

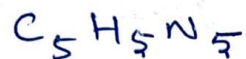
Genomics and Proteomics

Nomics means understanding computations
To be used in new computing device.

37.5 trillion cells

3 billion base-pairs

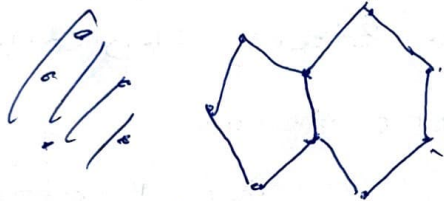
Adenine - Purin nucleotide base



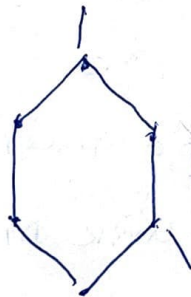
Cytosine (C), Guanine (G) Thymine (T)



Purine (A, G)



Pyrimidine (T, C)



Every base is added with a sugar and phosphorus

Nucleoside: Base + Sugar

Nucleotide: Base + Sugar + ^{own}Phosphorus

2 kinds of cells: Eukaryotes, Prokaryotes
Evolved. Primitive

Mitochondria → Power house.

Sugar → quality checks are performed here.

Protein Synthesis: ① Enzymes

② Hormones

— Pancreas
Insulin, Thyroid
Glands: Pituitary gland
Pineal gland

Protein Synthesis

Enzymes: created at a place and used at same place

Hormones: Created at one place and work at different place

RNA: Ribo Nucleic Acid

DNA: Deoxyribo Nucleic Acid.

T is replaced by U (Uracil)

TATGCCAG \rightarrow UAUGCCAG

Amino Acid: 3 bit sequence // Total 20 ^{Excluding} Start, Stop.

Start codon: AUG \rightarrow Methionine First Amino Acid in Protein

Stop Codon: UAG, UGA, UAA

Total 64 triplet Codes

Out of which 4 are Start, Stop Codes.

Male DNA - 20,000 genes.

Y Chromosome \rightarrow 100 Protein Coding genes.

X Chromosome \rightarrow 900 "

Female DNA - Up to 23,000 genes.

98% DNA refers to JUNK DNA. Non-Coding DNA

Steps in Protein Synthesis:

① Transcription

② Translation \rightarrow first, then comes

\rightarrow mRNA m stands for messenger

mRNA comes out of nucleus joins Ribosome.

Ribosomes are made up of rRNA

tRNA \rightarrow transfer RNA. \rightarrow brings complementary bases

3 bases at a time. (Codon \rightarrow 1/3 Anti Codon),
tRNA

\rightarrow Peptide bond: bond between two generated Amino Acids

\rightarrow Protein folding and Additional modification

- Central Dogma refers to flow of genetic information in cells as
DNA \rightarrow RNA \rightarrow Protein