

元智大學 102 學年度研究所 碩士班 招生試題卷

系(所)別： 生物與醫學資訊
碩士學位學程

組別： 不分組

科目： 生物資訊概論

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●不可使用電子計算機

1. (5%) Which of the following items contain DNA?
 (A) Chromosome (染色體) (B) Mitochondrial (粒線體) (C) Chromatin (染色質)
 (D) Ribosome (核糖體) (E) Lysosome (溶酶體) (F) Chloroplast (葉綠體)
2. (10%) Please define the **central dogma of molecular biology** in eukaryotes and prokaryotes, and briefly describe their differences.
3. (16%) Please briefly introduce the following biological databases and tools: (任選 8 個子題)
 (a) BLAST (Basic Local Alignment Sequence Tool)
 (b) WebLogo
 (c) MEME
 (d) ClustalW
 (e) Ensembl
 (f) UniGene
 (g) PubMed
 (h) OMIM (Online Mendelian Inheritance in Men)
 (i) KEGG
 (j) InterPro
 (k) BioMart
 (l) dbSNP
 (m) dbEST
 (n) miRBase
 (o) UniProt
 (p) NCBI GEO
 (q) RNAFold
4. (8%) Please illustrate what are the Exon, Intron, and Regulatory region for a gene.
5. (6%) Please define the following terms: Paralogs, Orthologs and Homology.
6. (1) What is the amino acid? (5%) (2) Please illustrate the basic chemical architecture of an amino acid (5%). (3) Please translate the mRNA sequence AUGACUUGGUCAUUUUA into an amino acid sequence using following table (5%).

| Second base in codon | | | | | |
|----------------------|---|--------------------------|----------------------------|---------------------------|------------------|
| | | A | G | | |
| First base in codon | U | Phe Phe Leu Leu | Ser Tyr STOP STOP | Cys Cys STOP Trp | U C A G |
| | C | Leu Leu Leu Leu | Pro Pro Gln Gln | His His Arg Arg | U C A G |
| | A | Ile Ile Ile Met | Thr Thr Lys Thr | Asn Asn Lys Lys | U C A G |
| | G | Val Val Val Val | Ala Ala Ala Ala | Asp Asp Glu Glu | U C A G |
| | | | Gly Gly Gly Gly | | |

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7. Please explain the following terms: (1) Global alignment (5%), (2) Local alignment (5%), and (3) Semiglobal alignment (5%).

8. Let $S_1 = \text{TGGACTTACTA}$ and $S_2 = \text{AAGGACTA}$ and let the scores of match, mismatch and gap penalty be 1, -1, and -2, respectively. Please finish the following table used in the dynamic programming algorithm for computing the local alignment of S_1 and S_2 (10%), and enumerate the best local alignment between S_1 and S_2 (5%).

| Local | S_1 | T | G | G | A | C | T | T | A | C | T | A |
|-------|-------|---|---|---|---|---|---|---|---|---|---|---|
| S_2 | 0 | | | | | | | | | | | |
| A | | | | | | | | | | | | |
| A | | | | | | | | | | | | |
| G | | | | | | | | | | | | |
| G | | | | | | | | | | | | |
| A | | | | | | | | | | | | |
| C | | | | | | | | | | | | |
| T | | | | | | | | | | | | |
| A | | | | | | | | | | | | |

9. Please explain: (1) What is the microRNA? (5%) (2) How to identify the targets of microRNA by Bioinformatics method? (5%)

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