05/25/2016

* DNA → RNA → protein
* DNA to RNA is transcription
* RNA to protein is translation
* Some RNAs can act as enzymes – tertiary structure forms
* Prokaryotes vs eukaryotes
  + Where/when
  + How do the enzymes know where to bind?
  + How does it start?
  + How does it end/
  + Post transcription processing?
* RNA types
  + MRNA: messenger RNA, code for proteins
  + rRNA: ribosomal RNA, form ribosome structure and catalyze protein synthesis
  + tRNA: transfer RNA, adaptors between mRNA and amino acids
  + snRNA: small nuclear RNA, nuclear processes
  + snoRNA: small nucleolar RNA: process rRNA
  + Other noncoding RNA: function in diverse cellular processes
    - telomere synthesis
    - X-chromosome inactivation
    - transport of proteins into ER
* RNA polymerases make RNA from DNA
  + RNA polymerase I: 5.8S, 18S, 28S rRNA genes
  + RNA polymerase II: all protein-coding genes, plus snoRNA genes and some snRNA genes\*
  + RNA polymerase III: rRNA genes, 5S rRNA genes, some snRNA genes and genes for other small RNAs
* sigma factor enables RNA polymerase in prokaryotes, transcription factors in eukaryotes
* Promoters allow transcription
  + Prokaryotes
    - Pribnow Box (-10 element) – TATAAT
    - -35 element – TTGACA
  + Eukaryotes
    - Assymetrical sequences
    - Basic core promoter: TATA box (TATAAA(A))
      * within 50 bp upstream of start site
      * found in unicellular eukaryotes
    - Core promoter PLUS
      * downstream promoters
      * proximal promoter elements
* On DNA: promoter, methianine, 200+ base pairs, stop codon
  + Open reading frame (ORF!!)
  + In eukaryotes, 200 bp have interspersed exons and introns
* RNA polymerase has gyrase function
* RNA polymerase builds from 5' to 3', reads from 3' to 5'
* Transcription initiation complex
* Lariat form – hairpin
* Post-transcription regulation
  + 5' cap
  + 3' poly A tail
  + Introns spliced out

|  |  |  |
| --- | --- | --- |
| Transcription | | |
|  | Prokaryotes | Eukaryotes |
| Where/when? | Cytoplasm | Nucleus |
| Where to bind? | Promoter | Promoter |
| Start? | Sigma factors, no repressor | Tfs on promoter contact enhancer |
| End? |  |  |
| Post transcription processing? |  |  |

05/26/2016

* Amino acids built from N end to C end
* Transfer RNA
  + anticodon – 3' to 5' sequence that matches the complementary 5' to 3' sequence (codon) on the mRNA
  + acceptor arm – amino acid code on 3' end
  + T and D loops provide structure for interface with aminoacyl-tRNA-synthetase
  + G-C hydrogen bonds force ccertain shape, allowing enzymatic behavior
* Introns: noncoding regions, eukaryotes only
* Exons: coding regions
* Codons are on mRNA and are 5' to 3', anticodons are on tRNA and are 3' to 5'
* 5' AUG 3' always first codon
* Wobble/redundancy
  + Anticodon in curcular loop doesn't exactly fit with codon
  + Third base pair in triplet doesn't matter as much in amino acid synthesis
  + Multiple ways to make each amino acid (except methionine)
* Ribosomes
  + 2 subunits
  + Eukaryotic bigger than prokaryotic
  + 16 subunits of rRNA used to figure out evolutionary distances
  + Exit hole, Aminoacyl hole, Peptidotransferase hole
  + Moves along mRNA
  + Assemble on top of mRNA
  + Made of rRNA and proteins
  + Read from 5' to 3'
  + P site is where growing peptide chain is kept and new AA are atttached
  + A site is where new codons are translated
  + E sites are where “naked” tRNA exit the ribosome'
  + Stop codons: UAA, UAG, UGA
    - No tRNA binds to this set of codons
    - One of these codons sat the A site attracts a release factor
    - Ribosome adds water to the last peptide, creating the carboxyl end
* Chaperone proteins aid formation of tertiary structure
* Improperly-folded proteins are tagged for deletion by Golgi apparatus
* Proteasome destroys and recycles proteins
* Klenow fragment
* Initiation, elongation, termination in transcription
* Introns spliced by spliceosome
* 5' cap, 3' poly A tails added
* Leaves nucleus through nuclear pore
* Three-letter codons
* Four special: 1 start, 3 stop
* mRNA binds to small ribosomal subunit upstream of start codon
* tRNAs bring amino acids, as determined by anticodons
* initiator tRNA binds, then large subunit to form translational complex

05/27/2016

* Bacteria need to respond quickly to changes in their environment
  + If they have enough of a product, they need to stop production
    - Why? Waste of energy to produce more
    - How? Stop production of enzymes for synthesis
  + If they find new food/energy source, need to utilize it quickly
    - Why? Metabolism, growth, reproduction
    - How? Start production of enzymes for digestion
* Lactose: beta-bonded glucose and galactose
* Structural genes make proteins
  + Beta-galactosidase allows breaking of beta bonds
  + Permase allows lactose to pass through membrane
  + Transacetylase enables lactose digestion (actual function unknown)
* Feedback inhibition
  + Product acts as an allosteric inhibitor of the first enzyme in the tryptophan pathway
    - Wasteful production of enzymes
* RNA polymerase binds to promoter site on DNA for mRNA transcription
  + Regulated by allosteric inhibitor on promoter site
* Gene regulation in bacteria
  + Cells vary amount of specific enzymes by regulating gene transcription
    - Induction: turning genes ON
    - Repression: turning genes OFF
* Operon
  + Genes grouped together with related functions
    - e.g. all enzymes in a metabolic pathway
  + Promoter: RNA polymerase binding site
    - Single promoter controls transcription of all genes in operon
    - Transcribed as one unit & a single mRNA is made
  + Operator: DNA binding site of repressor protein
  + Inducible operon
    - Lactose
      * Repressor always bound to operator except when lactose binds to lac repressor protein and triggeres repressor to release DNA
      * Allolactose is the inducer, byproduct of lactose fermentation
    - Usually functions in catabolic pathways
      * Digesting nutrients to simpler molecules
    - Produce enzymes only when nutrient is available
      * Cell avoids making proteins that have nothing to do
      * Cell allocates resources to other uses
  + Repressible operon
    - Tryptophan
    - Usually functions in anabolic pathways
      * Synthesizing end products
    - When end product is present in excess, cell allocates resources to other uses