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Protein Biosynthesis in Microorganisms: Mechanisms, Regulation, and Biotechnological Applications

Mustapha Abdulsalam *, Ahmad Tofa Salihu, Halima Yahaya Usman and Maryam Yahaya Usman

Department of Microbiology, School of Science and Technology, Skyline University Nigeria.

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Abstract

Protein biosynthesis in microorganisms is an essential process with in-depth implications in microbiology and biotechnology. This study aims to explore the mechanisms, regulations, applications, and prospects of this fundamental biological process. The objective was to provide a holistic understanding of protein biosynthesis, encompassing its mechanisms, regulation, and biotechnological relevance. In addressing the research problem, this study identifies a research gap while research has extensively covered aspects of translation in microorganisms, a notable gap exists in comprehending the consequences of ribosome pausing and mistranslation during translation elongation. While translation initiation and termination fidelity have gained attention, elongation fidelity is still a new area of study. Key discoveries include new insights into protein biosynthesis methods, the importance of regulatory elements such as riboswitches, and the possibility of precision engineering via synthetic biology. Surprisingly, effective biotechnological uses are highlighted, such as recombinant protein manufacturing and biofuel synthesis. Recommendations emphasize the need for further study in translational fidelity during elongation, precision engineering, and multi-omics integration. With advances in synthetic biology, single-cell technologies, and artificial intelligence applications, the future of protein biosynthesis research seems promising. Protein biosynthesis in microorganisms, on the other hand, is crucial to cellular life and holds great potential for biotechnological applications. This study is a great resource for academics, educators, and practitioners, providing insights into addressing microbiological and biotechnological difficulties through the use of protein biosynthesis.

Keywords: Protein biosynthesis; Microorganisms; Translational fidelity; Synthetic biology; Biotechnological applications

1. Introduction

Protein biosynthesis in microbes has been studied for decades, and there have been some pivotal moments in this regard. In 1961, Marshall Nirenberg and J. Heinrich Matthaei discovered the first codon – UUU which indicated the amino acid phenylalanine thereby revealing the genetic code. Therefore, this monumental discovery allowed us to understand the process by which genetic information is translated to proteins [1]. For decades, the protein production process over the years has exposed several important mechanisms like ribosome formation, mRNA processing process, and the discovery of transfer RNA (tRNA). It allows scientists to understand how the complex dance of molecular machinery occurs during the translation [2]. Microorganism protein synthesis cannot be taken for granted. Microorganisms play an essential role in biological technology, pharmaceutical, and ecological industries [3]. Monoclonal cells are important in the biopharmaceutical industry, where they play as horses working for insulin, vaccines, and high-yield protein biosynthesis. However, microorganisms are important players because they can be engineered to convert renewable resources into biofuels [4]. For example, microorganisms are applied in environmental studies for bioremediation which means the cleansing of polluted districts [5]. Protein biosynthesizing

* Corresponding author: Mustapha Abdulsalam

and its effect on pathogenicity could also shed light on microbial pathogenicity. The use of different proteins in the production of the pathogenic microbe gives treatment options.

This study seeks to review the mechanisms of protein synthesis in bacteria, control strategies, and potential industrial applications. This study will synthesize and analyze existing research and assess the extent to which this will address identified research gaps. By achieving this goal, the study hopes to be a useful resource for researchers, students, and practitioners in microbiology, biotechnology, and related fields. It also strives to bring together diverse disciplines that would help develop new ways of producing quality proteins and addressing bacterial problems that may cause damage. This study is a significant tool for increasing knowledge and development in the study and use of protein production in microorganisms.

2. Statement of the Problem

The study addresses a critical research gap and hurdles that impede the capacity to harness microorganisms for the efficient production of proteins with high translational fidelity. These challenges encompass the imperative to unravel the mechanisms governing translational accuracy, optimize regulatory networks, surmount biotechnological constraints, and navigate the intricacies of ethical and regulatory considerations. Addressing these predicaments is imperative for unlocking the full potential of protein biosynthesis in microorganisms, thus propelling advancements in biotechnological applications, scientific understanding, and industrial processes.

3. Literature Review

3.1. Overview of Protein Biosynthesis

The body of literature on protein biosynthesis in microorganisms serves as a robust foundation, with a plethora of studies shedding light on the fundamental processes integral to translation. Pioneering work by [1] established the groundwork for comprehending the genetic code and the crucial concept of codon-anticodon recognition. The revelation of transfer RNA (tRNA) molecules and their role in ferrying amino acids to the ribosome further enriched our understanding [6]. These seminal findings have laid the bedrock for subsequent research endeavors in this field.

3.2. Transcription: The Central Process

Transcription, a precursor to translation, has been extensively documented in the literature. Researchers have delved into the intricate dynamics of RNA polymerase binding to DNA, investigating initiation, elongation, and termination processes. The contributions of [7,8] have significantly advanced our comprehension of RNA polymerase functionality and its regulation.

3.3. The Genetic Code

The genetic code stands as a cornerstone of research in protein biosynthesis. [9] provided initial insights into the triplet nature of the genetic code. The comprehensive decoding of the entire genetic code marked a monumental achievement [10]. Nevertheless, the field has primarily focused on exploring the universality of the genetic code, leaving room for further exploration into potential deviations from this code within microorganisms.

3.4. Ribosomes and tRNA

Ribosome structure and function have been subjects of extensive scrutiny, with the elucidation of ribosomal RNA (rRNA) secondary structure representing a major milestone [11]. The roles of ribosomal proteins and tRNA in ribosome function are well-documented. Yet, a deeper analysis of the structural dynamics of ribosomes in microorganisms and their correlation with translational accuracy may unveil an uncharted research avenue.

3.5. Initiation, Elongation, and Termination of Translation

Meticulous studies have probed the initiation, elongation, and termination phases of translation. The functions of initiation factors and release factors have been comprehensively described [12,13]. However, an emerging research gap pertains to the repercussions of ribosome pausing and mistranslation events during translation elongation, which could impact the ultimate quality and functionality of the synthesized protein.

4. Identified Research Gap

While extensive research has addressed numerous facets of translation in microorganisms, there is a conspicuous void in comprehending the implications of ribosome pausing and mistranslation events during translation elongation. Although the fidelity of translation initiation and termination has undergone thorough exploration [14], the fidelity during elongation represents an emerging area of interest. Recent studies, including the work by [15] have underscored the prevalence of ribosome pausing and its potential to trigger mistranslation and premature termination of protein synthesis. These findings highlight the question of how such occurrences affect protein quality and function. Given the paucity of attention given to this gap by academics, it represents an intriguing prospect for future research in the domain of protein production in microbes.

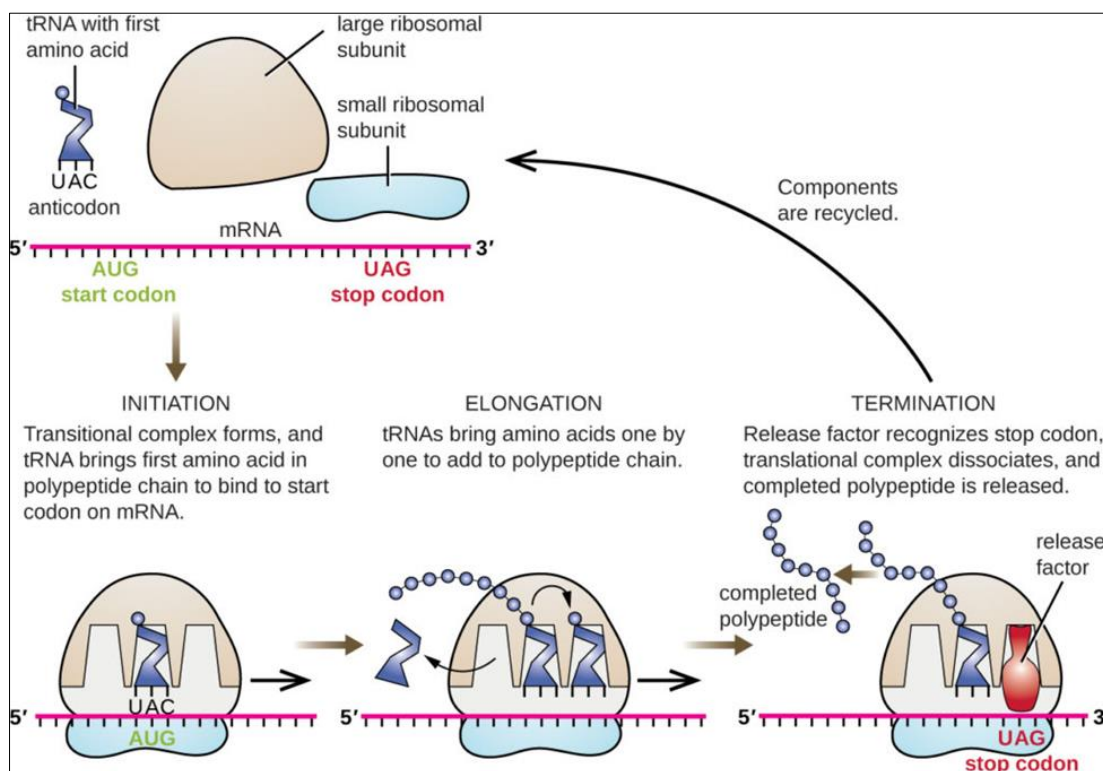
4.1. Filling the Research Gap

A multimodal approach might successfully address the research gap concerning the consequences of ribosome pausing and mistranslation during translation elongation in protein production in microorganisms. A thorough analysis can reveal how ribosome stalling and mistranslation events affect protein quality and functionality. The incorporation of controlled ribosome stalling and mistranslation experiments in a model micro-organism along with recent proteomic and structural investigations will provide more information about the impact these happenings exert on protein structure and function. Such research widens our knowledge about this issue and has applicability in terms of the protein industry as well as biotechnology. Further, this method allows for greater investigation of the evolutionary and ecological implications of microbial elongation fidelity. By doing so, we will achieve the full potential of microorganisms across various domains such as pharmaceutical, and biofuel, as well as in environmental pollution remediation.

5. Mechanisms of Protein Biosynthesis in Microorganisms

This section considers key principles of protein synthesis in microorganisms from transcription through protein biosynthesis.

5.1. Transcription and Translation



Source: <https://courses.lumenlearning.com/wm-biology1/chapter/prokaryotic-translation/>

Figure 1 In bacterial translation, the process starts with the initiation complex formation, comprising the small ribosomal subunit, mRNA, initiator tRNA with N-formyl-methionine, and initiation factors. Subsequently, the 50S subunit associates, forming a complete ribosome

Transcription and translation are the two necessary procedures during protein synthesis. In transcription, RNA polymerase transforms the DNA template into mRNA. The mRNA transports genetic information into ribosomes which is then converted into either eukaryotes' nuclei or prokaryotes' nuclei. It is a combined process whereby a set of ribosomes translates mRNA in the complementary base pairing of mRNA codon and tRNA [16]. This stage is important in understating how the genetic code is rightly translated into polypeptide chains. The first stage of bacterial translation starts with a commencement or pre-initiation phase. This stage comprises assembling the initiation complex that contains the small ribosomal subunit, mRNA, the initiator tRNA with N-formyl-methionine, and initiation factors [17]. This leads to the formation of functional ribosomes through 50S sub-unit bonding. This intact ribosome then advances to the elongation phase, where it moves along the mRNA, interpreting codons and facilitating the incorporation of corresponding amino acids brought by tRNA molecules. The process continues until a stop codon is encountered, signifying the termination of translation, as illustrated in Figure 1 below. At this juncture, the synthesized polypeptide is released from the ribosome, marking the end of the protein synthesis process. The meticulous orchestration of these steps ensures the precise translation of the genetic code into a functional protein.

5.2. The Role of RNA Polymerase

RNA polymerase, a critical enzyme in transcription, plays a pivotal role in the initiation, elongation, and termination of RNA synthesis. The initiation of transcription is initiated by the binding of RNA polymerase to the promoter region of a gene, a process regulated by various transcription factors and accessory proteins. This binding results in the synthesis of an mRNA strand complementary to the DNA template. The role of RNA polymerase is conserved across microorganisms and proves essential for the transcription of genes engaged in diverse cellular processes [18].

5.3. mRNA Processing

The expedition of mRNA processing involves a series of modifications to the initial transcript, known as pre-mRNA, to yield mature mRNA ready for translation. These modifications encompass capping, splicing, and polyadenylation. Capping at the 5' end entails the addition of a 7-methylguanosine cap, a pivotal step for mRNA stability and the initiation of translation. Splicing, conversely, involves the removal of introns (non-coding regions) and the joining of exons (coding regions) to craft a continuous coding sequence. Polyadenylation, at the 3' end, appends a poly-A tail, enhancing mRNA stability and facilitating export from the nucleus. An insightful understanding of these mRNA processing steps is acute for deciphering gene regulation and the control of protein expression in microorganisms [19].

5.4. Post-Translational Modifications

PTMs on four proteins which greatly change its structure and function. Processes such as phosphorylation, glycosylation, acetylation, and ubiquitination are referred to as PTMs. Such events as phosphorylation are also present in signal transduction pathways; microorganisms use them for response to the signals coming from outside and regulation of some inner biological process. Glycosylation may affect protein stability and interactions. PTM research must comprehend how bacteria utilize protein function optimization in response to shifting surroundings and for their stress management [20].

6. Post-translational Modifications

The following section explores different PTMs to microbial proteins. Therefore, this study examines chaperones and foldases functions, protein degradation, folding, processing, and maturation.

6.1. Protein Folding, Processing, and Maturation

Post-translational modification involves protein folding. Initially, Nascent polypeptide chains, which form in an unfolding and partly folded state, sometimes need complex modification. During and after translation proteins are subjected to complicated folding and ultimately lead to an active 3 dimensional structure structure. Chaperone proteins, such as GroEL-GroES in *Escherichia coli*, serve an important function in aiding polypeptide folding and inhibiting misfolding. Disulfide bond formation, glycosylation, and other alterations required for a protein's functional maturation are catalyzed by specialized enzymes. The timing and precision of these events hold paramount importance, as misfolded or incorrectly processed proteins can have detrimental effects on cellular function [21].

6.2. Role of Chaperones and Foldases

Chaperones and foldases emerge as indispensable agents guiding and facilitating the intricate process of protein folding and maturation. Molecular chaperones, including eminent figures like GroEL-GroES in bacteria, serve to prevent the misfolding and aggregation of nascent or denatured proteins. Foldases, typified by proteins like protein disulfide

isomerases (PDI), contribute to the formation and reshuffling of disulfide bonds, a pivotal process for protein stability and function. These specialized proteins ensure that the folding process transpires with accuracy and efficiency. Research conducted by [22] has unveiled the collaborative efforts of chaperones and foldases, revealing the intricate dance governing protein folding and the maintenance of cellular proteostasis.

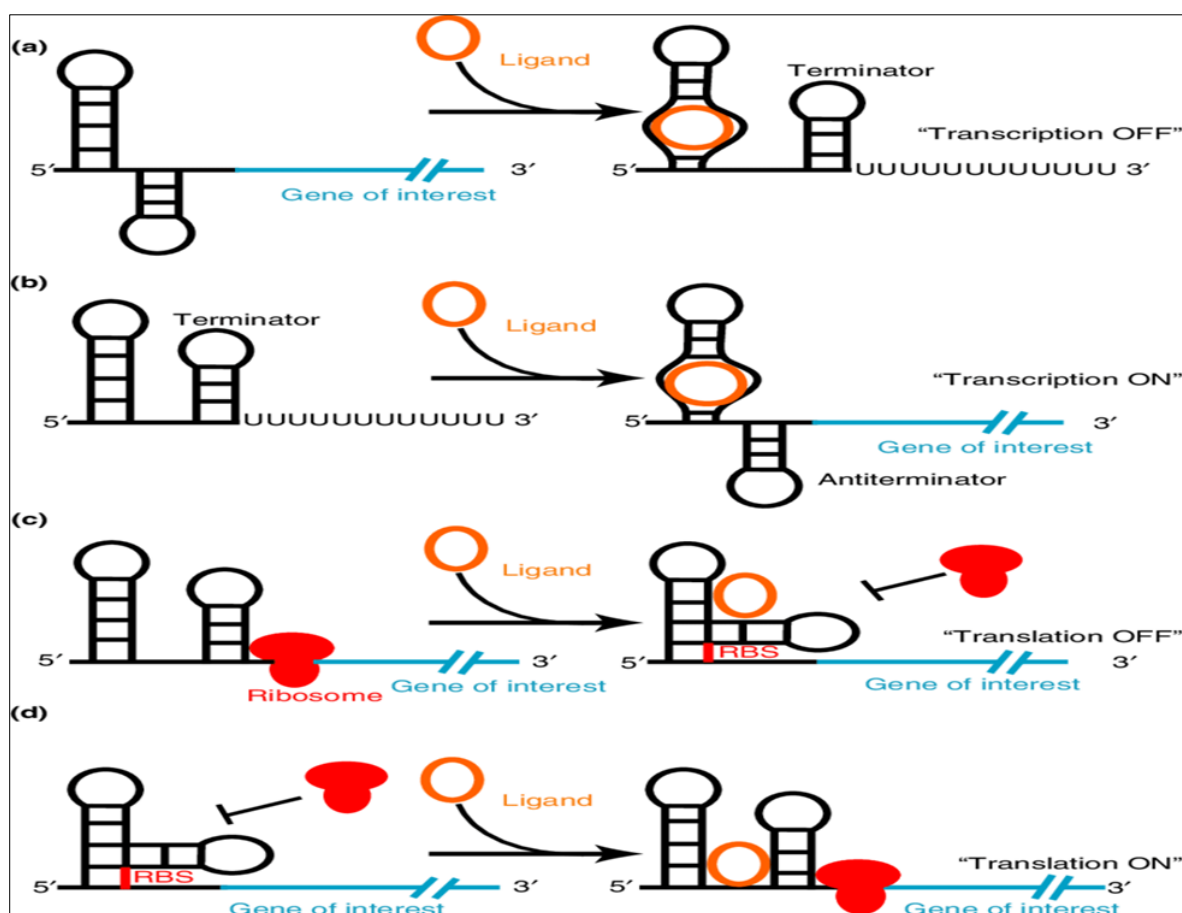
6.3. Protein Degradation and Turnover

Protein degradation and turnover represent essential mechanisms for maintaining cellular equilibrium and eliminating damaged or misfolded proteins. Microorganisms employ proteolytic systems, such as the proteasome and various proteases, to dismantle unwanted or malfunctioning proteins. For instance, the proteasome distinguishes and degrades proteins marked with ubiquitin, a small protein serving as a "degradation flag." Efficient protein turnover ensures the removal of potentially toxic proteins and recycles amino acids for new protein synthesis. Insights from research by [23] have significantly contributed to our understanding of the ubiquitin-proteasome system and its pivotal role in regulating protein degradation and turnover in microorganisms. However, post-translational modifications of proteins in microorganisms encompass crucial processes, including folding, processing, maturation, chaperone and foldase assistance, and protein degradation and turnover. These mechanisms are integral to the proper functioning of proteins, proteostasis, and overall cellular health. The exploration of these processes not only deepens our understanding of the fundamental biology of microorganisms but also unveils potential targets for biotechnological applications, drug development, and the elucidation of pathogenicity in microorganisms.

7. Regulation of Protein Biosynthesis

This section delves into the intricate regulatory mechanisms governing protein biosynthesis in microorganisms. It addresses multiple translational techniques and factors, such as the role of riboswitches and tiny RNAs, global regulators, stress responses, and feedback mechanisms that regulate protein synthesis.

7.1. Translational Regulation by Riboswitches and Small RNAs



Source: [26]

Figure 2 Schematic depiction of the mechanisms employed by riboswitches for gene expression regulation

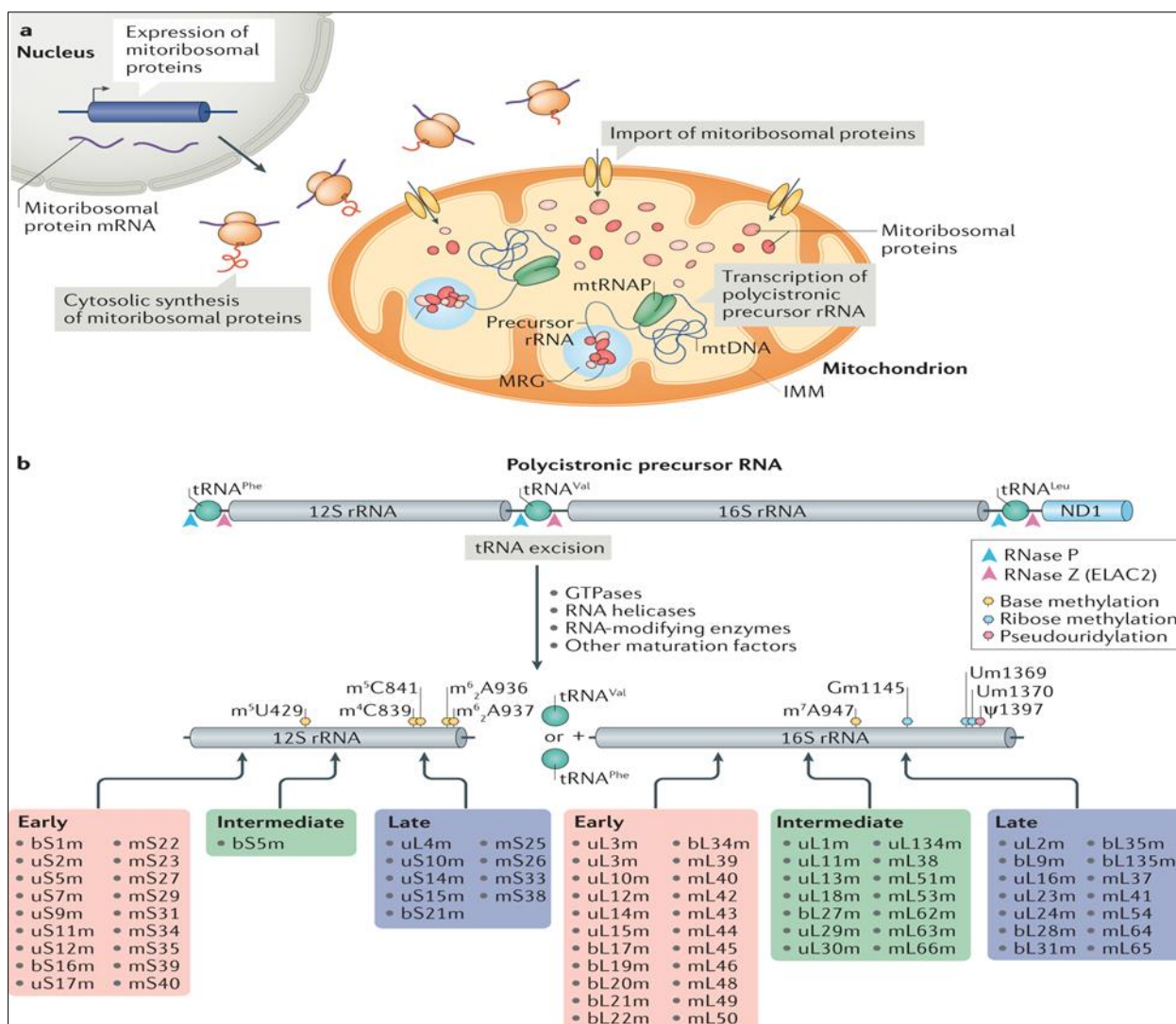
Riboswitches are mRNA molecule structural components that can directly control gene expression at the translational level in response to certain ligands. They are common in bacteria and govern a range of biological functions, including amino acid and coenzyme production. Small molecule binding to riboswitches causes structural changes in mRNA, which can either promote or impede translation start. Riboswitches in organisms such as *Bacillus subtilis* have been intensively researched, demonstrating how they allow bacteria to rapidly change their protein synthesis in response to environmental signals [24]. Similarly, small regulatory RNAs, such as microRNAs and small interfering RNAs, play pivotal roles in post-transcriptional regulation by guiding mRNA degradation or translational inhibition [25]. Riboswitches can be broadly classified into four categories based on their regulatory functions (a, b, c, d). They can either repress (a, c) or activate (b, d) gene expression. Transcriptional repression (a) occurs when riboswitches form a Rho-independent 'terminator' hairpin structure, leading to premature transcriptional termination. In contrast, gene activation (b) takes place when riboswitches adopt 'anti-terminator' secondary structures, preventing terminator formation and allowing the transcription of the complete message. Riboswitches can also repress the initiation of mRNA translation (c) by sequestering the Shine-Dalgarno (SD) ribosome-binding sequence (RBS) within a secondary structure, obstructing the small (30S) ribosomal subunit. On the other hand, exposing the RBS (d) facilitates binding by the 30S ribosomal subunit. In all cases, the secondary and tertiary structures of the riboswitch (represented as black stem loops) are controlled by the binding of a specific ligand (open oval). Figure 2 highlights the SD (RBS), the gene of interest, and represents the large and small ribosomal subunits as dual ovals. Understanding how these regulatory elements control protein biosynthesis is vital for comprehending the adaptability and response mechanisms of microorganisms to changing conditions.

7.2. Global Regulators and Stress Responses

Microorganisms employ global regulators to orchestrate gene expression on a large scale. These regulators, often transcription factors, control the expression of multiple genes involved in specific cellular processes. For example, the stringent response, governed by the alarmone (p)ppGpp, acts as a global regulator in bacteria. During stress conditions, (p)ppGpp helps microorganisms shift resources from growth to survival, impacting protein biosynthesis rates and overall physiology [27]. Moreover, stress responses such as the heat shock response or the cold shock response involve the rapid and coordinated regulation of protein synthesis. These responses help microorganisms cope with environmental challenges, ensuring the proper folding and functionality of proteins under stress [28]. Global regulators in bacteria are proteins that coordinate the expression of multiple genes, often in response to environmental or metabolic changes, ensuring cellular adaptation and survival. Stress responses, on the other hand, refer to the cellular reactions to adverse conditions, including heat, nutrient scarcity, or toxins, which can activate specific pathways, such as the heat shock response. Meanwhile, as shown in Figure 3, the biogenesis of the human mitochondrial ribosome involves the construction of ribosomal subunits within the mitochondria, which is required for the synthesis of proteins important for mitochondrial function. Global regulators and stress responses play a role in bacterial gene regulation, whereas mitochondrial ribosome biogenesis is essential for eukaryotic cellular respiration and energy generation [29]. Exploring the processes by which global regulators and stress responses impact protein production provides important insights into microbial adaptation and resilience.

7.3. Feedback Mechanisms Controlling Protein Synthesis

Feedback mechanisms play a significant role in protein biosynthesis regulation. Feedback inhibition is a well-known example, in which the result of a metabolic route acts as an inhibitor of early enzymes in the metabolic pathway. This procedure keeps cells from wasting resources by overproducing specific proteins. The availability of some proteins during translation can affect the translation of other genes. The quantity of specific ribosomal proteins, according to [29], can influence the translation of mRNA encoding other ribosomal components, resulting in coordinated protein synthesis. Understanding feedback mechanisms is crucial for comprehending how bacteria carefully control Protein biosynthesis to preserve cellular homeostasis and avoid imbalances. Protein biosynthesis in microbes, on the other hand, is governed by intricate interactions including riboswitches, short RNAs, global regulators, stress responses, and feedback mechanisms. These regulatory mechanisms are required by microorganisms to adapt to changing environments, optimize resource allocation, and maintain proper protein homeostasis. Her work sheds light on microbial dynamics and response behavior, which could be useful in biotechnology and the development of novel medical strategies.



Source: [30]

Figure 3 Biogenesis of the human mitochondrial ribosome

8. Protein Biosynthesis in Microbial Physiology

This section examines the various activities of protein biosynthesis in microbial physiology, including its role in antibiotic resistance, virulence and pathogenicity, and environmental adaptation.

8.1. Adaptation to Environmental Changes Through Protein Synthesis

Microbial physiology features biosynthesis as an extremely crucial process that helps bacteria survive in different extreme conditions. As far as microorganisms are concerned, they readily change their patterns of protein synthesis to optimize growth and survival. For instance, microbes can change their translation apparatus if nutrients are not available so they will start making stress proteins like molecular chaperones, ribosomal ones, amino acid biosynthetic ones, etc. Microbial resilience is associated with this type of flexibility in changing eco-types. More so, as per findings of [30], chaperones mediate such an adaptive response. Therefore, it is necessary to comprehend such adaptation mechanisms to establish the survival and diversity of microbes in different ecosystems.

8.2. Role in Microbial Virulence and Pathogenesis

Protein synthesis is essential for microbial virulence and disease. Pathogenic bacteria require precise gene expression and protein synthesis regulation to escape host immune responses and produce disease. Microbial pathogenicity necessitates the coordinated expression of virulence factors, toxins, and adhesins. Microorganisms such as *Escherichia coli* and *Staphylococcus aureus*, for example, modify protein biosynthesis during infection to create specific virulence

factors and toxins, allowing them to colonize host tissues and avoid the host's immune defenses [31]. Exploring the regulatory systems that govern protein production in pathogenic microbes reveals prospective treatment targets and techniques for fighting infectious diseases.

8.3. Antibiotic Resistance and Protein Biosynthesis

A crucial element of microbial physiology is the relationship between protein production and antibiotic resistance. Many antibiotics inhibit protein synthesis and cause cell death by targeting the bacterial ribosome. Antibiotic resistance mechanisms have evolved in microorganisms to counteract their effects. Modifications to the ribosome, such as ribosomal protective proteins, and efflux pumps that remove antibiotics from the cell are examples of these methods. To lower antibiotic susceptibility, certain microbes modify their protein production rates. Understanding how antibiotic resistance and protein production interact is critical for combating the growing problem of antibiotic-resistant bacteria. [32] discovered the structural basis of antibiotic binding to the ribosome, which will help in the development of new antibiotics. Protein biosynthesis, on the other hand, is a critical component of microbial physiology, regulating environmental adaptability, microbial virulence and disease, and antibiotic resistance [33]. These protein biosynthesis factors highlight their importance in microbial ecology and pathology, with ramifications spanning from microbiology and medicine to antibiotic development and environmental research.

9. Biotechnological Applications

This section focuses on successful case studies of protein biosynthesis in biotechnology, ranging from recombinant protein production and synthetic biology techniques to microbial cell factories, microbial fermentation, and bioprocessing for the production of biofuels and chemicals.

9.1. Recombinant Protein Production in Microbial Hosts

The production of recombinant proteins in microbial hosts such as *Escherichia coli*, yeast, and filamentous fungi is a key component of biotechnology. The advent of bioengineered proteins for specific protein mass production has brought changes in the medicine, and biopharmaceutical industries among others. Therapeutic proteins including insulin and monoclonal antibodies are most commonly produced in microbial systems. Knowledge of control of protein production in these hosts has to be understood when improving yield and quality along with optimizing the extraction process.

9.2. Synthetic Biology Approaches for Optimizing Protein Synthesis

Synthetic biology approaches have now revolutionized protein biosynthesis making it possible to assemble genetic circuits for optimum gene expression and protein production. Precise control of protein synthesis rates can be achieved with constructive promoters, ribosome-binding sites, etc. Synthetic circuits have also been speeded up with gene synthesis and CRISPR/Cas9-based genome editing through high throughput gene synthesis. Moreover, [34] highlights how CRISPR/Cas9 enhances protein yield. These breakthroughs are crucial for modifying microbes to produce desired proteins for a variety of applications ranging from medicines to industrial enzymes.

9.3. Engineering Microbial Cell Factories for Biofuel and Chemical Production

Microbial cell factories, such as bacteria and yeast, have been engineered for the sustainable production of biofuels and chemicals. This involves rewiring cellular metabolism and protein biosynthesis pathways to convert renewable resources into valuable products. For instance, microorganisms like *Saccharomyces cerevisiae* have been engineered to produce bioethanol from plant biomass [35]. Protein biosynthesis is integral to these processes as it governs the production of enzymes and pathways for biofuel and chemical synthesis. The development of such microbial cell factories aligns with the growing demand for eco-friendly, bio-based alternatives to traditional petrochemicals.

9.4. Microbial Fermentation and Bioprocessing

Microbial fermentation and bioprocessing play a pivotal role in the production of bio-based products. These processes leverage microbial protein biosynthesis to convert raw materials into valuable substances [36]. Fermentation tanks host microorganisms that synthesize and secrete proteins, enzymes, and metabolites for downstream processing. Advances in bioreactor design and control systems, along with our understanding of protein biosynthesis, have greatly improved the efficiency of microbial fermentation and bioprocessing [37]. Bioreactor systems utilized in biotechnological applications of protein biosynthesis are designed for large-scale protein production in controlled environments, optimizing conditions for efficient protein synthesis. On the contrary, early CFPS used "S30 extracts" to refer to the supernatants generated by centrifuged lysates from different cells. These "S30 extracts" served as a basis for CFPS system improvement by including enzymes like polymerases [figure 4](#) depicts the main elements of cell-free

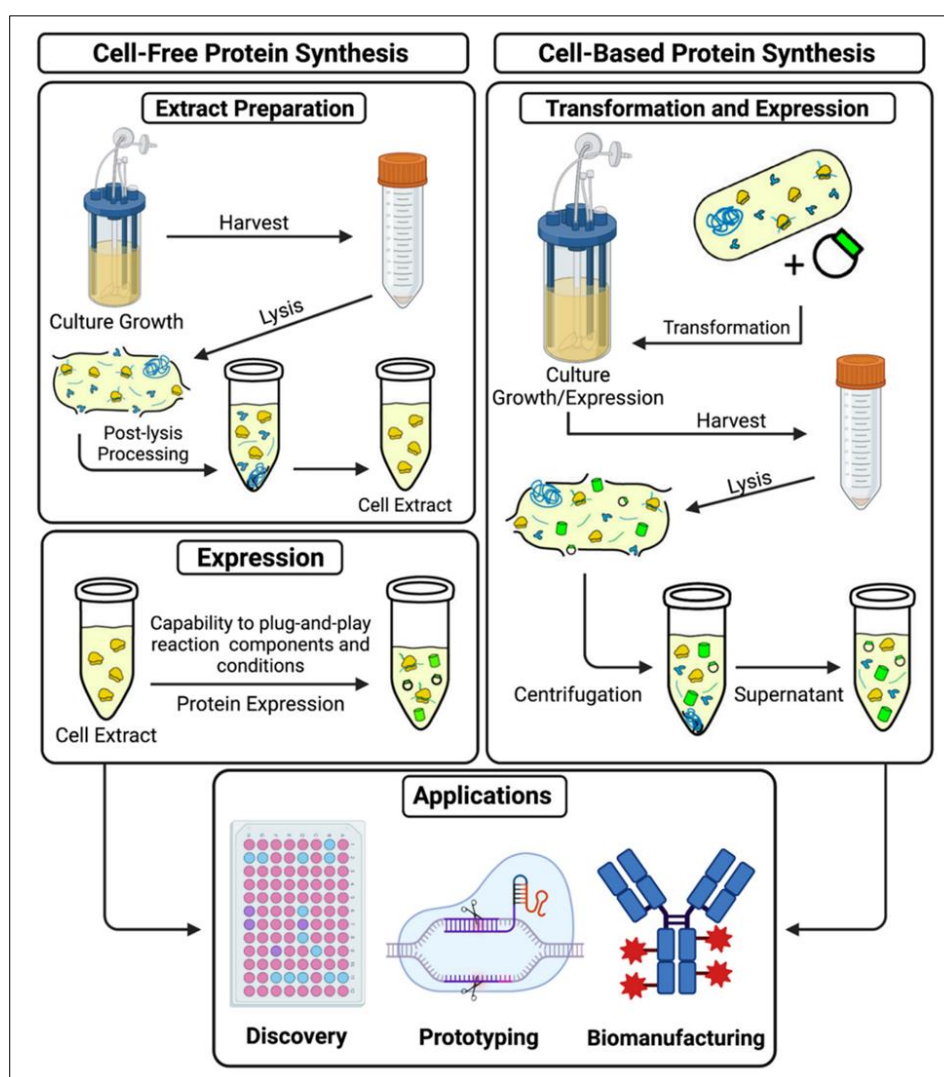
protein synthesis systems showing that they have evolved from the early S30 systems to more complex ones. Although the bioreactor is designed for commercial-scale production, CFPS based on S30 extract has produced a new direction for protein biosynthesis. Such a technique can be used in the manufacture of detergent enzymes, synthesis of biofuel, and biopolymer among other things.

9.5. Case Studies: Successful Biotechnological Applications

The discussion in this section centers on major biotechnological applications of protein biosynthesis including the production of recombinant insulin or bio-ethanol etc. These may have a significant impact on the industry and health care. These examples serve as powerful illustrations of how the knowledge of protein biosynthesis can translate into real-world solutions, benefiting both society and the economy. However, biotechnological applications of protein biosynthesis encompass a wide array of industries, from pharmaceuticals to biofuels and bioremediation [38]. Understanding the regulation and optimization of protein biosynthesis is central to harnessing the potential of microorganisms in biotechnology and driving innovation in sustainable product development.

10. Future Perspectives

This section provides a glimpse into the future of protein biosynthesis research, addressing the current challenges, emerging trends, and the potential for precision engineering in the realm of microorganisms.



Source: [39]

Figure 4 The constituents of a cell-free protein synthesis reaction are combined within a test tube, including DNA, amino acids, energy buffers, and the cellular lysate's molecular machinery. This mixture initiates the transcription and translation processes, ultimately leading to the creation of functional proteins

Table 1 The advantages and disadvantages of different microbial hosts for recombinant protein production

Microbial Host	Advantages	Disadvantages
<i>Escherichia coli</i>	- High growth rate	- Limited capacity for post-translational modifications
	- Well-established expression systems	- Formation of inclusion bodies may require refolding
	- Low cost and scalability	- May not be suitable for complex proteins
	- Efficient and high-yield expression	- Endotoxin production can complicate downstream processing
<i>Saccharomyces cerevisiae</i>	The eukaryotic system allows for proper folding	- Slower growth compared to bacteria
	- Can perform eukaryotic post-translational modifications	- Complexity of genetic manipulation
	- Suitable for secreted and glycosylated proteins	- Production costs may be higher
<i>Bacillus subtilis</i>	- Strong promoter systems	- Limited post-translational modifications
	- Efficient protein secretion	- Risk of proteolysis in the extracellular environment
	- Scalability in bioreactors	- May not be suitable for highly complex proteins
<i>Pichia pastoris</i>	- Efficient secretion system	- More expensive than bacterial expression systems
	- Can perform eukaryotic post-translational modifications	- Longer cultivation times
	- Suitable for the production of large quantities of proteins	- Potential glycosylation differences
<i>Baculovirus-Insect Cell</i>	- Appropriate for complex eukaryotic proteins	- Higher production costs
	- Allows for proper folding and post-translational modifications	- Slower growth compared to bacteria
	- High protein yields	- Insect cell culture expertise may be required

10.1. Current Challenges and Emerging Trends in Protein Biosynthesis Research

Protein biosynthesis research was advancing rapidly, but it still faced several challenges. One of the challenges was the exploration of translational fidelity during translation elongation, as mentioned earlier. Emerging trends included the integration of multi-omics approaches (genomics, transcriptomics, proteomics, and metabolomics) to provide a more comprehensive understanding of the interconnected processes in microorganisms [40]. The rise of single-cell technologies was another notable trend, enabling the study of heterogeneous populations of microorganisms and revealing hidden complexities in protein biosynthesis. The application of artificial intelligence and machine learning to predict and enhance protein synthesis is an ascending trend [41]. Concurrently, metagenomics and synthetic biology are expanding the frontiers of comprehending and manipulating protein biosynthesis within intricate microbial communities [42]. In the future, addressing these challenges and harnessing these trends will likely lead to innovative solutions and applications in various domains, including biotechnology, medicine, and environmental science.

10.2. Prospects for Precision Engineering of Protein Biosynthesis in Microbes

The future of protein biosynthesis in microorganisms is intrinsically intertwined with precision engineering. The capacity to finely manipulate and govern protein biosynthesis holds vast potential for tailored applications. This

precision engineering may encompass the optimization of translational machinery, the deliberate design of synthetic riboswitches, and the creation of high-performance expression systems. Advances in genome editing, such as CRISPR/Cas9 and related technologies, will persist in enabling meticulous control over gene expression and protein synthesis [43]. Synthetic biology and the construction of entirely new genetic circuits will facilitate the development of microorganisms designed for specific biotechnological purposes [44]. Furthermore, the evolution of cell-free protein synthesis systems will expedite the controlled production of proteins outside living cells [45]. These advancements promise elevated protein quality, accelerated bioprocessing, and the capacity to craft entirely novel proteins endowed with desired functionalities. Nevertheless, the future of protein biosynthesis research in microorganisms is marked by ongoing challenges and promising trends, from the integration of multi-omics data to the application of artificial intelligence and the rise of precision engineering. These advancements have the potential to reshape various industries and scientific domains, rendering protein biosynthesis in microorganisms a pivotal area of study with extensive implications.

11. Conclusion

Protein biosynthesis in microorganisms stands as the bedrock of cellular existence, providing the mechanism for translating genetic information into functional proteins. Key insights gleaned from our exploration encompass the intricate workings of transcription, translation, and post-translational modifications, along with the regulatory networks that oversee these processes. The revelation of riboswitches, small RNAs, global regulators, and feedback mechanisms has unveiled the intricacy of protein biosynthesis regulation. In the realm of biotechnology, the potential of protein biosynthesis is boundless. The production of recombinant proteins in microbial hosts has revolutionized the pharmaceutical and biopharmaceutical sectors, presenting cost-effective and scalable production methods. Synthetic biology approaches and precision engineering open doors to the customization of microorganisms for diverse applications, spanning from biofuel production to tailored drug synthesis. Microbial fermentation and bioprocessing continue to propel advancements in sustainable product development. The future of protein biosynthesis research offers exhilarating prospects, with hurdles like comprehending translational fidelity and burgeoning trends such as the integration of multi-omics techniques and the application of artificial intelligence. Precision engineering of protein biosynthesis will enable the creation of highly efficient and customizable microorganisms, expanding the possibilities for biotechnological applications. However, protein biosynthesis in microorganisms stands at the intersection of fundamental science and innovative applications. It is a field that continually unfolds its complexities and offers solutions to challenges in microbiology, biotechnology, and beyond. The potential of protein biosynthesis research is boundless, with far-reaching impacts on healthcare, industry, and environmental sustainability, making it a field of enduring significance and immense promise.

Compliance with ethical standards

Disclosure of conflict of interest

The authors acknowledged no conflicts of interest.

References

- [1] Matthaie, H., & Nirenberg, M. W. (1961). The dependence of cell-free protein synthesis in *E. coli* upon RNA prepared from ribosomes. *Biochemical and biophysical research communications*, 4(6), 404-408.
- [2] Ban, N., Nissen, P., Hansen, J., Moore, P. B., & Steitz, T. A. (2000). The complete atomic structure of the large ribosomal subunit at 2.4 Å resolution. *Science*, 289(5481), 905-920.
- [3] Rosano, G. L., & Ceccarelli, E. A. (2014). Recombinant protein expression in *Escherichia coli*: advances and challenges. *Frontiers in microbiology*, 5, 172.
- [4] Dien, J., Spencer, K. M., & Donchin, E. (2003). Localization of the event-related potential novelty response as defined by principal components analysis. *Cognitive Brain Research*, 17(3), 637-650.
- [5] Lors, C., Ryngaert, A., Périé, F., Diels, L., & Damidot, D. (2010). Evolution of bacterial community during bioremediation of PAHs in a coal tar contaminated soil. *Chemosphere*, 81(10), 1263-1271.
- [6] Holley, R. W., Apgar, J., Everett, G. A., Madison, J. T., Marquisee, M., Merrill, S. H., ... & Zamir, A. (1965). Structure of a ribonucleic acid. *Science*, 147(3664), 1462-1465.

- [7] Schier, A. C., & Taatjes, D. J. (2020). Structure and mechanism of the RNA polymerase II transcription machinery. *Genes & development*, 34(7-8), 465-488.
- [8] Darst, S. A., Opalka, N., Chacon, P., Polyakov, A., Richter, C., Zhang, G., & Wriggers, W. (2002). Conformational flexibility of bacterial RNA polymerase. *Proceedings of the National Academy of Sciences*, 99(7), 4296-4301.
- [9] Crick, F., Barnett, L., Brenner, S., & Watts-Tobin, R. J. (1961). General nature of the genetic code for proteins.
- [10] Ambrogelly, A., Palioura, S., & Söll, D. (2007). Natural expansion of the genetic code. *Nature Chemical Biology*, 3(1), 29-35.
- [11] Noller, H. F., Kop, J., Wheaton, V., Brosius, J., Gutell, R. R., Kopylov, A. M., ... & Woese, C. R. (1981). Secondary structure model for 23S ribosomal RNA. *Nucleic acids research*, 9(22), 6167-6189.
- [12] Kapp, L. D., & Lorsch, J. R. (2004). GTP-dependent recognition of the methionine moiety on initiator tRNA by translation factor eIF2. *Journal of molecular biology*, 335(4), 923-936.
- [13] Zavialov, A. V., Mora, L., Buckingham, R. H., & Ehrenberg, M. (2002). The release of peptides promoted by the GGQ motif of class 1 release factors regulates the GTPase activity of RF3. *Molecular cell*, 10(4), 789-798.
- [14] Mohler, K., & Ibba, M. (2017). Translational fidelity and mistranslation in the cellular stress response. *Nature Microbiology*, 2(9), 1-9.
- [15] Alejo, J. L., & Blanchard, S. C. (2017). Miscoding-induced stalling of substrate translocation on the bacterial ribosome. *Proceedings of the National Academy of Sciences*, 114(41), E8603-E8610.
- [16] de la Torre, D., & Chin, J. W. (2021). Reprogramming the genetic code. *Nature Reviews Genetics*, 22(3), 169-184.
- [17] Diez, S., Ryu, J., Caban, K., Gonzalez Jr, R. L., & Dworkin, J. (2020). The alarmone (p) ppGpp directly regulate translation initiation during entry into quiescence. *Proceedings of the National Academy of Sciences*, 117(27), 15565-15572.
- [18] Werner, F., & Grohmann, D. (2011). Evolution of multisubunit RNA polymerases in the three domains of life. *Nature Reviews Microbiology*, 9(2), 85-98.
- [19] Proudfoot, N. J. (2011). Ending the message: poly (A) signals then and now. *Genes & development*, 25(17), 1770-1782.
- [20] Walsh, C. T., Garneau-Tsodikova, S., & Gatto Jr, G. J. (2005). Protein posttranslational modifications: the chemistry of proteome diversifications. *Angewandte Chemie International Edition*, 44(45), 7342-7372.
- [21] Hartl, F. U., Bracher, A., & Hayer-Hartl, M. (2011). Molecular chaperones in protein folding and proteostasis. *Nature*, 475(7356), 324-332.
- [22] Fink, A. L. (1999). Chaperone-mediated protein folding. *Physiological reviews*, 79(2), 425-449.
- [23] Bhattacharyya, S., Yu, H., Mim, C., & Matouschek, A. (2014). Regulated protein turnover: snapshots of the proteasome in action. *Nature reviews Molecular cell biology*, 15(2), 122-133.
- [24] Mandal, M., & Breaker, R. R. (2004). Adenine riboswitches and gene activation by disruption of a transcription terminator. *Nature structural & molecular biology*, 11(1), 29-35.
- [25] Waters, L. S., & Storz, G. (2009). Regulatory RNAs in bacteria. *Cell*, 136(4), 615-628.
- [26] Nshogozabahizi, J. C., Aubrey, K. L., Ross, J. A., & Thakor, N. (2019). Applications and limitations of regulatory RNA elements in synthetic biology and biotechnology. *Journal of Applied Microbiology*, 127(4), 968-984.
- [27] Potrykus, K., & Cashel, M. (2008). (p) ppGpp: still magical? *Annu. Rev. Microbiol.*, 62, 35-51.
- [28] Mogk, A., Bukau, B., & Kampinga, H. H. (2018). Cellular handling of protein aggregates by disaggregation machines. *Molecular cell*, 69(2), 214-226.
- [29] Kummer, E., & Ban, N. (2021). Mechanisms and regulation of protein synthesis in mitochondria. *Nature Reviews Molecular Cell Biology*, 22(5), 307-325.
- [30] Chen, B., Feder, M. E., & Kang, L. (2018). Evolution of heat-shock protein expression underlying adaptive responses to environmental stress. *Molecular Ecology*, 27(15), 3040-3054.
- [31] Nizet, V. (2007). Understanding how leading bacterial pathogens subvert innate immunity to reveal novel therapeutic targets. *Journal of Allergy and Clinical Immunology*, 120(1), 13-22.

- [32] Poehlsgaard, J., & Douthwaite, S. (2005). The bacterial ribosome is a target for antibiotics. *Nature Reviews Microbiology*, 3(11), 870-881.
- [33] Abdulsalam, M., Usman, K. M. T., Nurudeen, A. A & Muhammad, F. Y. (2023). Analyzing COVID-19 on a global scale: Investigating its worldwide ramifications. *International Journal of Applied and Scientific Research*. 1(2):213-232.
- [34] Gaj, T., Gersbach, C. A., & Barbas, C. F. (2013). ZFN, TALEN, and CRISPR/Cas-based methods for genome engineering. *Trends in biotechnology*, 31(7), 397-405.
- [35] Hong, Y., Lam, J. W., & Tang, B. Z. (2011). Aggregation-induced emission. *Chemical Society Reviews*, 40(11), 5361-5388.
- [36] Abdulsalam, M., KalandarAmeer, S., Balakrishnan, S., & Pal, S. K. (2023). Maximizing Sustainability: Leveraging Indigenous Fungal Cellulases for Sugarcane Bagasse Bioethanol Production and Agricultural Waste Management in Kano. *Journal of Advanced Zoology*, 44(S-2), 2379-2393.
- [37] Mandenius, C. F., & Brundin, A. (2008). Review: Biocatalysts and bioreactor design. *Biotechnol. Prog*, 24, 1191-1203.
- [38] Abdulsalam, M., Fari, H.I., Tihamiyu, B.B., Salami, O. L. (2022). Optimizing α -amylase production from locally Isolated *Aspergillus* sp. using selected Agro waste as substrate. *Bioscience Biotechnology Research Communication*.15(3):424-430.
- [39] Brookwell, A., Oza, J. P., & Caschera, F. (2021). Biotechnology applications of cell-free expression systems. *Life*, 11(12), 1367.
- [40] Dias, M. I., Ferreira, I. C., & Barreiro, M. F. (2015). Microencapsulation of bioactives for food applications. *Food & function*, 6(4), 1035-1052.
- [41] Gupta, R., Srivastava, D., Sahu, M., Tiwari, S., Ambasta, R. K., & Kumar, P. (2021). Artificial intelligence to deep learning: machine intelligence approach for drug discovery. *Molecular diversity*, 25, 1315-1360.
- [42] Chatterjee, G., Negi, S., Basu, S., Faintuch, J., O'donovan, A., & Shukla, P. (2022). Microbiome systems biology advancements for natural well-being. *Science of The Total Environment*, 838, 155915.
- [43] Abdulsalam, M., Amina, A. A., Ummulkhair, A. Y and Zainab, H. F. (2023) Advances in understanding the interplay between Mutagenesis and DNA Repair: Implications for Genomic Stability and Evolution. *International Journal of Science Academic Research*. 04(10):6428-6438.
- [44] Naseri, G., & Koffas, M. A. (2020). Application of combinatorial optimization strategies in synthetic biology. *Nature communications*, 11(1), 2446.
- [45] Silverman, A. D., Karim, A. S., & Jewett, M. C. (2020). Cell-free gene expression: an expanded repertoire of applications. *Nature Reviews Genetics*, 21(3), 151-170.