YOUR MENTOR GURU

CSIR NET Life Sciences & Biotechnology — Unit 3

Fundamental Processes

Study & revision companion | Topic explanations, core facts, and active-recall questions

How to use this guide

Read each topic, explain the key mechanism in your own words, then answer the self-check prompts without looking at the notes. Use your detailed textbook or class notes for full derivations and additional examples.

Topic overview

1. 1. DNA Replication
2. 2. DNA Damage, Repair and Recombination
3. 3. Transcription and Promoters
4. 4. RNA Processing and Splicing
5. 5. Translation and Genetic Code
6. 6. Protein Processing and Degradation
7. 7. Gene Regulation and Epigenetics

1. DNA Replication

DNA polymerases extend a pre-existing primer 5′→3′ while reading the template 3′→5′.

Helicase unwinds duplex DNA; single-strand binding proteins stabilize exposed strands; topoisomerases relieve torsional stress.

Leading strands are synthesized continuously; lagging strands form Okazaki fragments joined after primer removal.

Proofreading by many replicative polymerases uses 3′→5′ exonuclease activity.

DNA polymerases extend DNA 5′ to 3′ from a primer. Leading and lagging strands differ because templates are antiparallel.

When solving a question, distinguish the underlying mechanism from its observable outcome. Compare the normal situation with the altered condition, and check whether the evidence supports a direct effect or only an association. The central distinction to retain is: proofreading and mismatch repair increase fidelity.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

2. DNA Damage, Repair and Recombination

Mismatch repair corrects replication errors escaping proofreading; defects elevate microsatellite instability.

Base-excision repair removes altered bases; nucleotide-excision repair excises bulky lesions such as UV photoproducts.

Homologous recombination uses a homologous template and is generally high fidelity; NHEJ joins ends without extensive homology.

RecA in bacteria and RAD51 in eukaryotes promote homologous strand exchange.

Base-excision repair corrects many small base lesions; nucleotide-excision repair removes bulky damage. Homologous recombination uses a homologous template.

When solving a question, distinguish the underlying mechanism from its observable outcome. Compare the normal situation with the altered condition, and check whether the evidence supports a direct effect or only an association. The central distinction to retain is: match lesion type with the repair mechanism.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

3. Transcription and Promoters

Bacterial RNA polymerase uses sigma factors for promoter recognition; eukaryotic Pol II transcribes most protein-coding genes.

RNA synthesis proceeds 5′→3′ and does not require a primer.

General transcription factors and mediator help assemble Pol II initiation complexes at many promoters.

Enhancers act through DNA-bound regulators and chromatin contacts; orientation and distance constraints vary.

RNA polymerase copies a DNA template into RNA. Promoters, transcription factors, activators and repressors regulate initiation.

When solving a question, distinguish the underlying mechanism from its observable outcome. Compare the normal situation with the altered condition, and check whether the evidence supports a direct effect or only an association. The central distinction to retain is: eukaryotic RNA polymerase II transcribes mRNA precursors.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

4. RNA Processing and Splicing

Eukaryotic pre-mRNA commonly receives a 5′ cap, intron removal and a 3′ poly(A) tail.

The spliceosome recognizes splice sites and branch point; two transesterification reactions release a lariat intron.

Alternative splicing produces distinct transcript isoforms from one gene.

rRNA and tRNA also undergo processing and chemical modifications.

Eukaryotic pre-mRNA is capped, spliced and usually polyadenylated. Alternative splicing generates different transcripts.

When solving a question, distinguish the underlying mechanism from its observable outcome. Compare the normal situation with the altered condition, and check whether the evidence supports a direct effect or only an association. The central distinction to retain is: splice-site mutations can change exon inclusion.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

5. Translation and Genetic Code

The ribosome reads mRNA codons 5′→3′ and synthesizes the polypeptide from N-terminus to C-terminus.

Aminoacyl-tRNA synthetases charge tRNAs and provide a major layer of translation fidelity.

The A site accepts incoming aminoacyl-tRNA, P site holds peptidyl-tRNA and E site releases deacylated tRNA.

Stop codons are recognized by release factors, not ordinary aminoacyl-tRNAs.

Ribosomes decode mRNA using charged tRNAs. Initiation, elongation and termination require specific factors.

When solving a question, distinguish the underlying mechanism from its observable outcome. Compare the normal situation with the altered condition, and check whether the evidence supports a direct effect or only an association. The central distinction to retain is: frameshifts often alter many downstream codons.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

6. Protein Processing and Degradation

Signal peptides can direct cotranslational targeting to the ER through SRP.

N-linked glycosylation begins in the ER; extensive glycan remodeling occurs in Golgi compartments.

Ubiquitin attachment commonly marks proteins for 26S proteasome degradation through E1, E2 and E3 enzymes.

Lysosomes degrade endocytosed material and many autophagic substrates.

Phosphorylation, glycosylation and cleavage modify protein function; ubiquitin-proteasome and lysosomal routes remove proteins.

When solving a question, distinguish the underlying mechanism from its observable outcome. Compare the normal situation with the altered condition, and check whether the evidence supports a direct effect or only an association. The central distinction to retain is: ubiquitination is not always a degradation signal.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

7. Gene Regulation and Epigenetics

The lac operon is induced when lactose-derived allolactose relieves LacI repression; glucose depletion favors cAMP–CRP activation.

The trp operon is repressible by tryptophan and additionally controlled by attenuation in bacteria.

Histone acetylation often correlates with accessible chromatin; DNA methylation effects depend on genomic context.

miRNAs guide post-transcriptional repression or RNA decay through Argonaute-containing complexes.

Operons illustrate bacterial gene control; enhancers, chromatin state and noncoding RNAs shape eukaryotic expression.

When solving a question, distinguish the underlying mechanism from its observable outcome. Compare the normal situation with the altered condition, and check whether the evidence supports a direct effect or only an association. The central distinction to retain is: changes in protein abundance need not reflect transcription alone.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

Active-recall practice

1. Explain the essential principles of 1. DNA Replication and give one experimental or real-world application.

2. Explain the essential principles of 2. DNA Damage, Repair and Recombination and give one experimental or real-world application.

3. Explain the essential principles of 3. Transcription and Promoters and give one experimental or real-world application.

4. Explain the essential principles of 4. RNA Processing and Splicing and give one experimental or real-world application.

5. Explain the essential principles of 5. Translation and Genetic Code and give one experimental or real-world application.

6. Explain the essential principles of 6. Protein Processing and Degradation and give one experimental or real-world application.

7. Explain the essential principles of 7. Gene Regulation and Epigenetics and give one experimental or real-world application.

Final revision checklist

- 1. DNA Replication
- 2. DNA Damage, Repair and Recombination
- 3. Transcription and Promoters
- 4. RNA Processing and Splicing
- 5. Translation and Genetic Code
- 6. Protein Processing and Degradation
- 7. Gene Regulation and Epigenetics

Further study

Use the corresponding unit notes, topic-wise detailed lessons, MCQs, practice tests and full-length mock tests on yourmentorguru.com. This compact PDF is a revision companion, not a replacement for full syllabus textbooks.