AG. https://doi.org/10.3390/foods12214027

6. Dent, T., & Maleky, F. (2022). Pulse protein processing: The effect of processing choices and enzymatic hydrolysis on ingredient functionality. In Critical Reviews in Food Science and Nutrition (Vol. 63, Issue 29, pp. 9914–9925). Informa UK Limited. https://doi.org/10.1080/10408398.2022.2070723
7. Wubshet, S. G., Måge, I., Böcker, U., Lindberg, D., Knutsen, S. H., Rieder, A., Rodriguez, D. A., & Afseth, N. K. (2017). FTIR as a rapid tool for monitoring molecular weight distribution during enzymatic protein hydrolysis of food processing by-products. In Analytical Methods (Vol. 9, Issue 29, pp. 4247–4254). Royal Society of Chemistry (RSC). https://doi.org/10.1039/c7ay00865a
8. Pascale, N. C., Chastinet, J. J., Bila, D. M., SantAnna, G. L., Jr, Quitério, S. L., & Vendramel, S. M. R. (2018). Enzymatic hydrolysis of floatable fatty wastes from dairy and meat food-processing industries and further anaerobic digestion. In Water Science and Technology (Vol. 79, Issue 5, pp. 985–992). IWA Publishing. https://doi.org/10.2166/wst.2018.508
9. Lim, J. Y., Chai, T.-T., Lam, M. Q., Ng, W. J., & Ee, K. Y. (2022). In silico enzymatic hydrolysis of soy sauce cake glycinin G4 to reveal the bioactive peptides as potential food ingredients. In Journal of Food Measurement and Characterization (Vol. 16, Issue 5, pp. 3477–3487). Springer Science and Business Media LLC. https://doi.org/10.1007/s11694-022-01433-y
10. Sharma, V., Tsai, M.-L., Nargotra, P., Chen, C.-W., Kuo, C.-H., Sun, P.-P., & Dong, C.-D. (2022). Agro-Industrial Food Waste as a Low-Cost Substrate for Sustainable Production of Industrial Enzymes: A Critical Review. In Catalysts (Vol. 12, Issue 11, p. 1373). MDPI AG. https://doi.org/10.3390/catal12111373
11. Hanlon, P., & Sewalt, V. (2020). GEMs: genetically engineered microorganisms and the regulatory oversight of their uses in modern food production. In Critical Reviews in Food Science and Nutrition (Vol. 61, Issue 6, pp. 959–970). Informa UK Limited. https://doi.org/10.1080/10408398.2020.1749026
12. EFSA Panel on Food Contact Materials, Enzymes and Processing Aids (CEP), Silano, V., Barat Baviera, J. M., Bolognesi, C., Brüschweiler, B. J., Cocconcelli, P. S., Crebelli, R., Gott, D. M., Grob, K., Lampi, E., Mortensen, A., Rivière, G., Steffensen, I., Tlustos, C., Van Loveren, H., Vernis, L., Zorn, H., Glandorf, B., Herman, L., … Chesson, A. (2019). Characterisation of microorganisms used for the production of food enzymes [JB]. EFSA Journal, 17(6). https://doi.org/10.2903/j.efsa.2019.5741
13. EFSA Panel on Food Contact Materials, Enzymes and Processing Aids (EFSA CEP Panel), Lambré, C., Barat Baviera, J. M., Bolognesi, C., Cocconcelli, P. S., Crebelli, R., Gott, D. M., Grob, K., Lampi, E., Mengelers, M., Mortensen, A., Rivière, G., Steffensen, I., Tlustos, C., Van Loveren, H., Vernis, L., Zorn, H., Glandorf, B., Herman, L., … Chesson, A. (2021). Scientific Guidance for the submission of dossiers on Food Enzymes [JB]. EFSA Journal, 19(10). https://doi.org/10.2903/j.efsa.2021.6851
14. Love, M., Bhandari, D., Dobson, R., & Billington, C. (2018). Potential for Bacteriophage Endolysins to Supplement or Replace Antibiotics in Food Production and Clinical Care. In Antibiotics (Vol. 7, Issue 1, p. 17). MDPI AG. https://doi.org/10.3390/antibiotics7010017
15. Blum, T. R., Liu, H., Packer, M. S., Xiong, X., Lee, P.-G., Zhang, S., Richter, M., Minasov, G., Satchell, K. J. F., Dong, M., & Liu, D. R. (2021). Phage-assisted evolution of botulinum neurotoxin proteases with reprogrammed specificity. In Science (Vol. 371, Issue 6531, pp. 803–810). American Association for the Advancement of Science (AAAS). https://doi.org/10.1126/science.abf5972
16. Packer, M. S., Rees, H. A., & Liu, D. R. (2017). Phage-assisted continuous evolution of proteases with altered substrate specificity. In Nature Communications (Vol. 8, Issue 1). Springer Science and Business Media LLC. https://doi.org/10.1038/s41467-017-01055-9
17. Ronau, J. A., Beckmann, J. F., & Hochstrasser, M. (2016). Substrate specificity of the ubiquitin and Ubl proteases. In Cell Research (Vol. 26, Issue 4, pp. 441–456). Springer Science and Business Media LLC. https://doi.org/10.1038/cr.2016.38
18. Meyer, J. G., Kim, S., Maltby, D. A., Ghassemian, M., Bandeira, N., & Komives, E. A. (2014). Expanding Proteome Coverage with Orthogonal-specificity α-Lytic Proteases. In Molecular & Cellular Proteomics (Vol. 13, Issue 3, pp. 823–835). Elsevier BV. https://doi.org/10.1074/mcp.m113.034710
19. Nguyen, L. M., & Fox, K. M. (2019). Enzyme Kinetic Characterization and Substrate Specificity of Schizophyllum commune Metacaspases. In The FASEB Journal (Vol. 33, Issue S1). Wiley. https://doi.org/10.1096/fasebj.2019.33.1_supplement.781.12
20. Rietschel, B., Bornemann, S., Arrey, T. N., Baeumlisberger, D., Karas, M., & Meyer, B. (2009). Membrane protein analysis using an improved peptic in-solution digestion protocol. In PROTEOMICS (Vol. 9, Issue 24, pp. 5553–5557). Wiley. https://doi.org/10.1002/pmic.200900532
21. Spolaore, B., Polverino de Laureto, P., Zambonin, M., & Fontana, A. (2004). Limited Proteolysis of Human Growth Hormone at Low pH: Isolation, Characterization, and Complementation of the Two Biologically Relevant Fragments 1−44 and 45−191. In Biochemistry (Vol. 43, Issue 21, pp. 6576–6586). American Chemical Society (ACS). https://doi.org/10.1021/bi049491g

22. Bai, Y., Wang, J., Zhang, Z., Shi, P., Luo, H., Huang, H., Feng, Y., & Yao, B. (2010). Extremely Acidic β-1,4-Glucanase, CelA4, from Thermoacidophilic Alicyclobacillus sp. A4 with High Protease Resistance and Potential as a Pig Feed Additive. In Journal of Agricultural and Food Chemistry (Vol. 58, Issue 3, pp. 1970–1975). American Chemical Society (ACS). https://doi.org/10.1021/jf9035595

23. Lim, S. J., & Oslan, S. N. (2021). Native to designed: microbial α-amylases for industrial applications. In PeerJ (Vol. 9, p. e11315). PeerJ. https://doi.org/10.7717/peerj.11315

24. Kumari, N., Sushil, Malik, K., & Avtar, R. (2019). Microbial amylases: An overview on recent advancement. In Journal of entomology and zoology studies (Vol. 7, p. 198–205). Society of Agricultural Research and Social Development.

25. Xie, X., Ban, X., Gu, Z., Li, C., Hong, Y., Cheng, L., & Li, Z. (2020). Structure-Based Engineering of a Maltooligosaccharide-Forming Amylase To Enhance Product Specificity. In Journal of Agricultural and Food Chemistry (Vol. 68, Issue 3, pp. 838–844). American Chemical Society (ACS). https://doi.org/10.1021/acs.jafc.9b07234

26. Janeček, Š., Svensson, B., & MacGregor, E. A. (2013). α-Amylase: an enzyme specificity found in various families of glycoside hydrolases. In Cellular and Molecular Life Sciences (Vol. 71, Issue 7, pp. 1149–1170). Springer Science and Business Media LLC. https://doi.org/10.1007/s00018-013-1388-z

27. Rittenauer, M., Gladis, S., Gastl, M., & Becker, T. (2021). Gelatinization or Pasting? The Impact of Different Temperature Levels on the Saccharification Efficiency of Barley Malt Starch. In Foods (Vol. 10, Issue 8, p. 1733). MDPI AG. https://doi.org/10.3390/foods10081733

28. Yuan, J., Wang, X., Yin, D., Wang, M., Yin, X., Lei, Z., & Guo, Y. (2017). Effect of different amylases on the utilization of cornstarch in broiler chickens. In Poultry Science (Vol. 96, Issue 5, pp. 1139–1148). Elsevier BV. https://doi.org/10.3382/ps/pew323

29. Barbosa, M. S., Freire, C. C. C., Almeida, L. C., Freitas, L. S., Souza, R. L., Pereira, E. B., Mendes, A. A., Pereira, M. M., Lima, Á. S., & Soares, C. M. F. (2019). Optimization of the enzymatic hydrolysis of Moringa oleifera Lam oil using molecular docking analysis for fatty acid specificity. In Biotechnology and Applied Biochemistry (Vol. 66, Issue 5, pp. 823–832). Wiley. https://doi.org/10.1002/bab.1793

30. Souza, G. P. R., Correia, T. B. A., Reis, W. S. M., Bredda, E. H., Da Rós, P. C. M., & Pereira, E. B. (2022). Enzymatic Hydrolysis of Waste Cooking Oil by Lipase Catalysis: Simplex Mixture Design Optimization. In Catalysis Letters (Vol. 153, Issue 3, pp. 689–697). Springer Science and Business Media LLC. https://doi.org/10.1007/s10562-022-04025-z

31. Qiao, H., Zhang, F., Guan, W., Zuo, J., & Feng, D. (2016). Optimisation of combi-lipases from Aspergillus niger for the synergistic and efficient hydrolysis of soybean oil. In Animal Science Journal (Vol. 88, Issue 5, pp. 772–780). Wiley. https://doi.org/10.1111/asj.12718

32. HIRAYAMA, O. (1964). Glyceride Structure and Biosynthesis of Natural Fats. In Agricultural and Biological Chemistry (Vol. 28, Issue 4, pp. 193–200). Oxford University Press (OUP). https://doi.org/10.1271/bbb1961.28.193

33. Jensen, R. G., Sampugna, J., & Pereira, R. L. (1964). Intermolecular Specificity of Pancreatic Lipase and the Structural Analysis of Milk Triglycerides. In Journal of Dairy Science (Vol. 47, Issue 7, pp. 727–732). American Dairy Science Association. https://doi.org/10.3168/jds.s0022-0302(64)88753-1

34. Lim, S. Y., Steiner, J. M., & Cridge, H. (2022). Lipases: it's not just pancreatic lipase! In American Journal of Veterinary Research (Vol. 83, Issue 8). American Veterinary Medical Association (AVMA). https://doi.org/10.2460/ajvr.22.03.0048

35. Xiao, X., & Lowe, M. E. (2015). The β5-Loop and Lid Domain Contribute to the Substrate Specificity of Pancreatic Lipase-related Protein 2 (PNLIPRP2). In Journal of Biological Chemistry (Vol. 290, Issue 48, pp. 28847–28856). Elsevier BV. https://doi.org/10.1074/jbc.m115.683375

36. Qamar, S. A., Qamar, M., Bilal, M., Bharagava, R. N., Ferreira, L. F. R., Sher, F., & Iqbal, H. M. N. (2021). Cellulose-deconstruction potential of nano-biocatalytic systems: A strategic drive from designing to sustainable applications of immobilized cellulases. In International Journal of Biological Macromolecules (Vol. 185, pp. 1–19). Elsevier BV. https://doi.org/10.1016/j.ijbiomac.2021.06.079

37. Zajki-Zechmeister, K., Kaira, G. S., Eibinger, M., Seelich, K., & Nidetzky, B. (2021). Processive Enzymes Kept on a Leash: How Cellulase Activity in Multienzyme Complexes Directs Nanoscale Deconstruction of Cellulose. In ACS Catalysis (Vol. 11, Issue 21, pp. 13530–13542). American Chemical Society (ACS). https://doi.org/10.1021/acscatal.1c03465

38. Berlemont, R. (2022). The Potential for Cellulose Deconstruction in Fungal Genomes. In Encyclopedia (Vol. 2, Issue 2, pp. 990–1003). MDPI AG. https://doi.org/10.3390/encyclopedia2020065

39. Resch, M. G., Donohoe, B. S., Baker, J. O., Decker, S. R., Bayer, E. A., Beckham, G. T., & Himmel, M. E. (2013). Fungal cellulases and complexed cellulosomal enzymes exhibit synergistic mechanisms in cellulose

deconstruction. In Energy & Environmental Science (Vol. 6, Issue 6, p. 1858). Royal Society of Chemistry (RSC). https://doi.org/10.1039/c3ee00019b

40. You, C., Liu, Y.-J., Cui, Q., & Feng, Y. (2023). Glycoside Hydrolase Family 48 Cellulase: A Key Player in Cellulolytic Bacteria for Lignocellulose Biorefinery. In Fermentation (Vol. 9, Issue 3, p. 204). MDPI AG. https://doi.org/10.3390/fermentation9030204

41. Halliwell, G., & Griffin, M. (1973). The nature and mode of action of the cellulolytic component C1 of Trichoderma koningii on native cellulose. In Biochemical Journal (Vol. 135, Issue 4, pp. 587–594). Portland Press Ltd. https://doi.org/10.1042/bj1350587

42. Venezia, V., Califano, V., Pota, G., Costantini, A., Landi, G., & Di Benedetto, A. (2020). CFD Simulations of Microreactors for the Hydrolysis of Cellobiose to Glucose by β-Glucosidase Enzyme. In Micromachines (Vol. 11, Issue 9, p. 790). MDPI AG. https://doi.org/10.3390/mi11090790

43. Yepes, C., Estévez, J., Arroyo, M., & Ladero, M. (2022). Immobilization of an Industrial β-Glucosidase from Aspergillus fumigatus and Its Use for Cellobiose Hydrolysis. In Processes (Vol. 10, Issue 6, p. 1225). MDPI AG. https://doi.org/10.3390/pr10061225

44. Wei, H., Wang, W., Alper, H. S., Xu, Q., Knoshaug, E. P., Van Wychen, S., Lin, C.-Y., Luo, Y., Decker, S. R., Himmel, M. E., & Zhang, M. (2019). Ameliorating the Metabolic Burden of the Co-expression of Secreted Fungal Cellulases in a High Lipid-Accumulating Yarrowia lipolytica Strain by Medium C/N Ratio and a Chemical Chaperone. In Frontiers in Microbiology (Vol. 9). Frontiers Media SA. https://doi.org/10.3389/fmicb.2018.03276

45. Wang, J., Liu, S., Li, Y., Wang, H., Xiao, S., Li, C., & Liu, B. (2017). Central carbon metabolism influences cellulase production in Bacillus licheniformis. In Letters in Applied Microbiology (Vol. 66, Issue 1, pp. 49–54). Oxford University Press (OUP). https://doi.org/10.1111/lam.12813

46. Sultana, S., Sawrav, Md. S. S., Das, S. R., Alam, M., Aziz, Md. A., Hossain, Md. A.-A., & Haque, Md. A. (2022). Isolation and Biochemical Characterization of Cellulase Producing Goat Rumen Bacteria. In Proceedings of International Conference on Emerging Trends in Engineering and Advanced Science. International Conference on Emerging Trends in Engineering and Advanced Science. AIJR Publisher. https://doi.org/10.21467/proceedings.123.12

47. Singh Jadaun, J. (2018). Pectinase: A Useful Tool in Fruit Processing Industries. In Nutrition & Food Science International Journal (Vol. 5, Issue 5). Juniper Publishers. https://doi.org/10.19080/nfsij.2018.05.555673

48. Adapa, V., Ramya, L. N., Pulicherla, K. K., & Rao, K. R. S. S. (2014). Cold Active Pectinases: Advancing the Food Industry to the Next Generation. In Applied Biochemistry and Biotechnology (Vol. 172, Issue 5, pp. 2324–2337). Springer Science and Business Media LLC. https://doi.org/10.1007/s12010-013-0685-1

49. Satapathy, S., Rout, J. R., Kerry, R. G., Thatoi, H., & Sahoo, S. L. (2020). Biochemical Prospects of Various Microbial Pectinase and Pectin: An Approachable Concept in Pharmaceutical Bioprocessing. In Frontiers in Nutrition (Vol. 7). Frontiers Media SA. https://doi.org/10.3389/fnut.2020.00117

50. Haile, S., & Ayele, A. (2022). Pectinase from Microorganisms and Its Industrial Applications. In S. Rodriguez-Couto (Ed.), The Scientific World Journal (Vol. 2022, pp. 1–15). Hindawi Limited. https://doi.org/10.1155/2022/1881305

51. Wormit, A., & Usadel, B. (2018). The Multifaceted Role of Pectin Methylesterase Inhibitors (PMEIs). In International Journal of Molecular Sciences (Vol. 19, Issue 10, p. 2878). MDPI AG. https://doi.org/10.3390/ijms19102878

52. Biz, A., Farias, F. C., Motter, F. A., de Paula, D. H., Richard, P., Krieger, N., & Mitchell, D. A. (2014). Pectinase Activity Determination: An Early Deceleration in the Release of Reducing Sugars Throws a Spanner in the Works! In V. N. Uversky (Ed.), PLoS ONE (Vol. 9, Issue 10, p. e109529). Public Library of Science (PLoS). https://doi.org/10.1371/journal.pone.0109529

53. Wu, H.-C., Bulgakov, V. P., & Jinn, T.-L. (2018). Pectin Methylesterases: Cell Wall Remodeling Proteins Are Required for Plant Response to Heat Stress. In Frontiers in Plant Science (Vol. 9). Frontiers Media SA. https://doi.org/10.3389/fpls.2018.01612

54. Yadav, S., Yadav, P. K., Yadav, D., & Yadav, K. D. S. (2009). Pectin lyase: A review. In Process Biochemistry (Vol. 44, Issue 1, pp. 1–10). Elsevier BV. https://doi.org/10.1016/j.procbio.2008.09.012

55. Biz, A., Farias, F. C., Motter, F. A., de Paula, D. H., Richard, P., Krieger, N., & Mitchell, D. A. (2014). Pectinase Activity Determination: An Early Deceleration in the Release of Reducing Sugars Throws a Spanner in the Works! In V. N. Uversky (Ed.), PLoS ONE (Vol. 9, Issue 10, p. e109529). Public Library of Science (PLoS). https://doi.org/10.1371/journal.pone.0109529

56. Toy, J. Y. H., Lu, Y., Huang, D., Matsumura, K., & Liu, S.-Q. (2020). Enzymatic treatment, unfermented and fermented fruit-based products: current state of knowledge. In Critical Reviews in Food Science and

Nutrition (Vol. 62, Issue 7, pp. 1890–1911). Informa UK Limited. https://doi.org/10.1080/10408398.2020.1848788

57. Keggi, C., & Doran-Peterson, J. (2020). The Homogalacturonan Deconstruction System of Paenibacillus amylolyticus 27C64 Requires No Extracellular Pectin Methylesterase and Has Significant Industrial Potential. In E. R. Master (Ed.), Applied and Environmental Microbiology (Vol. 86, Issue 12). American Society for Microbiology. https://doi.org/10.1128/aem.02275-19

58. Zhao, Li-li., Tian, CH-r., Hua, J. I., & Shuang, L. (2007). Research Actuality of Microbe Pectinases and its Application in Fruits and Vegetables Processing. In Progress in Modern Biomedicine (Issue 6, pp. 951–953). Ministry of Science and Technology of China Statistic.

59. Duvetter, T., Sila, D. N., Van Buggenhout, S., Jolie, R., Van Loey, A., & Hendrickx, M. (2009). Pectins in Processed Fruit and Vegetables: Part I—Stability and Catalytic Activity of Pectinases. In Comprehensive Reviews in Food Science and Food Safety (Vol. 8, Issue 2, pp. 75–85). Wiley. https://doi.org/10.1111/j.1541-4337.2009.00070.x

60. Rafique, N., Bashir, S., Khan, M. Z., Hayat, I., Orts, W., & Wong, D. W. S. (2021). Metabolic engineering of Bacillus subtilis with an endopolygalacturonase gene isolated from Pectobacterium. carotovorum; a plant pathogenic bacterial strain. In K. S. Ahmad (Ed.), PLOS ONE (Vol. 16, Issue 12, p. e0256562). Public Library of Science (PLoS). https://doi.org/10.1371/journal.pone.0256562

61. Hashim, H., Maskat, M. Y., Mustapha, W. A. W., Mamot, S., & Saadiah, I. (2013). Optimization of enzymatic hydrolysis of cockle (Anadara Granosa) meat wash water precipitate for the development of seafood flavor. In International Food Research Journal (Vol. 20, Issue 6, pp. 3053–3059). Universiti Putra Malaysia.

62. Dong, Y., Yan, W., Zhang, X.-D., Dai, Z.-Y., & Zhang, Y.-Q. (2021). Steam Explosion-Assisted Extraction of Protein from Fish Backbones and Effect of Enzymatic Hydrolysis on the Extracts. In Foods (Vol. 10, Issue 8, p. 1942). MDPI AG. https://doi.org/10.3390/foods10081942

63. Liang, X., Qian, G., Yang, H., Chen, N., Ai, Z., Xing, Y., Huang, W., Xu, L., Li, M., Wang, Z., Zheng, Y., & Yue, X. (2023). Evaluation of IgG/IgE-binding capacity and functional properties of enzymatic hydrolysis in skimmed cow milk system. In Journal of Food Science (Vol. 88, Issue 7, pp. 2780–2795). Wiley. https://doi.org/10.1111/1750-3841.16579

64. Fang, Fu-y., Miao, Y-l., & Song, W-d. (2009). Compound Enzymatic Hydrolysis of Paphia undulate Meat and Development of Its Functional Oral Liquid. In Food Science (Vol. 30, Issue 18, pp. 412–415). China Food Publishing Co.

65. Izadyar, L., Friboulet, A., Remy, M. H., Roseto, A., & Thomas, D. (1993). Monoclonal anti-idiotypic antibodies as functional internal images of enzyme active sites: production of a catalytic antibody with a cholinesterase activity. In Proceedings of the National Academy of Sciences (Vol. 90, Issue 19, pp. 8876–8880). Proceedings of the National Academy of Sciences. https://doi.org/10.1073/pnas.90.19.8876

66. Lu, J., Jiang, X., Zhen, L., Luan, H.-F., Chen, H., Wang, X.-J., & Ching, C.-B. (2010). Cloning, expression, purification and characterization of the carboxylesterase Yeig from Escherichia coli k12. In African Journal of Microbiology Research (Vol. 4, Issue 9, pp. 757–765). Academic Journals.

67. Inagami, T., & Mitsuda, H. (1964). The Mechanism of the Specificity of Trypsin Catalysis. In Journal of Biological Chemistry (Vol. 239, Issue 5, pp. 1388–1394). Elsevier BV. https://doi.org/10.1016/s0021-9258(18)91326-8

68. Navanietha Krishnaraj, R., David, A., & Sani, R. K. (2017). Fundamentals of Enzymatic Processes. In Extremophilic Enzymatic Processing of Lignocellulosic Feedstocks to Bioenergy (pp. 5–29). Springer International Publishing. https://doi.org/10.1007/978-3-319-54684-1_2

69. Lingenfelder, M., Tomba, G., Costantini, G., Colombi Ciacchi, L., De Vita, A., & Kern, K. (2007). Tracking the Chiral Recognition of Adsorbed Dipeptides at the Single-Molecule Level. In Angewandte Chemie International Edition (Vol. 46, Issue 24, pp. 4492–4495). Wiley. https://doi.org/10.1002/anie.200700194

70. Pan, R., Zhang, X.-J., Zhang, Z.-J., Zhou, Y., Tian, W.-X., & He, R.-Q. (2010). Substrate-induced Changes in Protease Active Site Conformation Impact on Subsequent Reactions with Substrates. In Journal of Biological Chemistry (Vol. 285, Issue 30, pp. 22950–22956). Elsevier BV. https://doi.org/10.1074/jbc.m110.103549

71. Venditto, I., Najmudin, S., Luís, A. S., Ferreira, L. M. A., Sakka, K., Knox, J. P., Gilbert, H. J., & Fontes, C. M. G. A. (2015). Family 46 Carbohydrate-binding Modules Contribute to the Enzymatic Hydrolysis of Xyloglucan and β-1,3–1,4-Glucans through Distinct Mechanisms. In Journal of Biological Chemistry (Vol. 290, Issue 17, pp. 10572–10586). Elsevier BV. https://doi.org/10.1074/jbc.m115.637827

72. Venditto, I., Najmudin, S., Luís, A. S., Ferreira, L. M. A., Sakka, K., Knox, J. P., Gilbert, H. J., & Fontes, C. M. G. A. (2015). Family 46 Carbohydrate-binding Modules Contribute to the Enzymatic Hydrolysis of

Xyloglucan and β-1,3–1,4-Glucans through Distinct Mechanisms. In Journal of Biological Chemistry (Vol. 290, Issue 17, pp. 10572–10586). Elsevier BV. https://doi.org/10.1074/jbc.m115.637827

73. Morgillo, C. M., Lupia, A., Deplano, A., Pirone, L., Fiorillo, B., Pedone, E., Luque, F. J., Onnis, V., Moraca, F., & Catalanotti, B. (2022). Molecular Basis for Non-Covalent, Non-Competitive FAAH Inhibition. In International Journal of Molecular Sciences (Vol. 23, Issue 24, p. 15502). MDPI AG. https://doi.org/10.3390/ijms232415502

74. Kisselev, A. F., Akintola, O., & Smith, J. (2021). Abstract 1396: Non-competitive inhibition of proteasome by kinase inhibitors. In Cancer Research (Vol. 81, Issue 13_Supplement, pp. 1396–1396). American Association for Cancer Research (AACR). https://doi.org/10.1158/1538-7445.am2021-1396

75. Sanchez, O. F., Lee, J., Yu King Hing, N., Kim, S.-E., Freeman, J. L., & Yuan, C. (2017). Lead (Pb) exposure reduces global DNA methylation level by non-competitive inhibition and alteration of dnmt expression. In Metallomics (Vol. 9, Issue 2, pp. 149–160). Oxford University Press (OUP). https://doi.org/10.1039/c6mt00198j

76. Cole, R. N., Chen, W., Pascal, L. E., Nelson, J. B., Wipf, P., & Wang, Z. (2022). (+)-JJ-74–138 is a Novel Noncompetitive Androgen Receptor Antagonist. In Molecular Cancer Therapeutics (Vol. 21, Issue 4, pp. 483–492). American Association for Cancer Research (AACR). https://doi.org/10.1158/1535-7163.mct-21-0432

77. Mondal, A., Bhat, I. A., Karunakaran, S., & De, M. (2021). Supramolecular Interaction of Molecular Cage and β-Galactosidase: Application in Enzymatic Inhibition, Drug Delivery and Antimicrobial Activity. In ChemBioChem (Vol. 22, Issue 11, pp. 1955–1960). Wiley. https://doi.org/10.1002/cbic.202100008

78. Sampedro, L. J. G., Grimaldos, N. A. G., Pereañez, J. A., & Montoya, J. E. Z. (2019). Lipids as competitive inhibitors of subtilisin carlsberg in the enzymatic hydrolysis of proteins in red tilapia (oreochromis sp.) viscera: insights from kinetic models and a molecular docking study. In Brazilian Journal of Chemical Engineering (Vol. 36, Issue 2, pp. 647–655). FapUNIFESP (SciELO). https://doi.org/10.1590/0104-6632.20190362s20180346

79. Brazdausks, P., Godina, D., & Puke, M. (2023). Phosphorus-Containing Catalyst Impact on Furfural and Glucose Production during Consecutive Hydrothermal Pretreatment and Enzymatic Hydrolysis. In Fermentation (Vol. 9, Issue 9, p. 803). MDPI AG. https://doi.org/10.3390/fermentation9090803

80. ZHANG, R.-H., HU, Q.-Z., KANG, Q., QI, L.-B., PANG, Y.-P., & YU, L. (2021). Research on Competitive Enzymatic Hydrolysis-Assisted Liquid Crystal-based Acetylcholine Sensor. In Chinese Journal of Analytical Chemistry (Vol. 49, Issue 2, pp. e21014–e21019). Elsevier BV. https://doi.org/10.1016/s1872-2040(20)60081-0

81. Padron-Regalado, E., Mejía-Olvera, E. E., Marruffo-Carmona, A. M., Solís-Suárez, J. C., Peralta-Agapito, D., & Medina-Rivero, E. (2023). Efficient enzymatic hydrolysis for enriching the antioxidant content of agro-food industrial residues. In JSFA reports (Vol. 3, Issue 9, pp. 420–428). Wiley. https://doi.org/10.1002/jsf2.145

82. Areeya, S., Tawai, A., & Sriariyanun, M. (2020). Model-Based Control for Fed-Batch Enzymatic Hydrolysis Reactor of Lignocellulosic Biomass. In 2020 6th International Conference on Control, Automation and Robotics (ICCAR). 2020 6th International Conference on Control, Automation and Robotics (ICCAR). IEEE. https://doi.org/10.1109/iccar49639.2020.9108066

83. Baranwal, J., Lhospice, S., Kanade, M., Chakraborty, S., Gade, P. R., Harne, S., Herrou, J., Mignot, T., & Gayathri, P. (2019). Allosteric regulation of a prokaryotic small Ras-like GTPase contributes to cell polarity oscillations in bacterial motility. In A. M. Stock (Ed.), PLOS Biology (Vol. 17, Issue 9, p. e3000459). Public Library of Science (PLoS). https://doi.org/10.1371/journal.pbio.3000459

84. Guzmán-Ortiz, F. A., Castro-Rosas, J., Gómez-Aldapa, C. A., Mora-Escobedo, R., Rojas-León, A., Rodríguez-Marín, M. L., Falfán-Cortés, R. N., & Román-Gutiérrez, A. D. (2018). Enzyme activity during germination of different cereals: A review. In Food Reviews International (Vol. 35, Issue 3, pp. 177–200). Informa UK Limited. https://doi.org/10.1080/87559129.2018.1514623

85. Chang-po, S. (2013). Study on the factors to affect the activity of zearalenone degrading enzyme ZLHY6. In Science and Technology of Cereals, Oils and Foods. National Food Authority only non-profit research institutions - Academy of State Grain Administration.

86. BravoRodriguez, V., JuradoAlameda, E., MartinezGallegos, J. F., ReyesRequena, A., & GarciaLopez, A. I. (2006). Enzymatic Hydrolysis of Soluble Starch with an α-Amylase from Bacillus licheniformis. In Biotechnology Progress (Vol. 22, Issue 3, pp. 718–722). Wiley. https://doi.org/10.1021/bp060057a

87. Donovan, J. W., & Hansen, L. U. (1971). The β-n-acetylglucosaminidase activity of egg white. 1. Kinetics of the Reaction and Determination of the Factors Affecting the Stability of the Enzyme in Egg White. In

Journal of Food Science (Vol. 36, Issue 1, pp. 174–177). Wiley. https://doi.org/10.1111/j.1365-2621.1971.tb02063.x

88. Nazarov, K., Sagdiyev, X., Shukurxonova, M., & Karimova, K. (2022). Features of enzymatic hydrolysis of fibers of genetically different cotton lines. In S. Sadullozoda, Z. Usmanov, & A. Gibadullin (Eds.), International Conference on Remote Sensing of the Earth: Geoinformatics, Cartography, Ecology, and Agriculture (RSE 2022). SPIE. https://doi.org/10.1117/12.2643189

89. Vogelsang-O'Dwyer, M., Sahin, A. W., Arendt, E. K., & Zannini, E. (2022). Enzymatic Hydrolysis of Pulse Proteins as a Tool to Improve Techno-Functional Properties. In Foods (Vol. 11, Issue 9, p. 1307). MDPI AG. https://doi.org/10.3390/foods11091307

90. Saini, R., Patel, A. K., Saini, J. K., Chen, C.-W., Varjani, S., Singhania, R. R., & Di Dong, C. (2022). Recent advancements in prebiotic oligomers synthesis via enzymatic hydrolysis of lignocellulosic biomass. In Bioengineered (Vol. 13, Issue 2, pp. 2139–2172). Informa UK Limited. https://doi.org/10.1080/21655979.2021.2023801

91. Sharikov, A., Amelyakina, M., Serba, E., Ivanov, V., Polivanovskaya, D., & Abramova, I. (2022). Steam Extraction System Use in the Gluten-Free Cereal Snacks Technology. In Food Industry (Vol. 7, Issue 4, pp. 6–14). Ural State University of Economics. https://doi.org/10.29141/2500-1922-2022-7-4-1

92. Sharikov, A. Yu., Ivanov, V. V., Sokolova, E. N., Amelyakina, M. V., & Serba, E. (2023). Technological aspects of obtaining gluten-free cereal products based on biocatalytic and hydrothermomechanical processes. In Proceedings of the 1st International Congress "The Latest Achievements of Medicine, Healthcare, and Health-Saving Technologies." I International Congress "The Latest Achievements of Medicine, Healthcare, and Health-Saving Technologies." Kemerovo State University. https://doi.org/10.21603/-i-ic-152

93. Medvid, I., Shydlovska, O., & Dotsenko, V. (2019). The use of sunflower lecithin in the technology on gluten-free bread with enzymatic modification of flour starch. In Journal of Faculty of Food Engineering (Vol. 17, Issue 4, pp. 352–362). Stefan cel Mare University of Suceava.

94. Kroghsbo, S., Andersen, N. B., Rasmussen, T. F., Jacobsen, S., & Madsen, C. B. (2014). Acid Hydrolysis of Wheat Gluten Induces Formation of New Epitopes but Does Not Enhance Sensitizing Capacity by the Oral Route: A Study in "Gluten Free" Brown Norway Rats. In N. J. Mantis (Ed.), PLoS ONE (Vol. 9, Issue 9, p. e107137). Public Library of Science (PLoS). https://doi.org/10.1371/journal.pone.0107137

95. Dotsenko, V., Medvid, I., Shydlovska, O., & Ishchenko, T. (2019). Studying the possibility of using enzymes, lecithin, and albumen in the technology of gluten-free bread. In Eastern-European Journal of Enterprise Technologies (Vol. 1, Issue 11 (97), pp. 42–51). Private Company Technology Center. https://doi.org/10.15587/1729-4061.2019.154957

96. Espinoza-Herrera, J., Martínez, L. M., Serna-Saldívar, S. O., & Chuck-Hernández, C. (2021). Methods for the Modification and Evaluation of Cereal Proteins for the Substitution of Wheat Gluten in Dough Systems. In Foods (Vol. 10, Issue 1, p. 118). MDPI AG. https://doi.org/10.3390/foods10010118

97. Wang, J., Bai, H., Zhang, R., Ding, G., Cai, X., Wang, W., Zhu, G., Zhou, P., & Zhang, Y. (2023). Effect of a Bacterial Laccase on the Quality and Micro-Structure of Whole Wheat Bread. In Journal of Microbiology and Biotechnology (Vol. 33, Issue 12, pp. 1671–1680). Korean Society for Microbiology and Biotechnology. https://doi.org/10.4014/jmb.2305.05008

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Contact Address:

Dinara Akimova, Shakarim University, Department of Food technology and biotechnology, 20A Glinki Street, 071412, Semey, Kazakhstan; Kazakh Research Institute of Processing and Food Industry (Semey Branch), 29 Bairursynov Street, 071410, Semey, Kazakhstan,
Tel.: + 7 7222 314 602; +7 7222 770026
E-mail: akdilife@mail.ru
ORCID: https://orcid.org/0000-0001-8922-2854

Aitbek Kakimov, Shakarim University, Department of Food technology and biotechnology, 20A Glinki Street, 071412, Semey, Kazakhstan,
Tel.: + 7 7222 314 602
E-mail: bibi.53@mail.ru
ORCID: https://orcid.org/0000-0002-9607-1684

***Anuarbek Suychinov**, Kazakh Research Institute of Processing and Food Industry (Semey Branch), 29 Bairursynov Street, 071410, Semey, Kazakhstan,
Tel.: +7 7222 770026
E-mail: asuychinov@gmail.com
ORCID: https://orcid.org/0000-0003-4862-3293

Zhumatay Urazbayev, Kazakh Research Institute of Processing and Food Industry, Gagarin Ave., 238 "G", 050060, Almaty, Kazakhstan,
Tel.: +7 7222 770026
E-mail: sb.info@rpf.kz
ORCID: https://orcid.org/0000-0003-1898-0564

Yerlan Zharykbasov, Shakarim University, Department of Food technology and biotechnology, 20A Glinki Street, 071412, Semey, Kazakhstan,
Tel.: + 7 7222 314 602
E-mail: erlan-0975@mail.ru
ORCID: https://orcid.org/0000-0001-9707-0539

Nadir Ibragimov, Shakarim University, Department of Technological Equipment and Mechanical Engineering, 20A Glinki Street, 071412, Semey, Kazakhstan,
Tel.: + 7 7222 314 602
E-mail: ibragimnk@mail.ru
ORCID: https://orcid.org/0000-0001-9607-823X

Aigul Bauyrzhanova, Shakarim University, Department of Food technology and biotechnology, 20A Glinki Street, 071412, Semey, Kazakhstan,
Tel.: + 7 7222 314 602
E-mail: bauyrzhanova@shakarim.kz
ORCID: https://orcid.org/0009-0007-5031-8411

Assiya Utegenova, Shakarim University, Department of Food technology and biotechnology, 20A Glinki Street, 071412, Semey, Kazakhstan,
Tel.: + 7 7222 314 602
E-mail: asia_aksu@mail.ru
ORCID: https://orcid.org/0000-0003-3378-6815

Corresponding author: *