



Narrative Review

From Genetic Code to Biological Structure: A Biochemical Analysis of Protein Synthesis from Replication to Folding

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ABSTRACT

Protein biosynthesis is a highly coordinated and tightly regulated molecular process essential for maintaining cellular function and organismal homeostasis. This process encompasses a continuum of events, beginning with DNA replication to preserve genetic integrity, followed by transcription, which generates messenger RNA (mRNA) as an intermediary, and translation, where genetic information is decoded into a polypeptide chain. Subsequently, post-translational modifications and protein folding ensure the formation of stable and functionally active three-dimensional protein structures. Each stage is interdependent, and disruption at any level, whether through genetic mutations, translational errors, or protein misfolding, can lead to dysfunctional proteins and contribute to disease pathogenesis.

This review highlights the integrated nature of protein biosynthesis and emphasizes the importance of regulatory mechanisms at transcriptional, translational, and epigenetic levels. Furthermore, it underscores the clinical relevance of these processes, particularly in genetic disorders, cancer, and neurodegenerative diseases associated with protein misfolding. A comprehensive understanding of the molecular coordination underlying protein synthesis provides critical insights into the mechanisms of disease and offers potential avenues for the development of targeted therapeutic strategies in modern medicine.

Introduction

Protein synthesis is a fundamental process in cellular biochemistry that plays a crucial role in maintaining cellular function and organismal homeostasis. Virtually all biological activities—ranging from metabolism, gene regulation, immune responses, to intercellular communication—depend on the presence of structurally precise and functionally specific proteins. Therefore, understanding the mechanisms of protein synthesis is essential not only in molecular biology but also in medical science, particularly in elucidating the pathogenesis of diseases associated with dysregulated gene expression and protein misfolding.^{1,2}

Proteins represent the final products of gene expression and directly determine cellular phenotype. Genetic information stored within deoxyribonucleic acid (DNA) is translated into biological structure and function through a series of coordinated molecular processes. Gene expression reflects the activation or repression of specific genes under particular conditions, resulting in phenotypic variability despite identical genotypes. Consequently, proteins serve not only as structural components but also as enzymes, hormones, and regulatory molecules that define cellular identity and function.³

In general, protein synthesis involves several interconnected stages, including DNA replication, transcription, translation, and post-translational modification. DNA replication ensures accurate duplication of genetic material for transmission to daughter cells and is characterized by semiconservative replication, proofreading activity, and coordinated replication fork dynamics.^{4,8} Following replication, transcription converts genetic information from DNA into ribonucleic acid (RNA), particularly messenger RNA (mRNA),

which serves as the template for protein synthesis.⁹

Translation subsequently occurs at the ribosome, where mRNA is decoded into a polypeptide chain through interactions with transfer RNA (tRNA) and multiple translation factors. This process is tightly regulated to ensure fidelity and efficiency of protein production.¹⁰ After synthesis, polypeptides undergo post-translational modifications and protein folding to achieve a stable three-dimensional conformation essential for biological activity. Molecular chaperones play a critical role in maintaining proteostasis and preventing misfolding or aggregation.¹¹

Although these stages are often studied separately, in reality they function as a highly integrated and coordinated system within the cellular environment. Disruptions at any stage may lead to protein dysfunction, contributing to various pathological conditions such as genetic disorders, cancer, and neurodegenerative diseases associated with protein misfolding. Therefore, a comprehensive approach that examines the interconnection among these molecular processes is essential to understand how functional proteins are generated from genetic information.

Based on the above considerations, the primary research question of this essay is: how does protein synthesis occur in an integrated manner from DNA replication to the formation of functional protein structures through folding processes? Additionally, how does each stage contribute to ensuring the accuracy and efficiency of gene expression?

The objective of this essay is to provide a biochemical analysis of the integrated molecular processes involved in protein synthesis, encompassing DNA replication, transcription, translation, post-translational modification, and protein folding. A comprehensive understanding of these interconnected stages is expected to offer

a holistic perspective on the mechanisms underlying functional protein formation and their implications in health and disease.

Discussions

A. DNA Replication as the Foundation of Genetic Information Inheritance

DNA replication is a core process in molecular biology that ensures the faithful transmission of genetic information from one cell generation to the next. This mechanism underpins protein synthesis by preserving the integrity of nucleotide sequences that will later be transcribed into RNA and translated into functional proteins. Any compromise in replication fidelity may disrupt genomic stability, leading to mutations that can alter protein structure and impair cellular homeostasis.^{1,9}

At the conceptual level, DNA replication follows a semiconservative model, in which each newly formed DNA molecule consists of one parental strand and one newly synthesized strand. This principle was experimentally validated in the landmark study by Matthew Meselson and Franklin Stahl in 1958, demonstrating that genetic information is conserved through strand separation and complementary base pairing. Such a mechanism guarantees that daughter cells inherit an essentially identical copy of the genome.^{5,3}

The replication process is carried out by a coordinated set of enzymes assembled into a multiprotein complex known as the replisome. Key enzymatic components include DNA polymerase, helicase, primase, and DNA ligase. Helicase unwinds the double helix by breaking hydrogen bonds between complementary bases, generating a structure known as the replication fork. Primase synthesizes short RNA primers, providing a free 3'-OH group required for DNA polymerase to initiate nucleotide addition. DNA polymerase then elongates the new strand in a

5'→3' direction, incorporating nucleotides complementary to the template strand while simultaneously performing proofreading to maintain replication accuracy. DNA ligase subsequently seals discontinuities in the DNA backbone by forming phosphodiester bonds, ensuring strand continuity.^{2,7}

Due to the antiparallel nature of DNA and the unidirectional activity of DNA polymerase, replication proceeds asymmetrically. The leading strand is synthesized continuously in the direction of replication fork progression, whereas the lagging strand is synthesized discontinuously as short segments known as Okazaki fragments. These fragments are later processed through primer removal and ligation to form a continuous strand. This strategy reflects the remarkable adaptability and efficiency of the replication machinery in overcoming structural constraints of the DNA molecule.^{6,1}

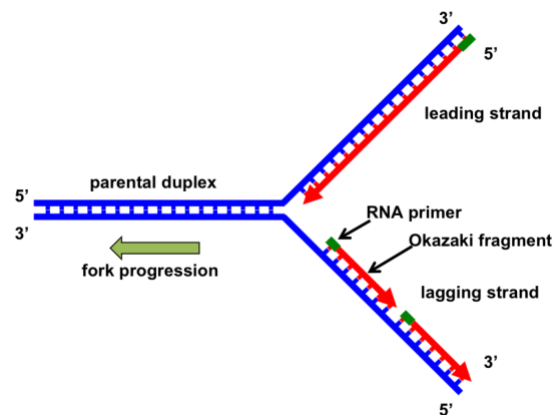


Figure 1. Replication fork. Leading strand synthesis proceeds continuously in the 5'→3' direction, whereas lagging strand synthesis also occurs in the 5'→3' direction but in a discontinuous manner. RNA/DNA primers (indicated in green) initiate synthesis of the leading strand and each Okazaki fragment on the lagging strand.⁸

Beyond its role in duplicating genetic material, DNA replication is also critical for maintaining genomic integrity through proofreading and DNA repair mechanisms. High fidelity during replication is essential, as even minor errors in nucleotide incorporation may

lead to altered protein structure and function. In the medical context, defects in replication fidelity and repair pathways are strongly associated with the development of various diseases, including malignancies and inherited genetic disorders resulting from mutation accumulation.^{7,1}

In summary, DNA replication serves not only as a mechanism for genetic inheritance but also as the fundamental basis for all subsequent gene expression processes, including protein synthesis. The precision and stability of replication directly influence the quality of genetic information that is transcribed and translated, ultimately determining the formation of functional proteins. Therefore, an in-depth understanding of DNA replication is indispensable for comprehending the integrated molecular continuum from genetic code to biological structure and function.

B. Transcription: RNA Synthesis from DNA

Transcription represents a pivotal stage in gene expression, linking genetic information encoded in DNA to protein synthesis through RNA intermediates. In this process, the nucleotide sequence of DNA is transcribed into messenger RNA (mRNA), which subsequently conveys genetic instructions to the ribosome for translation into protein. As such, transcription serves as a principal regulatory checkpoint that determines which genes are expressed and to what extent, thereby exerting a direct influence on cellular phenotype.^{1,2}

In general, transcription is catalysed by RNA polymerase, an enzyme that synthesizes RNA in the 5'→3' direction using one strand of DNA as a template. Unlike DNA replication, this process does not require a primer; instead, it depends on the recognition of specific DNA sequences known as promoters, which define the transcription start site.⁹ RNA polymerase, together with transcription factors, binds to promoter regions—such as the TATA box in

eukaryotic cells—leading to localized unwinding of the DNA double helix and the formation of a transcription bubble. This configuration allows access to the template strand, enabling the initiation of RNA synthesis through the incorporation of complementary ribonucleotides.²

During the elongation phase, RNA polymerase traverses the DNA template strand, sequentially adding nucleotides to extend the growing RNA chain. As transcription progresses, the DNA helix re-anneals behind the enzyme, while the nascent RNA transcript dissociates from the DNA–RNA hybrid. Although elongation is a rapid process, RNA polymerase retains limited proofreading capability to maintain transcriptional fidelity.¹

The final stage, termination, occurs when RNA polymerase encounters specific termination signals. In prokaryotic systems, termination may occur intrinsically via the formation of a hairpin structure in the RNA transcript or through the action of the rho factor. In contrast, termination in eukaryotic cells is more complex and is often associated with polyadenylation signals, which are subsequently processed during post-transcriptional modification.⁹

In eukaryotes, the initial transcript—pre-mRNA—requires extensive post-transcriptional processing before becoming a mature and functional mRNA molecule. These modifications are essential for RNA stability, nuclear export, and translational efficiency. Key processes include:

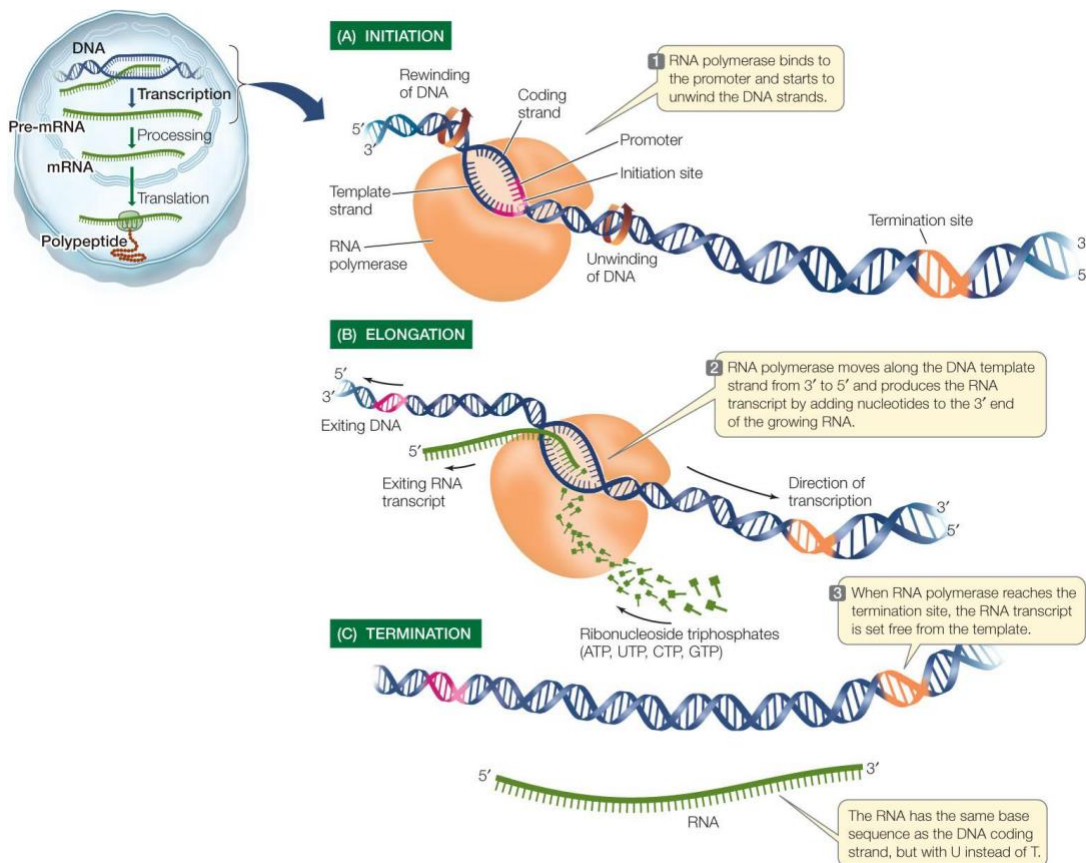


Figure 2. Transcription Process

First, **5' capping**, which involves the addition of a 7-methylguanosine moiety at the 5' end of the mRNA. This cap structure protects the transcript from exonucleolytic degradation and facilitates ribosomal recognition during translation initiation.³

Second, **polyadenylation**, characterized by the addition of a poly-A tail at the 3' end of the mRNA. This modification enhances mRNA stability, promotes nuclear export, and increases translational efficiency.²

Third, **RNA splicing**, a process in which non-coding introns are removed and coding exons are ligated by the spliceosome complex. Beyond generating a functional transcript, splicing enables alternative splicing mechanisms that significantly expand proteomic diversity from a single gene.¹

Regulation of transcription constitutes a critical determinant of gene expression levels. In eukaryotic systems, this regulation involves

intricate interactions among DNA regulatory elements, transcription factors, enhancers, silencers, and epigenetic modifications such as DNA methylation and histone modification. Through these coordinated mechanisms, cells are able to respond dynamically to environmental and physiological stimuli by modulating gene expression patterns. Dysregulation of transcriptional control is strongly implicated in the pathogenesis of numerous diseases, including cancer, developmental disorders, and inherited genetic conditions.^{10, 1}

In conclusion, transcription is not merely a process of RNA synthesis from DNA but serves as a central regulatory hub in gene expression. The integration of transcriptional mechanisms with post-transcriptional modifications ensures that genetic information is accurately and efficiently processed into functional mRNA, ultimately guiding the synthesis of proteins that define cellular structure and function.

C. Translation: Protein Synthesis at the Ribosome

Translation represents the subsequent phase of gene expression in which genetic information encoded in messenger RNA (mRNA) is decoded into a specific sequence of amino acids, forming a polypeptide chain. This process occurs at the ribosome and involves coordinated interactions among mRNA, transfer RNA (tRNA), and multiple protein factors. Translation is a critical step because it determines how the genetic code is interpreted into a precise and functional protein structure.^{1,2}

The ribosome is a ribonucleoprotein complex composed of two subunits: a small subunit and a large subunit. In eukaryotic cells, the small (40S) subunit is responsible for binding mRNA and ensuring accurate codon recognition, whereas the large (60S) subunit possesses catalytic activity, functioning as a peptidyl transferase that facilitates peptide bond formation. The ribosome contains three essential binding sites: the A (aminoacyl) site, where incoming tRNA molecules carrying amino acids bind; the P (peptidyl) site, where the growing polypeptide chain is held; and the E (exit) site, where deacylated tRNA exits the ribosome.⁹

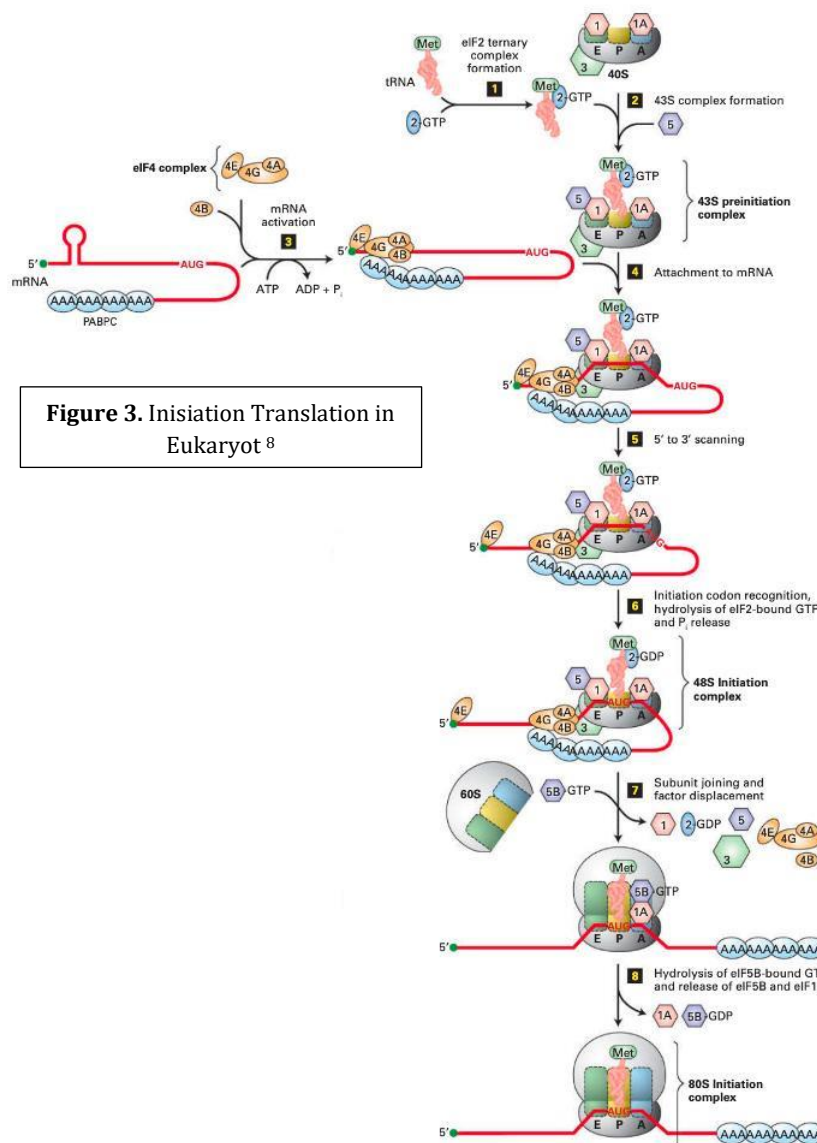


Figure 3. Inisiation Translation in Eukaryot⁸

Transfer RNA acts as a molecular adaptor that links codons in mRNA to their corresponding amino acids. Each tRNA molecule exhibits a characteristic cloverleaf structure and contains an anticodon region that pairs complementarily with the mRNA codon. At its 3' end, tRNA binds a specific amino acid that has been activated by aminoacyl-tRNA synthetase enzymes. The fidelity of codon–anticodon pairing is essential for maintaining translational accuracy.³

Translation proceeds through three major stages: initiation, elongation, and termination. During initiation, the small ribosomal subunit binds to the 5' end of the mRNA and scans for the start codon (AUG). This codon is recognized by the initiator tRNA carrying methionine. Subsequently, the large ribosomal subunit assembles to form a complete ribosome, positioning the initiator tRNA in the P site.² Elongation constitutes the phase of polypeptide chain extension. In this stage, an aminoacyl-tRNA corresponding to the next codon enters the A site. The peptidyl transferase activity of the large subunit catalyses the formation of a peptide bond between the amino acid in the P site and the one in the A site. Following this reaction, the ribosome undergoes translocation: the tRNA in the A site shifts to the P site, the empty tRNA moves to the E site and exits, and the ribosome advances along the mRNA. This cycle repeats until all codons are translated.¹

Termination occurs when the ribosome encounters a stop codon (UAA, UAG, or UGA). These codons are not recognized by tRNA but instead by release factors, which promote the hydrolysis of the bond between the polypeptide chain and the tRNA in the P site, resulting in the release of the newly synthesized protein. The ribosomal subunits then dissociate and become available for subsequent rounds of translation.⁹

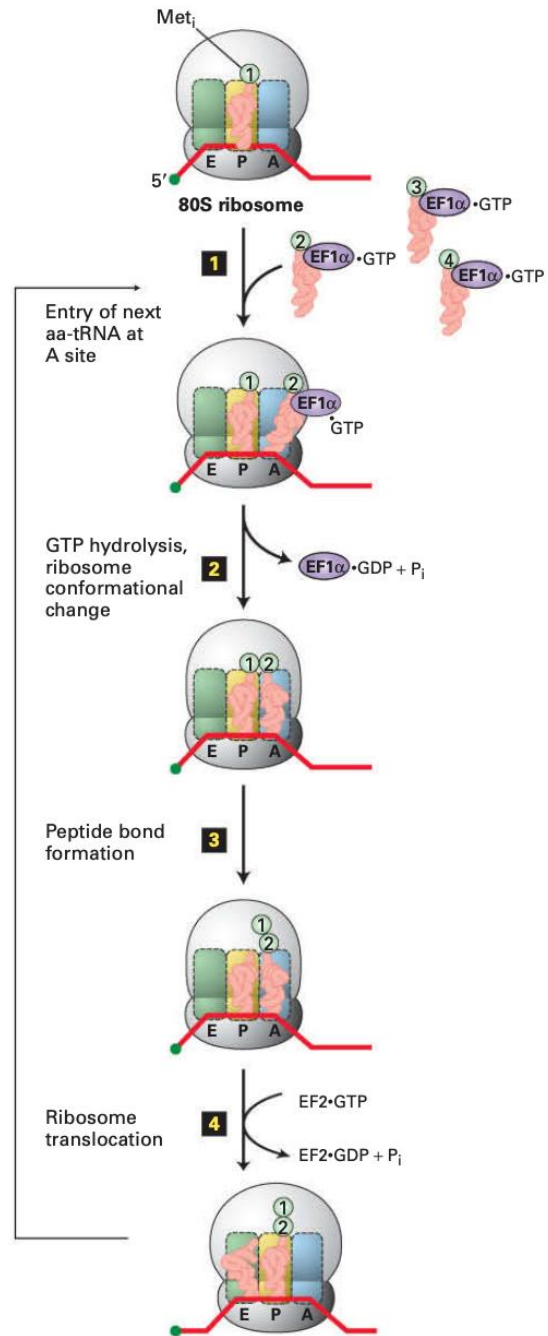


Figure 5. Elongation Translation in Eukaryot⁸

A fundamental concept underlying translation is the genetic code, which defines the relationship between nucleotide triplets (codons) and specific amino acids. The genetic code is degenerate, meaning that a single amino acid can be encoded by multiple codons—for example, leucine is specified by several codons. This redundancy provides a degree of tolerance against point mutations, particularly at the third

nucleotide position (the wobble position). Furthermore, the genetic code is nearly universal across organisms, reflecting a highly conserved evolutionary origin.^{3,1}

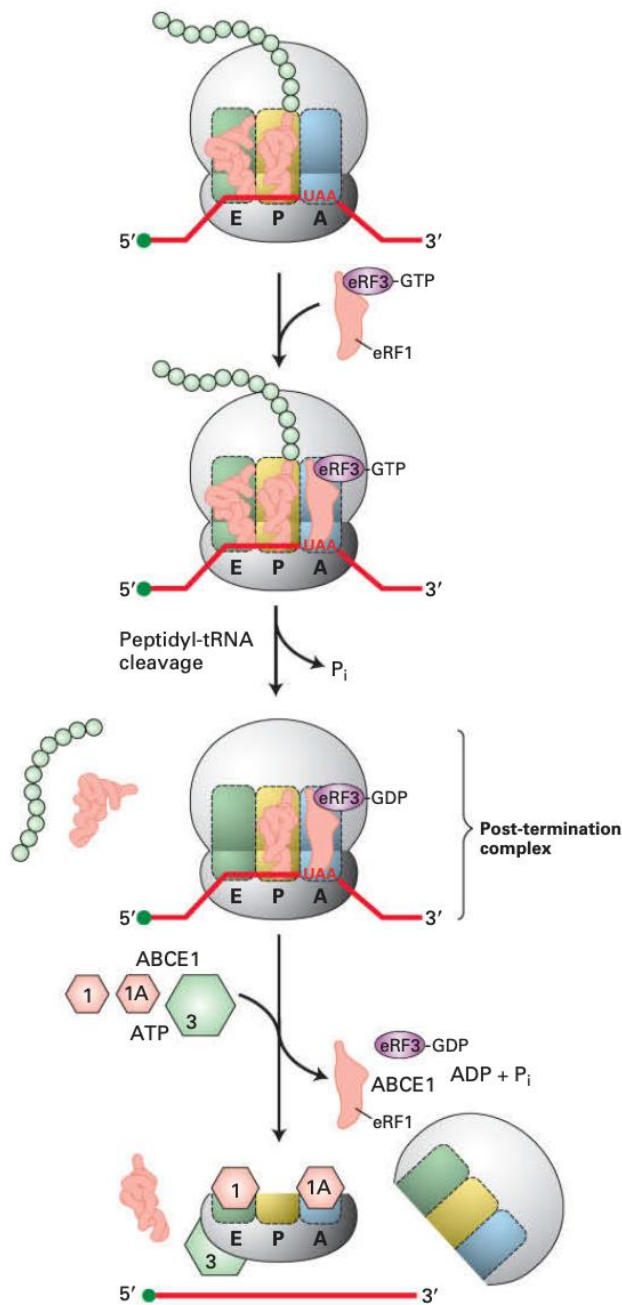


Figure 6. Elongation Translation in Eukaryot⁸

In summary, translation is a highly coordinated molecular process that converts genetic information into a functional polypeptide chain. The accuracy of each stage is essential, as even minor errors in codon interpretation may

result in non-functional or deleterious proteins. Consequently, translation represents a critical control point in protein synthesis, ultimately determining the successful formation of biologically active proteins.

D. Post-Translational Modifications and Protein Folding

Proteins emerging from the translational machinery are not inherently biologically active. The newly synthesized polypeptide chains exist as linear sequences that must undergo precise folding and a range of chemical modifications to attain a stable and functional three-dimensional conformation. This stage is critical, as errors in folding or post-translational processing may result in loss of function or the formation of toxic protein species that disrupt cellular homeostasis.^{1,9}

1. Protein Folding and the Role of Molecular Chaperones

Protein folding is the process by which a linear polypeptide chain adopts its specific three-dimensional structure, dictated primarily by its amino acid sequence. This hierarchical organization progresses from primary structure to secondary elements such as α -helices and β -sheets, followed by tertiary and, in some cases, quaternary structures. The final conformation is essential for biological activity, as it determines the protein's ability to interact with ligands, substrates, or other biomolecules.³

Within the crowded intracellular environment, spontaneous folding is often inefficient and prone to error. Therefore, cells utilize specialized proteins known as molecular chaperones, including heat shock proteins (Hsp), to facilitate proper folding. These chaperones do not encode structural information but act by preventing inappropriate intermolecular interactions and stabilizing intermediate folding states. In cases of misfolding, proteins may be

refolded or targeted for degradation via the ubiquitin–proteasome system. Failure of these quality control mechanisms is closely associated with neurodegenerative disorders such as Alzheimer’s disease and Parkinson’s disease, both characterized by the accumulation of misfolded protein aggregates.^{11,1}

2. Post-Translational Chemical Modifications

In addition to folding, many proteins undergo post-translational modifications (PTMs) that alter their chemical properties and functional capacities. These modifications regulate enzymatic activity, stability, intracellular localization, and protein–protein interactions. Major forms of PTMs include:

Phosphorylation involves the addition of a phosphate group to amino acid residues such as serine, threonine, or tyrosine, catalysed by kinases. This reversible modification plays a central role in cellular signalling pathways, functioning as a molecular switch that can activate or inhibit protein activity.⁹

Glycosylation refers to the attachment of carbohydrate moieties to proteins, particularly those destined for secretion or membrane localization. Occurring primarily in the endoplasmic reticulum and Golgi apparatus, glycosylation is essential for protein stability, cell recognition, and intercellular communication.²

Methylation entails the addition of methyl groups to residues such as lysine or arginine. This modification is frequently involved in the regulation of gene expression, particularly through histone modification, which influences chromatin structure and transcriptional accessibility.³

Acetylation, commonly occurring on lysine residues, modulates protein function and gene expression. Histone acetylation, for instance, enhances chromatin accessibility, thereby facilitating transcriptional activation.¹

3. The Relationship Between Three-Dimensional Structure and Protein Function

The biological function of a protein is intrinsically linked to its three-dimensional conformation. Specific interactions between proteins and other molecules—such as enzyme–substrate binding, receptor–ligand recognition, or structural assembly—depend on both shape complementarity and the physicochemical properties of the protein surface. Even subtle alterations in protein structure, whether due to genetic mutations or folding defects, may lead to loss of function or the emergence of aberrant, potentially toxic activities.⁹

From a biomedical perspective, understanding the relationship between protein structure and function is essential, particularly in the context of targeted therapy development. Many modern pharmacological agents are designed to interact selectively with specific protein conformations, making the structural integrity of target proteins a key determinant of therapeutic efficacy.

In conclusion, post-translational modifications and protein folding represent the final and decisive stages in protein biogenesis. These processes determine whether a synthesized polypeptide will achieve its functional state. The integration of genetic information, translational mechanisms, and post-synthetic biochemical dynamics underscores that protein function is not solely dictated by the genetic code but also by complex regulatory processes that occur after synthesis.

E. Integration and Regulation of Gene Expression

Gene expression is a highly integrated process encompassing a sequence of molecular events, from DNA replication and transcription to translation and post-translational modification. Although these stages are often described

independently for conceptual clarity, within the cellular environment they operate in a coordinated and dynamic manner. DNA replication preserves genetic fidelity, transcription governs the production of RNA intermediates, and translation converts this information into functional proteins. This integration enables cells to adapt efficiently to environmental changes and physiological demands.^{1,2}

1. Transcriptional Regulation

Transcriptional regulation represents the primary level of control in gene expression. This process involves interactions between RNA polymerase and specific DNA regulatory elements, including promoters, enhancers, and silencers, as well as a diverse array of transcription factors. Promoters serve as the binding sites for RNA polymerase initiation, whereas enhancers can significantly increase transcriptional efficiency even when located distal to the target gene. Transcription factors function as modulators that either activate or repress gene expression through sequence-specific DNA binding.³

This regulatory framework allows gene expression to be highly selective and tissue-specific. For instance, hepatocytes and neurons share identical genomic content but exhibit distinct gene expression profiles corresponding to their specialized functions. Disruption of transcriptional regulators or DNA control elements may result in aberrant gene expression, a phenomenon commonly observed in malignancies and other pathological conditions.¹

2. Translational Regulation

Beyond transcription, gene expression is further regulated at the level of translation. Translational control enables cells to modulate protein synthesis from existing mRNA pools, thereby providing a rapid and energy-efficient

response to cellular needs. This regulation involves multiple mechanisms, including modulation of translation initiation factors, control of mRNA stability, and interaction with regulatory RNA molecules such as microRNA (miRNA).²

miRNAs bind to complementary sequences on target mRNA molecules, leading to translational repression or mRNA degradation. This layer of regulation is particularly important during cellular stress, differentiation, and development, where rapid adjustments in protein production are required without the need for new transcriptional events.

3. Epigenetic Regulation of Gene Expression

In addition to sequence-dependent mechanisms, gene expression is also regulated by epigenetic modifications, which alter gene activity without changing the underlying DNA sequence. Two principal epigenetic mechanisms include DNA methylation and histone modification.

DNA methylation involves the addition of methyl groups to cytosine residues, particularly within CpG islands, and is generally associated with transcriptional repression due to reduced accessibility of transcription factors.⁹

Histone modifications, such as acetylation and methylation, influence chromatin structure and gene accessibility. Histone acetylation typically promotes gene expression by relaxing chromatin into a more open (euchromatin) configuration, whereas deacetylation leads to chromatin condensation (heterochromatin) and transcriptional silencing.¹

4. Clinical Relevance

Dysregulation of gene expression has significant clinical implications, particularly in the pathogenesis of genetic disorders and cancer. Mutations in genes encoding critical proteins may disrupt normal protein synthesis at either the

transcriptional or translational level, resulting in dysfunctional or absent proteins. A classic example is sickle cell anaemia, caused by a mutation in the β -globin gene that alters haemoglobin structure and function.³

In oncogenesis, aberrant gene expression frequently arises from activation of oncogenes and inactivation of tumour suppressor genes. In addition to genetic mutations, epigenetic alterations—such as hyper methylation of tumour suppressor gene promoters—also contribute significantly to cancer development. These observations highlight that gene expression regulation is not only essential for normal cellular function but also central to understanding disease mechanisms and developing targeted molecular therapies.^{1,2}

In summary, the integration and regulation of gene expression constitute a complex, multi-layered system that operates from the level of DNA to functional protein products. Precise coordination among these regulatory mechanisms ensures that proteins are produced in appropriate quantities and with correct structural integrity. A comprehensive understanding of these processes is fundamental in both biochemistry and medical science, particularly for elucidating the molecular basis of disease.

Critical Discussion

Protein synthesis represents a highly integrated molecular continuum, encompassing DNA replication, transcription, translation, and post-translational processing, including protein folding. These stages are not isolated events but are functionally and structurally interdependent. Consequently, disruption at any level can propagate downstream effects, ultimately altering protein structure and function. Within this framework, protein synthesis can be viewed as a complex biological system requiring high precision, where genomic stability and accuracy

of gene expression are essential determinants of cellular integrity.^{1,2}

At the level of DNA replication, errors in nucleotide incorporation may result in permanent mutations within the genome. These alterations are subsequently transmitted to daughter cells and serve as templates during transcription. When mutations occur within coding regions, they can modify the codon sequence of mRNA, thereby influencing the amino acid sequence during translation. Such changes in primary protein structure may lead to alterations in higher-order conformations and compromise biological function.³

A well-established example is sickle cell disease, which arises from a single point mutation in the β -globin gene. This mutation leads to the substitution of glutamic acid with valine, significantly altering the physicochemical properties of haemoglobin. Despite being a single amino acid change, this modification promotes abnormal haemoglobin polymerization under hypoxic conditions, resulting in erythrocyte deformation and impaired oxygen transport. This case illustrates how a molecular defect at the genetic level can translate into profound structural and clinical consequences.⁹

Beyond genetic mutations, errors may also occur during post-translational stages, particularly in protein folding. Proper folding is essential for achieving functional three-dimensional structures. Misfolded proteins may become unstable or aggregate into toxic complexes, a phenomenon known as protein misfolding. This process is strongly associated with several degenerative disorders.

For instance, Alzheimer's disease is characterized by the accumulation of β -amyloid plaques resulting from aberrant protein folding. Similarly, prion diseases such as Creutzfeldt-Jakob disease arise from conformational changes in normal proteins into pathogenic isoforms capable of inducing misfolding in other proteins.

These conditions highlight that not only the amino acid sequence but also the fidelity of folding processes is critical for maintaining protein function.^{11,1}

Furthermore, dysregulation of gene expression at both transcriptional and translational levels can lead to imbalances in protein production. Overexpression or under expression of specific proteins may disrupt cellular homeostasis. In cancer, for example, activation of oncogenes or inactivation of tumour suppressor genes results in uncontrolled cell proliferation due to aberrant protein expression. This underscores the importance of tightly regulated gene expression mechanisms in preserving normal cellular function.²

Overall, the interdependence among the processes involved in protein synthesis demonstrates that this system operates as a unified and coordinated network. DNA replication ensures the fidelity of genetic information, transcription regulates its transmission, translation converts it into polypeptide structures, and post-translational processes ensure the acquisition of functional conformation. Disruption at any stage can compromise the entire system, ultimately leading to pathological conditions.

From a biomedical perspective, adopting an integrative approach to understanding protein synthesis is essential. Analyzing the causal relationships between these molecular stages enables the identification of critical control points that may serve as therapeutic targets. This perspective provides a foundation for the development of gene-based therapies, protein-targeted interventions, and pharmacological strategies aimed at specific molecular pathways, thereby advancing precision medicine and improving clinical outcomes.

Conclusions

Protein biosynthesis is a complex, highly structured, and tightly integrated biochemical process that begins with DNA replication as the foundation for the inheritance of genetic information. This is followed by transcription, which generates RNA intermediates, and translation, which decodes genetic information into a polypeptide chain. Importantly, this process does not conclude with polypeptide formation; it is further refined through post-translational modifications and protein folding, which ensure that proteins attain a stable and biologically functional three-dimensional conformation.^{1,9}

Each stage of protein biosynthesis plays a distinct yet interdependent role. High fidelity during DNA replication preserves genetic integrity, accurate transcription determines the quality of mRNA transcripts, and precise translation ensures the correct amino acid sequence according to the genetic code. Subsequently, protein folding and post-translational modifications are essential for finalizing protein structure and enabling proper biological activity. Disruption at any stage may have systemic consequences, potentially leading to the production of abnormal proteins and the development of pathological conditions.²

Overall, the success of protein biosynthesis depends on precise coordination and regulation across all levels of molecular processes. Properly synthesized proteins perform essential biological functions, including enzymatic catalysis, structural support, and regulatory signaling, thereby maintaining cellular and organismal homeostasis. A comprehensive understanding of this integrated process is therefore fundamental not only in biochemistry but also in clinical medicine, particularly for elucidating the molecular basis of disease and advancing targeted therapeutic strategies.

Author Contribution Statement

The authors performed all aspects of this study.

References

- [1] Alberts B, Johnson A, Lewis J, Morgan D, Raff M, Roberts K, et al. Molecular biology of the cell. 7th ed. Garland Science; 2022.
- [2] Lodish H, Berk A, Kaiser CA, Krieger M, Scott MP, Bretscher A, et al. Molecular cell biology. 9th ed. W.H. Freeman and Company; 2021.
- [3] Berg JM, Tymoczko JL, Gatto GJ, Stryer L. Biochemistry. 9th ed. W.H. Freeman and Company; 2019.
- [4] Bell SP, Labib K. Chromosome duplication in *Saccharomyces cerevisiae*. *Nat Rev Mol Cell Biol*. 2016;17(10):553–564. <https://doi.org/10.1038/nrm.2016.70>.
- [5] Meselson M, Stahl FW. The replication of DNA in *Escherichia coli*. *Proc Natl Acad Sci U S A*. 1958;44(7):671–682.
- [6] Okazaki R, Okazaki T, Sakabe K, Sugimoto K, Sugino A. Mechanism of DNA chain growth. *Proc Natl Acad Sci U S A*. 1968;59(2):598–605.
- [7] Reha-Krantz LJ. DNA polymerase proofreading: multiple roles maintain genome stability. *Biochim Biophys Acta*. 2010;1804(5):1049–1063. 1804(5), 1049–1063.
- [8] Leman AR, Noguchi E. The replication fork: understanding the eukaryotic replication machinery and the challenges to genome duplication. *Genes (Basel)*. 2013;4(1):1–32. <https://doi.org/10.3390/genes4010001>
- [10] Nelson DL, Cox MM. Lehninger principles of biochemistry. 8th ed. W.H. Freeman and Company; 2021.
- [11] Hershey JWB, Sonenberg N, Mathews MB. Principles of translational control: an overview. *Cold Spring Harb Perspect Biol*. 2019;11(9):a032607. <https://doi.org/10.1101/cshperspect.a032607>.
- [12] Hartl FU, Bracher A, Hayer-Hartl M. Molecular chaperones in protein folding and proteostasis. *Nature*. 2011;475(7356):324–332. <https://doi.org/10.1038/nature10317>.
- [13] Corella D, Ordovas JM. Basic concepts in molecular biology related to genetics and epigenetics. *Rev Esp Cardiol*. 2017;70:696–810. <http://dx.doi.org/10.1016/j.rec.2017.03.012>.