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並不得書寫、畫記、作答。

國立清華大學 111 學年度碩士班考試入學試題


系所班組別：生命科學院

甲組(生物與醫學科學組)

科目代碼：0404

考試科目：分子生物學

### —作答注意事項—

1. 請核對答案卷(卡)上之准考證號、科目名稱是否正確。
2. 考試開始後，請於作答前先翻閱整份試題，是否有污損或試題印刷不清，得舉手請監試人員處理，但不得要求解釋題意。
3. 考生限在答案卷上標記「由此開始作答」區內作答，且不可書寫姓名、准考證號或與作答無關之其他文字或符號。
4. 答案卷用盡不得要求加頁。
5. 答案卷可用任何書寫工具作答，惟為方便閱卷辨識，請儘量使用藍色或黑色書寫；答案卡限用 2B 鉛筆畫記；如畫記不清(含未依範例畫記)致光學閱讀機無法辨識答案者，其後果一律由考生自行負責。
6. 其他應考規則、違規處理及扣分方式，請自行詳閱准考證明上「國立清華大學試場規則及違規處理辦法」，無法因本試題封面作答注意事項中未列明而稱未知悉。

# 國立清華大學 111 學年度碩士班考試入學試題

系所班組別：生命科學院甲組、丁組

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\*請在【答案卡】作答

## I. 選擇題 - multiple choice questions and select One or More Answer Choices according to the specific question directions (70 points, 2 points for each).

1. Chi sites are \_\_\_\_\_.

- (A) generated from Holliday junctions
- (B) inverted repeats
- (C) binding sites for RecA protein
- (D) specific sequences in prokaryotic genomes where crossovers occur
- (E) specialized single-stranded region

2. A single nucleotide deletion occurred in a gene. The change is indicated below. What is the consequence of the mutation?

..... AGT CGA TGA GTT AGC CTA ..... → ..... AGT CGA TGG TTA GCC TA.....

- (A) The mutation occurs in the third position of a codon so it is likely to be a silent mutation because of the Wobble effect.
- (B) It leads to frameshift so the downstream amino acid sequence will alter and the protein is unlikely to be functional.
- (C) It results in premature termination of translation so a truncated polypeptide will be produced.
- (D) A longer polypeptide will be made but the protein might still be functional.
- (E) It changes the single amino acid, which may or may not cause a problem.

3. What is the purpose of the inverted repeats at the ends of DNA-based transposons?

- (A) The inverted repeats are recognized by enzymes that move the elements.
- (B) The inverted repeats are the sites of transfer.
- (C) The inverted repeats are recognized by restriction enzymes that cut out the transposon.
- (D) The inverted repeats are magnets for nucleases.
- (E) The inverted repeats protect transposons from degradation.

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4. What is 5' UTR?

- (A) 5' untranscribed region: it refers only to the promoter region.
- (B) 5' untranscribed region: it includes promoter and enhancer.
- (C) 5' untranscribed region: it regulates transcription activity.
- (D) 5' untranslated region: it is removed during RNA splicing.
- (E) 5' untranslated region: it must contain the first exon.

5. Rolling circle replication \_\_\_\_\_.

- (A) begins when the origin of replication is pulled apart to generate a replication bubble
- (B) occurs at the origin of vegetative replication
- (C) begins when the origin of replication is nicked and one strand is unrolled
- (D) occurs when a plasmid replicates in step with host cell division
- (E) occurs bidirectionally that can rapidly synthesize multiple copies

6. Regarding molecular cloning using restriction enzyme and ligase.

- (A) Blunt end is clean and thus easier to be ligated.
- (B) Ligase also mediates joining of sticky ends by catalyzing the formation of hydrogen bonds.
- (C) Two sticky ends with complementary overhangs can be perfectly ligated but the restriction enzyme recognition site is not necessarily restored.
- (D) Restriction enzyme more efficiently cuts at the ends of DNA fragments.
- (E) Phosphatase treatment of both digested vector and digested insert reduces self-ligation so that correct ligation is enhanced.

7. The size of a gene in the genome is 3kb. What is the expected size of the polypeptide product encoded from the 3kb sequence? It appears as a single 60kD band on a SDS-PAGE gel. What could be the explanation for the difference?

- (A) 110kD; presence of introns
- (B) 110kD; protein degradation
- (C) 55kD; post-translational modifications
- (D) 55kD; amino acid composition bias
- (E) 30kD; dimer formation

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\*請在【答案卡】作答

8. Which of the following factor(s) promote dissociation of 70S ribosome to 50S and 30S?

- (A) IF-2
- (B) IF-3
- (C) EF-Tu
- (D) EF-G
- (E) RRF

9. Which of the following factor(s) mediates the binding of the Shine-Dalgarno sequence with the complementary sequence of the 16S rRNA?

- (A) IF-2
- (B) IF-3
- (C) EF-Tu
- (D) EF-G
- (E) RRF

10. Which of the following descriptions is **NOT** correct for comparison of protein translation between eukaryotes and bacteria?

- (A) Bacterial translation begins with methionine
- (B) Bacterial translation requires Shine-Dalgarno sequence to show ribosomes where to start
- (C) Eukaryotic mRNA has caps at 5' end
- (D) Eukaryotic initiating tRNA is not same as tRNA for interior
- (E) Eukaryotic translation requires Kozak sequence to show ribosomes where to start

11. Which of the following factor(s) can bind Pab1p, a poly[A]-binding protein?

- (A) eIF1
- (B) eIF1A
- (C) eIF4A
- (D) eIF4E
- (E) eIF4G



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\*請在【答案卡】作答

12. Which of the following factor(s) has an RNA helicase activity in translation initiation complex?

- (A) eIF1
- (B) eIF1A
- (C) eIF4A
- (D) eIF4E
- (E) eIF4G

13. Which of the following factor(s) are involved in dissociating improper complexes between 40S subunits and mRNA?

- (A) eIF1
- (B) eIF1A
- (C) eIF4A
- (D) eIF4E
- (E) eIF4G

14. Which of the following descriptions is **NOT** correct for the peptidyl transferase in ribosome?

- (A) The peptidyl transferase resides on the 50S ribosomal particle
- (B) The peptidyl transferase activity is GTP-dependent
- (C) Minimum components necessary for its activity are 23S rRNA and proteins L2 and L3
- (D) 23S rRNA is at the catalytic center of peptidyl transferase
- (E) puromycin can be its substrate

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\*請在【答案卡】作答

15. Which of the following description about histone is (are) correct?

- (A) The molecular mass of Histone H4 is bigger than the other types of histones.
- (B) Histones H2A/H2B and H3/H4 dimerize through the non-covalent interaction of a highly conserved structural motif found in each core histone.
- (C) The histone H3 is extreme highly conserved from pea to cow, which differs by only two residues.
- (D) Histones H1 and H5 bind as monomers to nucleosomes and internucleosomal linker DNA to facilitate higher-order DNA compaction.
- (E) The heterogeneity of histone proteins is due to alternative splicing.

16. Which of the following description about histones modification is (are) correct?

- (A) Histone acetylation specifically occurs in the nucleus.
- (B) The bromodomain domain of HAT(histone acetyltransferase) recognizes acetylated lysine residues on the N-terminal tails of histones.
- (C) The type B HAT does not contain the bromodomain.
- (D) The SANT domain of the type A HAT binds to DNA instead of histone.
- (E) HDAC deacetylates lysine on the N-terminal tail of core histone, leading to activation of gene transcription.

17. Which of the following description about RNA polymerase II (Pol II) is (are) correct?

- (A) Pol II is a multiprotein complex that transcribes DNA into precursors of mRNA and microRNA.
- (B) The C-terminal domain (CTD) of the RNA polymerase binding protein (Rpb1) subunit of Pol II interacts with the splicing factor and stimulates splicing of substrates in organisms that use exon definition.
- (C) The facilitates chromatin transcription (FACT) complex is a histone chaperone comprising Spt16 and SSRP1, which is involved in transcription elongation by RNA polymerases II.
- (D) The CTD of the Rbp1 subunit is involved in capping and splicing but not in polyadenylation.
- (E) The cotranscriptional cleavage (CoTC) element is essential for transcription termination.

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18. Which of the following description about polyadenylation is (are) correct?

- (A) The polyA binding protein I (PAB I) binds to mRNA Poly(A), which recruits polysomes and enhances the translatability of mRNA.
- (B) Continuously translating mRNA to protein causes Poly(A) turnover, leading to mRNA degradation.
- (C) PAB II is critical for the initiation of polyadenylation.
- (D) Occurrence of pre-mRNA cleavage triggers the assembling the of precleavage complex bound to the cleavage site.
- (E) The cleavage and polyadenylation specificity factor (CPSF) is required for both initiation and elongation phases of Poly(A).

19. Which of the following description about RNA editing is (are) correct?

- (A) RNA editing occurs in kinetoplasts.
- (B) RNA editing proceeds in a 5'→3' direction
- (C) gRNAs form wobble base pairs with pre-mRNA and direct both insertion and deletion of UMPs in pre-mRNA
- (D) The cytidine deaminases acting on RNA (CDAR) carries out C to G transversion for RNA editing.
- (E) Endonuclease, terminal uridylyl transferase (TUTase), and ligase are required for removing UTP from pre-mRNA.

20. Which of the following is (are) involved in RNA interference?

- (A) Dicer
- (B) Argonaut 2 (ago2)
- (C) ATP
- (D) R2D2
- (E) C3PO

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\*請在【答案卡】作答

21. Which of the following is (are) description about miRNA is (are) correct?
- (A) miRNA blocks translation initiation and elongation
  - (B) miRNA causes mRNA degradation
  - (C) miRNA activates translation
  - (D) miRNA can be processed from spliced introns
  - (E) Biogenesis of miRNA occurs in both the nucleus and cytoplasm.
22. Recombinant spike protein of SARS-CoV-2 is currently used for COVID-19 vaccination. Which of the following approach is NOT applied for the recombinant protein production from eukaryotic cells?
- (A) Identify coding sequence of target protein from NCBI, gene bank or GIASID database
  - (B) Generate an expression construct with the target gene driven by a T7 promoter
  - (C) Generate an expression construct with the target gene driven by a CMV promoter
  - (D) Incorporate the target gene with an extra tag (such as his, Fc, myc, flag etc) for purification
  - (E) Transfection the expression construct into a cell line such as CHO cells
23. Which of the following approach is NOT generally used to reduce or diminish a specific target gene expression in the cell?
- (A) small interference RNA (siRNA)
  - (B) CRISPR/Cas9
  - (C) MicroRNA
  - (D) Small hairpin RNA (shRNA)
  - (E) Long non-coding RNA (lncRNA)
24. Which of the following epigenetic modification is NOT maintained in daughter cells after cell division?
- (A) DNA methylation
  - (B) DNA phosphorylation
  - (C) Histone methylation
  - (D) Histone acetylation
  - (E) Histone phosphorylation

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25. Which of the following enzyme is essential for the replication of a virus with a minus-strand RNA genome?

- (A) DNA-dependent DNA polymerase
- (B) RNA-dependent DNA polymerase
- (C) DNA-dependent RNA polymerase
- (D) RNA-dependent RNA polymerase
- (E) Reverse transcriptase

26. Which of the following approach does NOT discriminate the Omicron variant from the wild type SARS-CoV-2 in nasal swabs?

- (A) Next generation sequencing
- (B) RT-PCR using variant-specific primer sets
- (C) Neutralizing antibody detection
- (D) Viral antigen detection
- (E) Hybridization gene chip

27. What is the key enzyme complex which activity is blocked by the G2/M DNA damage repair mechanism before mitotic entry?

- (A) Cyclin A/Cdk2
- (B) Cyclin D/Cdk6
- (C) Cyclin A/Cdk1
- (D) Cyclin B/Cdk1
- (E) Cyclin D/Cdk4

28. Which of the following technology can be used for genome editing?

- (A) CRISPR/Cas9
- (B) Transcription activator-like effector nucleases (TALEN)
- (C) Zinc Finger Nuclease (ZFN)
- (D) Editing by Nucleobase Modification (BASE editing)
- (E) All of the above

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29. Small ribosome subunits scan for initiation sites on eukaryotic mRNA. Which of the following descriptions is not correct?

- (A) Cap binding complex contains eIF4G.
- (B) Cap binding complex contains eIF4A.
- (C) Cap binding complex contains eIF5.
- (D) 43S pre-initiation complex contains eIF1.
- (E) 43S pre-initiation complex contains eIF2.

30. Initiation Factor eIF2. Which of the following descriptions is not correct?

- (A) eIF2 unwinds secondary structure of mRNA.
- (B) eIF2 is a heterotrimeric protein.
- (C) eIF2 is active when bound to GTP.
- (D) eIF2 binds to Met-tRNA<sub>i</sub>.
- (E) eIF2B is the GDP exchange factor for eIF2.

31. Bacteriophages. Which of the following descriptions is not correct?

- (A) Bacteriophages specifically infect bacteria.
- (B) Their genetic material is surrounded by a protein capsid.
- (C) This is connected to the elongated sheath by a collar region.
- (D) The sheath forms a hollow tube through which the viral proteins are injected into the host.
- (E) At the bottom is the base plate.

32. Spliceosome Assembly. Which of the following descriptions is not correct?

- (A) The commitment complex is the E complex.
- (B) The E complex contains U13 snRNP bound at the 5' splice site
- (C) The E complex contains the protein U2AF bound to a pyrimidine tract.
- (D) U2AF is a heterodimer consisting of the U2AF65 and U2AF35.
- (E) The E complex progresses to the A complex in the presence of ATP.

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33. Iron-response element (IRE). Which of the following descriptions is not correct?

- (A) IRE consists of multiple stem-loop structures.
- (B) The affinity of the IRE-binding protein for the IRE is altered by ion binding.
- (C) The IRE-binding protein exhibits low affinity when its iron-binding site is full.
- (D) The IRE-binding protein exhibits high affinity when its iron-binding site is not full.
- (E) The IRE-binding protein destabilizes the mRNA.

34. MicroRNA. Which of the following descriptions is not correct?

- (A) The precursor is primary miRNA (pri-miRNA).
- (B) Pri-miRNAs fold into stem-loop structures.
- (C) The loop region of pri-miRNA is cut by Drosha.
- (D) The pre-miRNA exits the nucleus.
- (E) The pre-miRNA is trimmed by Dicer to form miRNA.

35. Using the genetic code. Which of the following descriptions is not correct?

- (A) The bases of mRNA are read off in groups of three, the codon.
- (B) There are 128 different codons in the genetic code.
- (C) Bases are read from 5' to 3'.
- (D) UAA, UAG, and UGA have signal stop.
- (E) AUG act as start codons.

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## II. 簡答題 - essay questions (30 points, 6 points for each)

36. Which molecular biology method is the most reliable approach to examine the current status of SARS-CoV-2 infection? What kind of viral information is required for the assay? Please explain how CT value is determined and what it means.

37. What is a TA vector and how is TA cloning done?

38. Please describe how post-transcriptional control of transferrin receptor (TfR) expression by cytosolic aconitase under high and low cellular iron levels (4 points). Please predict the outcomes if a mutation prevents aconitase from binding iron in the cell that contains abundant TfR mRNA (2 points).

39. SARS-CoV-2 is a coronavirus that causes the COVID-19 pandemic. The virus carries a positive strand “polycistronic” RNA genome.

Please explain “polycistronic RNA”? (2 points)

Please explain the mechanism of “ribosomal frameshifting” for the translation of viral products of SARS-CoV-2. (4 points)

40. Non-coding RNAs (ncRNAs) do not code for proteins. Column I lists ncRNAs. Match each one in column I to its correct description in Column II.

### Column I

small cytoplasmic RNAs (scRNA)

small nuclear RNA (snRNA)

small nucleolar RNA (snoRNA)

### Column II

A. RNAs that are present in the cytoplasm.

B. One of many small RNA species confined to the nucleus; several of them are involved in splicing or other RNA processing reactions.

C. A small nuclear RNA that is localized in the nucleolus.