Please choose the most appropriate terms/phrases/statements that complete or answer the questions.
Attention: <u>More than one</u> of the choices provided may be correct.
(2.5 points for each question)

1. Which physical or chemical factor of the following list can cause DNA mutation?
   (A) Heat
   (B) Ultra-violet light
   (C) Ethidium bromide
   (D) Nitrous acid
   (E) 5-Bromouracil

2. Which following mutation repairing mechanism in bacteria is the most likely to repair DNA in an error-prone way?
   (A) Photoreactivation
   (B) Excision repair
   (C) Recombination repair
   (D) Alkyltransferase repair
   (E) SOS response

3. Which following description(s) is/are **CORRECT** about Okazaki fragments?
   (A) Short RNA primers needed for initiation of polymerization
   (B) Short stretches of DNA formed on the lagging strand
   (C) The smallest subunit of DNA polymerase III
   (D) Fragment of DNA polymerase I that lack 5' to 3' exonuclease activity
   (E) The non-specific side products of DNA replication

4. Which enzyme(s) is/are needed for bacterial genome DNA replication?
   (A) gyrase
   (B) RNA primase
   (C) Restriction enzymes
   (D) DNA polymerase III
   (E) RNase H

5. Which mechanism(s) is/are often used in bacterial horizontal gene transfer?
   (A) Transformation
   (B) Transfection
   (C) Transduction
   (D) Conjugation
   (E) Transposon

6. Which of the following biological mechanism(s) in the cell could be regulatory targets regarding gene expression?
   (A) Transcription
   (B) mRNA processing
   (C) mRNA export and localization
   (D) Translation
   (E) Protein modification

7. Which RNA molecule(s) is/are transcribed by RNA polymerase II?

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(A) tRNA
(B) rRNA
(C) snRNA
(D) mRNA
(E) microRNA

8. Which organism listed below would need spliceosome-based pre-mRNA splicing to remove introns?
(A) *Homo sapiens*
(B) *Drosophila melanogaster*
(C) *Caenorhabditis elegans*
(D) *Saccharomyces cerevisiae*
(E) *Escherichia coli*

9. U-rich small nuclear RNAs (snRNAs) are important for base pairing with the pre-mRNA and are required for pre-mRNA splicing. They include
(A) U1
(B) U2
(C) U4
(D) U5
(E) U6

10. Which following description(s) is/are **CORRECT** about ribozyme?
(A) A catalyst that uses RNA as substrate
(B) An enzyme that synthesizes RNA as a part of the transcription process
(C) An enzyme that catalyzes the association between the large and small ribosomal subunits
(D) An RNA with catalytic activity
(E) An important component of RNA transport from the nucleus to the cytoplasm

11. RNA interference (RNAi) is an evolutionarily conserved mechanism to degrade RNA molecules in a sequence-specific manner. This mechanism does **NOT** exist in
(A) *Homo sapiens*
(B) *Drosophila melanogaster*
(C) *Caenorhabditis elegans*
(D) *Saccharomyces cerevisiae*
(E) *Escherichia coli*

12. MicroRNAs are small non-coding regulatory RNAs that down regulate gene expression by the mechanisms including
(A) Repress translation of target mRNAs
(B) Trigger cleavage of target mRNAs
(C) Trigger decapping of target mRNAs
(D) Enhance polyadenylation of target mRNAs
(E) Trigger the nonsense-mediated decay (NMD) pathway

13. During the first stage of translation, the small and large ribosomal subunits assemble around an mRNA that has an aminoacylated initiator tRNA correctly positioned at the start codon. The process is mediated by a special set of proteins known as translation initiation (IFs). In eukaryotes, the translation initiation complex contains the 40S subunit, the Met-tRNA and IFs **NOT** including
(A) eIF1

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(B) eIF2
(C) eIF3
(D) eIF4
(E) eIF6

14. Which of the following techniques can be used to measure the amount of a specific mRNA in a sample?
(A) Real-Time quantitative reverse transcription PCR
(B) Primer extension analysis
(C) Northern blot analysis
(D) Southern blot analysis
(E) Western blot analysis

15. Which enzyme(s) is/are **NOT** required for setting up a Real-Time quantitative reverse transcription PCR experiment?
(A) *E. coli* DNA polymerase I
(B) T4 DNA ligase
(C) Taq DNA polymerase
(D) Reverse transcriptase
(E) T7 RNA polymerase

16. Protein-Protein interaction can be examined by yeast two-hybrid and co-immunoprecipitation. Which methods can be used for the same purpose as well?
(A) Electrophoretic mobility shift assay (EMSA)
(B) Farwestern blot analysis
(C) Glutathione-S-transferase (GST) fusion protein pull-down
(D) Förster resonant energy transfer (FRET)
(E) Bimolecular fluorescence complementation (BiFC)

17. Which method(s) can be used for detecting RNA-Protein interaction?
(A) Electrophoretic mobility shift assay (EMSA)
(B) Real-Time quantitative reverse transcription PCR
(C) Protein-RNA pull-down assays
(D) Fluorescent in situ hybridization (FISH)
(E) Oligonucleotide-targeted RNase H protection assays

18. Which method(s) can be used to functionally inactivate a gene without changing its DNA sequence?
(A) CRISPR/Cas9 genome editing
(B) RNAi interference
(C) Site directed mutagenesis
(D) TALEN genome edditing
(E) Cre-Lox and FLP/FRT recombinase target-based gene inactivation

19. Which consensus sequences will define a typical intron?
(A) 5' splice site
(B) 3' splice site
(C) Branch points (BPs)
(D) Polypyrimidine tract
(E) Kozak consensus sequence

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20. Which of the following evidence will indicate a discovery of a gene in a DNA sequence?
(A) The sequence is aligned partially to a known cDNA sequence
(B) The sequence is similar to a known genes in other organisms
(C) The sequence is AT-rich
(D) Typical intron splice sites are found
(E) Typical poly(A) sites are found

21. Please select the **CORRECT** description from the following options related to nucleic acids:
(A) A is mostly base paired with C
(B) Structure of nucleotides are composed of six-member ring sugar, base and phosphate group.
(C) The linkage between nucleotides is phosphodiester bond
(D) Nucleic acids at neutral pH buffer (pH=7) are highly negatively charged
(E) Quantification of DNA is based on absorbance 280nm

22. Please select the **CORRECT** description from the following options which are related to DNA synthesis during cell replication
(A) DNA synthesis can be either direction depends on where the primer is located
(B) The short DNA fragments formed during DNA replication is called okazaki fragment
(C) During DNA replication, short DNA will serve as a primer for the synthesis of new DNA strand
(D) Ligation between DNA fragments only occurs during DNA repair, not standard DNA replication process
(E) Since DNA polymerase can faithfully replicate the other strand of DNA, the length of DNA is always the same

23. Which of following statement regarding chromatin regulation is/are **CORRECT**:
(A) Histone methylation only results in suppression of gene expression
(B) Both DNA and histones can be methylation in human cells
(C) Euchromatin represent a highly packed chromatin
(D) RNA polymerase II occupancy on DNA region represent the lightly packed DNA region
(E) Histone Acetylation results in gene activation of the modified genes

24. Which of the following statements related to eukaryotic RNA is/are **TURE**:
(A) mRNA is made by RNA polymerase II
(B) Cap structure and polyA is an RNA modification after RNA is made, thus it is independent of the type of RNA polymerase that is used to make the RNA.
(C) PolyA tail is a string of A encoded in the DNA sequence
(D) The standard RNA degradation is initiated by decaping and polyA shortening.
(E) Nonsense-mediated decay (NMD) is an RNA degradation mechanism depends on the translation status of the RNAs.

25. Which of the following statements related to noncoding RNA is/are **TURE**:
(A) The noncoding RNA represent RNAs that are not coded for proteins, including tRNA and ribosomal RNAs
(B) Noncoding RNAs can be made by all three types of RNA polymerase
(C) MicroRNAs are made by RNA polymerase I
(D) Nucleotides in both ribosomal RNA and tRNA are heavily modified.
(E) microRNA regulate gene expression is most often at their DNA level

26. Which of following statements regarding eukaryotic translation is/are **TURE**:
(A) Translation is a protein making process, but this process still requires the capping structure of the mRNAs

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(B) One transcript could encode multiple coding sequences in both eukaryotic and prokaryotic system
(C) RNA splicing and translation occur simultaneously in both eukaryotic and prokaryotic system.
(D) Prior to 5' mRNA capping, the 5' end group of mRNA is tri-phosphate.
(E) A premature stop codon will not only affect the production of functional proteins, will also cause the instability of mRNAs

27.CRISPR is a famous genome-editing tool. Which of following statement is/are **TRUE**:
(A) CRISPR is discovered as a bacterial immune system
(B) Cas-9 protein is found in all bacterial CRISPR system
(C) Two major components that introduced into mammalian cell for genome editing are cas-9 protein and guide DNA
(D) Creating gene deletion using CRISPR rely on the mistake of DNA repairing system in the host cell
(E) Introducing GFP tagging endogenous protein using CRISPR relies on non-homologous end joining DNA repairing system.

28.For the following statements of various biological processes in different cell compartments, which statements is/are **TURE**:
(A) Nucleolus is located in the nucleus
(B) Ribosomal RNAs are made in the cytoplasm
(C) RNA splicing takes place in the cytoplasm
(D) Mitochondria has its own DNA and RNA
(E) The function of ribosomal RNAs is protein translation.

29.Which of the following amino acid residues are positively charged in buffer with pH 7:
(A) Arginine
(B) Aspartate
(C) Phenylalanine
(D) Lysine
(E) Tryptophan

30.What the following statements for enzyme is/are **TURE**:
(A) Catalytic activity and substrate binding activity can not be separated
(B) Catalytic function of an enzyme mostly relies on the charged group on the amino acid side chains
(C) In Michaelis-Menten curve, same amount of enzyme with defects in substrate binding can never reach to the same Vmax as wild-type
(D) The velocity (V) of catalysis of an enzyme is constant and it is independent of substrate concentration
(E) Dissociation constant (Kd) can be used to represent the binding affinity between enzyme and substrate

31.Regulation of transcription in mammalian cells
(A) altering the spacing between promoter-proximal elements or enchancers and the TATA box has been shown to have more effect on transcription from some eukaryotic promoters.
(B) some transcription factors can form heterodimers, and have less advantages to cells.
(C) DNA-binding domain and activation domain can be in different protein subunits.
(D) involves hormone receptors normally found in the nucleus.
(E) as the number of initiation-complex components bound to the promoter increases, the gel migration of the DNA-protein complex will decrease.

32.Structure and function of RNA in vivo and in vitro
(A) has fewer hydroxy groups than DNA.

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(B) can fold back on itself to form double-helical regions with DNA.
(C) is less susceptible than DNA to degradation at high pH.
(D) like DNA, is a long, unbranched macromolecule consisting of nucleotides joined by 5' → 3' phosphodiester bonds.
(E) can act as a catalyst.

33. What is the concentration of an adenine solution whose absorbance at 257= 0.330? (εm = 15,100) Assume path length = 1.00 cm.
(A) 2.18×10^{-6} M
(B) 2.18×10^{-5} M
(C) 3.3×10^{-6} M
(D) 3.3×10^{-5} M
(E) 6.6×10^{-4} M

34. A single amino acid changes in a protein may
(A) eliminate all antigenicity
(B) have no effect on antigenicity
(C) make protein more stable.
(D) produce cross-reacting material
(E) change its subcellular localization

35. Which of the following statement(s) is/are **TURE**?
(A) Cloned cDNA can be translated *in vitro* to yield labeled proteins.
(B) Suppressor mutations can identify genes encoding interacting proteins.
(C) Transcription start sites can be mapped by S1 protection and primer extension.
(D) DNA polymorphisms are used to map human mutations.
(E) Nuclease-protection method can quantitate specific RNAs in a mixture and mapping them.

36. What is the cell density of a bacterial culture if plating 0.2 ml of a 10^5-fold dilution of the culture yields 45 colonies.
(A) 4.5×10^6
(B) 9.0×10^6
(C) 2.25×10^7
(D) 4.5×10^7
(E) 9.0×10^7

37. Which of the following statement(s) is/are **TURE**?
(A) An entire genome can be cloned as fragments in a heterogeneous population of microbial cell or viruses that is called a cDNA library.
(B) Single stranded nucleic acids with complementary of nucleotide sequence will find and hybridize to each other in solution.
(C) Protein-coding regions of eukaryotic genes can be obtained by synthetizing genomic DNA from mRNA populations.
(D) The variant phenotypes associated with organellar DNA variants are transmitted by cytoplasmic contact alone.
(E) Mitochondria and chlroroplasts have their own unique linear DNA "chromosomes" distinct from nuclear DNA.

38. Which of the following characteristic(s) is/are **TURE** for enhancer regions in eukaryotic DNA?

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(A) DNA Pol I binding sites
(B) orientation and position dependent
(C) promote transcription
(D) bind transcription factors
(E) promote better cloning efficiency

39. Which of the following techniques CAN be used to check DNA binding proteins?
(A) DNAase I sensitivity assay
(B) Southern blot
(C) Chromatin immunoprecipitation assay
(D) Primer extension assay
(E) Electrophoretic mobility shift assay

40. Which of the following statement(s) is/are **TURE** about the proteins in ER?
(A) may be retained in ER.
(B) may be glycosylation.
(C) cytosolic ribosomes have proteins with N-terminal sequences that enter the ER during synthesis.
(D) may flow through to plasma membrane by C-terminal KDEL signal.
(E) may be diverted to other destinations by specific N-terminal signals.

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