Institute for Advanced Studies in Basic Sciences – Zanjan Department of Computer Science and Information Technology

By: Mahdi Vasighi

BOILDINGES

Molecular Biology Primer RNA, Proteins & Translation

Part 4

Mahdi Vasighi





Alternative splicing is an important mechanism for production of different forms of a protein from a single gene, called **isoforms**.



Central dogma of molecular biology







Proteins (polypeptides) are organic compounds made of amino acids arranged in a linear chain and folded into a globular form. Amino acids are molecules containing:

- a central α-carbon
- an amine group (NH₂)
- a carboxylic acid group (COOH)
- a side-chain (R) that varies between different amino acids.
- a hydrogen atom







The central α -carbon is asymmetric, these molecules can exist in two mirror-image forms called by convention the D (dextro) and the L (levo) isomers



Chirality and enantiomers

109.5°

109.5°

109.5°

 With rare exceptions, only the L forms of amino acids are found in proteins.







Most proteins are linear polymers built from series of different amino acids.





Proteins



Figure 4-2 Essential Cell Biology, 2/e. (© 2004 Garland Science)

















Proteins







Proteins can be grouped into several broad functional classes:

- Structural proteins, which provide structural rigidity to the cell.
- Transport proteins, which control the flow of materials across cellular membranes.
- Regulatory proteins, which act as sensors and switches to control protein activity and gene function.
- Signaling proteins, including cell surface receptors and other proteins that transmit external signals to the cell interior.
- Motor proteins, which cause motion.









Translation is the second process of **protein biosynthesis** (part of the overall process of **gene expression**). In translation, Messenger RNA (mRNA) is **decode**d to produce a specific polypeptide according to the rules specified by the **genetic code**.

For translation Three different type of RNA is required:

- messenger RNA (mRNA)
- transfer RNA (tRNA)
- ribosomal RNA (rRNA)







The sequence of codons that runs from a specific start codon to a stop codon is called a **reading frame**.





RNA secondary structure strand folds upon itself to form base pairs so it can have a diverse form of secondary structure.

The secondary structure of biological RNA's can often be uniquely decomposed into stems and loops.





Nature Reviews | Molecular Cell Biology





Dynamic programming algorithms for RNA secondary structure prediction with pseudoknots

Discrete Applied Mathematics Volume 104, Issues 1–3, 15 August 2000, Pages 45–62

Predicting RNA secondary structures from sequence and probing data

Methods Volume 103, 1 July 2016, Pages 86–98 Advances in RNA Structure

A Dynamic 3D Graphical Representation for RNA Structure Analysis and Its Application in Non-Coding RNA Classification PLoS ONE Volume11, issue 5, e0152238.





Transfer RNA (tRNA) is a molecule composed of RNA, typically 73 to 93 nucleotides in length.



Large

Small subunit





Ribosomal RNA (rRNA)

Ribosomal ribonucleic acid (rRNA) is the RNA component of the ribosome. It constitutes the predominant material within the ribosome, which is approximately 60% rRNA and 40% protein by weight.

The ribosomal RNAs form two subunits:

- the large subunit (LSU)
- small subunit (SSU)

Ribosomal RNA provides a mechanism for decoding mRNA into amino acids and interacts with tRNAs during translation.









SSU

LSU





1. Activation: the correct amino acid is covalently bonded to the correct transfer RNA (tRNA).













2. Initiation: Initiation involves the small subunit of the ribosome binding to the 5' end of mRNA







3. Elongation: During chain elongation, each additional amino acid is added to the nascent polypeptide chain







3. Termination: No tRNA can recognize or bind to this codon. Instead, the stop codon induces the binding of a release factor protein.



















Genetic Code

The genetic code is the set of rules by which information encoded in genetic material (DNA or mRNA sequences) is translated into proteins (amino acid sequences) by living cells.

Degeneracj

The code defines how sequences of three nucleotides, called **codons**, specify which amino acid will be added next during protein synthesis.

- 4 different base
- 3 position for each Codon
- 4^3 = 64 different combination There is only 20 amino acids!





	Second position						
Translation		U	С	А	G		
	IJ	UUU phe	UCU UCC _{ser}	UAU UAC ^{tyr}	UGU UGC	U C	
on (5'-end)	Ū	UUA UUG	UCA UCG	UAA Stop UAG Stop	UGA Stop UGG trp	AG	
	С	CUU _{leu} CUC	CCU CCC	CAU CAC ^{his}	CGU CGC	Thire	
		CUA CUG	CCA ^{pro} CCG	CAA gln CAG	CGA ^{drig} CGG	A U	
positi	Α	AUU AUC ile	ACU ACC	AAU AAC ^{asn}	AGU AGC ^{ser}	on (3'-	
First	~	AUA AUG met	ACA "" ACG	AAA <i>lys</i> AAG	AGA arg AGG	A G	
	G	GUU GUC GUA ^{val}	GCU GCC _{ala} GCA	GAU GAC ^{asp} GAA _{glu}	GGU GGC GGA ^{gly}	U C A	
		GUG	GCG	GAG Terminat	GGG	G	

Translation

TPA

U
C
p A
G
U _
, C
Ap
G
US
C $\widehat{\omega}$
A

Codon	Universal Code	Unusual Code*	Occurrence	U
UGA	Stop	Trp	Mycoplasma, Spiroplasma, mitochondria of many species	A
CUG	Leu	Thr	Mitochondria in yeasts	C
UAA, UAG	Stop	Gln	Acetabularia, Tetrahymena, Paramecium, etc.	
UGA	Stop	Cys	Euplotes	

*"Unusual code" is used in nuclear genes of the listed organisms and in mitochondrial genes as indicated. SOURCE: S. Osawa et al., 1992, *Microbiol. Rev.* **56**:229.







Institute for Advanced Studies in Basic Sciences – Zanjan Department of Computer Science and Information Technology





