

1. One organism contains 31% adenosine in genome. Which statement is correct?
  - (A) it should have 31% cytosine
  - (B) it should have 31% guanine
  - (C) it should have 24% thymine
  - (D) it should have 24% guanine
  - (E) None of them is correct
2. Which of statements is **INCORRECT** for the comparisons of euchromatin and heterochromatin?
  - (A) euchromatin is more open than heterochromatin in term of its structure
  - (B) heterochromatin is easier to be accessed by transcription factors
  - (C) DNAs and histones in heterochromatin all can be modified by methylation
  - (D) heterochromatin is not modified by acetylation
  - (E) euchromatin and heterochromatin are regulated by histone modifications
3. Which organelle is engaged in lipid oxidation?
  - (A) mitochondria (B) endoplasmic reticulum (C) golgi (D) lysosome (E) peroxisome
4. Which statement is correct for gene expression in prokaryotic organisms?
  - (A) mRNA is transported from nucleus to cytosol
  - (B) mRNA is subject to splicing for removing intron
  - (C) transcription occurs on the linear chromosome
  - (D) nascent mRNA is simultaneously bound by RNA polymerase and ribosomes
  - (E) most gene regulations happen at epigenetic, post-translational and post-translational levels
5. Which of the description of microRNAs (miRNAs) is **INCORRECT** ?
  - (A) silence gene expression
  - (B) lead to RNA degradation
  - (C) reduce protein production
  - (D) interact with proteins
  - (E) encode proteins
6. Which statement of transposon is **INCORRECT**?
  - (A) double-stranded DNA intermediate is integrated into the target site
  - (B) repeated sequence is common in transposon
  - (C) RNA has no role in transposon
  - (D) it is used for random mutagenesis
  - (E) transposons are present in prokaryotes and eukaryotes
7. Which of the following restriction enzymes is likely to produce a blunt end? (\* marks the cutting site)
  - (A) SmaI (CCC\*GGG)
  - (B) XmaI (C\*CCGGG)
  - (C) KpnI (GGTAC\*C)
  - (D) SacII (CCGC\*GG)
  - (E) FseI (GGCCGG\*CC)
8. Protein sequence is the **LEAST** likely to be used to:
  - (A) predict mRNA sequence
  - (B) predict DNA binding sites
  - (C) predict post-translational modification sites
  - (D) predict secondary structures
  - (E) predict subcellular localization
9. Which of the statement is **INCORRECT** for GTPase?
  - (A) GTP-bound as the "on" state

- (B) GDP-bound as the "off" state  
(C) GTPase activating proteins switch GTPases from "off" to "on" state  
(D) guanine nucleotide-exchange factor release GDP from GTPases  
(E) Two major classes of GTPases: trimeric and monomeric G proteins
10. Sandy wants to amplify a DNA sequence by Polymerase Chain Reaction (PCR). What is **NOT** essential for this experiment?  
(A) primers  
(B) oligo dT  
(C) dNTP  
(D) DNA polymerase  
(E)  $Mg^{2+}$  buffer
11. Single-molecular *in situ* hybridization **CANNOT** be used to:  
(A) measure endogenous protein expression  
(B) measure the mRNA expression of particular genes  
(C) visualize nucleolus  
(D) visualize telomere  
(E) reveal gene duplication in genome
12. Which of statements is correct?  
a. mitochondrial genome is circular  
b. bacteria genome is linear  
c. eukaryotic animals have linear and circular genome  
(A) only a  
(B) only b  
(C) only c  
(D) a and c  
(E) a, b and c
13. Post-translational modifications on histones regulate gene expression, and which of the modification is **NOT** observed on histones up to date?  
(A) phosphorylation  
(B) methylation  
(C) acetylation  
(D) ubiquitination  
(E) adenylation
14. Which of statements is **INCORRECT** for Hox gene?  
(A) Hox genes are controlled by transcription factors  
(B) Hox genes control body segmentation  
(C) The arrange of Hox genes in genomic locus is similar to body patterning  
(D) Hox genes only function in mammals  
(E) Hox genes encode transcription factors
15. Comparing the denature of proteins and DNAs, which one is correct:  
(A) all of them are reversible  
(B) all of them can be denatured by heat  
(C) denature changes the composition of proteins and DNAs  
(D) denature of proteins and DNAs does not change the conformation  
(E) Heat is the only way to denature proteins and DNAs
16. Which is **INCORRECT** for microtubules?  
(A)  $\alpha$ - and  $\beta$ -tubulin are essential for polymerization of microtubules

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- (B) myosin is the major motor protein that transport cargos along microtubules
  - (C) MTOCs is the seed to assemble microtubules
  - (D) polymerization of microtubules is uni-directional
  - (E) GTP hydroxylation is required for polymerization of microtubules
17. Which of the following statement is **INCORRECT** for cell cycle?
- (A) S-phase requires active DNA polymerases
  - (B) microtubules are attaching chromosomes at M phase
  - (C) G1-phase has duplicated chromosomes
  - (D) repairing of chromosomes occurs in G2-phase
  - (E) the cell cycle is ceased in G0-phase.
18. Which of the following has the enzyme activity?
- (A) ribonucleoprotein
  - (B) rRNA
  - (C) mRNA
  - (D) sgRNA
  - (E) ribozyme
19. Marry wants to clone a gene from a cDNA library. She designed a pair of primers and performed PCR, but she surprisingly found two PCR products. She then sequenced it, and found that two PCR products are mostly matching to the target gene except for having an intron in one of them. What could be the most possible reason?
- (A) incomplete splicing of the gene
  - (B) trans-splicing of the gene
  - (C) point mutation in primers
  - (D) low  $T_m$  for PCR reaction
  - (E) wrong buffer condition
20. Which statement about RNA is **INCORRECT**?
- (A) it can have enzyme activity
  - (B) it can form secondary structure
  - (C) it can form tertiary structure
  - (D) it can associate with protein
  - (E) it can associate with lipid
21. Which post-translational modification is usually associated with protein degradation?
- (A) ubiquitination
  - (B) SUMOylation
  - (C) phosphorylation
  - (D) glycosylation
  - (E) lipidation
22. Endosomal pathways in cells are critical for protein trafficking. Which of statements is correct?
- (A) ER-localized proteins have signal peptide KDEL at C-terminal
  - (B) proteins are completely synthesized in cytosol and being transported into ER
  - (C) the cargo vesicles are transported with COPII from golgi to ER
  - (D) mis-sorted proteins for ER residents in golgi are transported to lysosome for degradation
  - (E) the cargo vesicles are transported with COPI from ER to golgi
23. John is studying a protein with Zinc-finger motif. What is the most likely function for this protein?
- (A) cell adhesion protein
  - (B) enzyme
  - (C) ribozyme

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- (D) transcription factor  
(E) ribosome
24. CRISPR is a novel technique that generates double strands break with the guidance of "guide RNA". Sandy wants to target a gene with the sequence " ATTCTGATACGATGCATAAATATGCTGAGGAAATGTC", and which one is likely to work as a guide RNA sequence? (PAM site is marked)
- (A) 5'-TACGATGCATAAATATGCTG-3'  
(B) 5'-GATGCATAAATATGCTGAGG-3'  
(C) 5'-CCTCAGCATATTTATGCATC-3'  
(D) 5'- CAGCATATTTATGCATCGTA-3'  
(E) None of above
25. Which of the following **CANNOT** be determined by NGS (next generation sequencing)?
- (A) enzyme activity  
(B) mRNA level of particular genes  
(C) long non-coding RNA  
(D) the genes expressed by mitochondria  
(E) expression of small RNAs
26. Which of statements of Mitochondrial DNA is **INCORRECT**?
- (A) mtDNA is only inherited from mother in mammals  
(B) mtDNA is only inherited from cytoplasmically  
(C) duplication of mtDNA only happens at S phase in cell cycle  
(D) mtDNA encodes proteins for lipid metabolism  
(E) mitochondrial genetic codes differ from the standard nuclear codes
27. A mutation that changes a lysine codon to a stop codon is called a :
- (A) missense mutation  
(B) nonsense mutation  
(C) silence mutation  
(D) frameshift mutation  
(E) suppressor mutation
28. Which statement of mitosis is **INCORRECT**?
- (A) metaphase- chromosomes aligned at the metaphase plate  
(B) telophase- assembly of contractile ring  
(C) anaphase-spindle pole separation  
(D) prophase-contractile ring forms cleavage furrow  
(E) interphase- chromosome duplication
29. Which statement of SARS-Cov-2 is **INCORRECT**?
- (A) similar to HIV, it is an RNA virus with single strand RNA  
(B) spike proteins on the surface are essential for the infection  
(C) the genomic RNA is not integrated in host genome  
(D) it produces all essential proteins in ER  
(E) similar to HIV, it undergoes lytic cycle
30. SDS-polyacrylamide gel electrophoresis (PAGE) is a useful technique with the following descriptions **EXCEPT** for:
- (A) evaluate the protein size  
(B) need antibodies to reveal the presence of particular proteins  
(C) cannot distinguish dimers associated with non-covalent bonds  
(D) can visualize proteins with coomassie blue staining  
(E) can distinguish proteins with different pI

31. Which statement of ribosome is **INCORRECT**?
- (A) prokaryotic and eukaryotic ribosomes are composed of a large and a small subunit.
  - (B) an additional rRNA in large subunit of eukaryotic ribosome
  - (C) conformational changes of ribosomes require ATP hydrolysis
  - (D) ribosomes will accommodate release factors when encounter UAA, UAG and UGA
  - (E) the assembly of initial complex for translation usually requires tRNA of methionine
32. Splicing of mRNA must require the following **EXCEPT** for:
- (A) nucleophilic attack
  - (B) adenosine
  - (C) spliceosome
  - (D) transesterification
  - (E) splice sites

**Answer the question groups:**

**Group1:**

33. Mark is a graduate student studying the function of a gene called X in neurodevelopment in *Drosophila*. In the mutant animals without X gene, the transportation of synaptic vesicles is abolished. He did research on protein sequence of X, and found that there is a nuclear localization sequence. He cloned the gene and confirmed the subcellular localization of X protein. Based on it, he predicts that the function of X is **unlikely** to be:
- (A) a histone
  - (B) a transcription factor
  - (C) a factor in spliceosome
  - (D) a mitochondria protein
  - (E) a DNA polymerase
34. In order to gain understanding of gene X, he wants to investigate whether this protein is interacting with other proteins or nuclear acids. He listed out a few methods, but his advisor pointed out one of it is not going to help. Which one is likely the answer?
- (A) chromatin immunoprecipitation
  - (B) yeast two hybrid
  - (C) RNAseq
  - (D) co-immunoprecipitation
  - (E) electrophoretic mobility-shift assay
35. He then carried out the experiments, and found that X is interacting with a DNA sequence upstream of translational start site of Y gene. The transcription of Y gene is dependent on the presence of X, and he listed out a few hypotheses. Which one is the **LEAST** likely to be true?
- (A) X can epigenetically modify DNA sequence
  - (B) X can interact with PCNA
  - (C) X can interact with RNA polymerase
  - (D) X can unwind DNA double helix
  - (E) X can interact with activator sequence
36. Finally, he understood the biological function of gene X, but wanted to inspect the protein structure. Which approach is not appropriate?
- (A) X-ray crystallography
  - (B) NMR spectroscopy

- (C) cryo-electron microscopy
- (D) scanned electron microscopy
- (E) homology modeling

**Group2:**

37. James expressed a mRNA sequence from bacteria to generate a small peptide (RNA sequence- "UCAGACCAUGGCGAGCAAUUGCAUUA"). How many amino acids in this peptide?
- (A) 3
  - (B) 4
  - (C) 5
  - (D) 6
  - (E) 7
38. After sequencing, he found out a mutation in the RNA sequence that change a C into U as the following "UCAGACCAUGGCGAGCUAAAUUGCAUUA". Now, how many amino acids in this peptide?
- (A) 3
  - (B) 4
  - (C) 5
  - (D) 6
  - (E) 7
39. He then purified the peptide with the correct sequence from bacteria, but could not elicit the same response as endogenous peptides when he supplied it to culture neuronal cells. What is likely going wrong?
- (A) peptide is engulfed by autophagosome
  - (B) peptide is degraded by Cas9-CRISPR
  - (C) peptide is degraded by E3 ubiquitin ligases
  - (D) lack of covalent bonds
  - (E) lack of post-translational modification on the peptide
40. Finally, he figured out what went wrong, and successfully found a receptor on neuronal cells. Based on sequence homologous analysis, the receptor has 7 transmembrane domains. What is likely to be the receptor?
- (A) integrin
  - (B) G-protein couple receptor
  - (C) NMDA receptor
  - (D) frizzled receptor
  - (E) receptor tyrosine kinase

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