

Edit Mode is: **OFF****MCB-3421-Introduction to Molecular Evolution and Bioinformatics-SEC001-1188**

Assessments

Review Test Submission: Take home exam #1

## Review Test Submission: Take home exam #1

User	Johann Gogarten
Course	MCB-3421-Introduction to Molecular Evolution and Bioinformatics-SEC001-1188
Test	Take home exam #1
Started	9/13/18 5:33 PM <small>LATE</small>
Submitted	9/13/18 5:40 PM <small>LATE</small>
Due Date	9/12/18 11:15 AM
Status	Needs Grading
Attempt Score	Grade not available.
Time Elapsed	7 minutes
Results Displayed	Correct Answers

**Question 1**

Needs Grading

1. Give a one sentence description of the field known as Bioinformatics.

Correct

Answer: Bioinformatics is the science at the intersection of Computer Sciences (informatics) and Genomics and the analysis of other biological data sets related to the acquisition of large amounts of data.

**Question 2**

1 out of 1 points

Bioinformatics does NOT include which of the following activities?

Correct Answer: B. Figuring out a protein structure from X-ray crystallography

**Question 3**

1 out of 1 points

Can a protein be 84% homologous to another protein?

Correct Answer:  B. Mostly no, with the exception of cases of domain shuffling.

#### Question 4

Needs Grading

How many peptides (short proteins) of 70 amino acids in length are possible, given that there are 20 possible amino acids? For your answer only consider the principles of combinatorics and ignore possible incompatibilities between amino acids.

How does this number compare to the estimated number of protons in the universe?

Correct Answer: 1.18E91  $\leftarrow$   $20^{70}$   
 It is larger by ~~about ten~~ orders of magnitude

#### Question 5

Needs Grading

How many **types** of subunits (note: this asks for the **different types** of subunits, encoded by separate genes, not the number of subunits) form the hexamer (the head) of nucleotide binding subunits in the F1 ATPase? (In your answer, do not count the subunit that is rotated.)

Correct Answer:  2  $3\alpha$  &  $3\beta$

#### Question 6

1 out of 1 points

Proteins that evolved from the same ancestral protein

Correct Answer:  D. Do not necessarily retain detectable similarity in primary sequence.

#### Question 7

1 out of 1 points

True/False In the catalytic cycle of the ATPase, all of the catalytic subunits work in different phases of the catalytic cycle at any one point in time.

Correct Answer:  True

#### Question 8

1 out of 1 points

True/False The ancestral ATPase could have looked like a homohexamer with six identical subunits.

Correct Answer:  True

### Question 9

1 out of 1 points

True/False The different ATP binding subunit types that form the **hexamer** of the F1- ATP synthase are homologous to each other.

Correct Answer:  True

### Question 10

1 out of 1 points

What is homology?

Correct Answer:  C.  
Similarity due to shared ancestry, i.e. both got it from a common ancestor.

### Question 11

1 out of 1 points

What might be the reason for proteins that show significant similarity in their primary sequence (when no simple repeats or low complexity regions are present) to be homologous.

Correct Answer:  A.  
Sequence space is so big that stumbling onto a significantly similar sequence by chance is very unlikely

### Question 12

1 out of 1 points

Which elements make up the secondary structure of proteins?

Correct Answer:  C. Beta sheets, alpha helices, and loops.

### Question 13

1 out of 1 points

Which of the following is NOT part of the explanation for how complex functional molecules were assembled, despite the vastness of protein space?



Correct Answer:  A.  
Gaia directs protein evolution, through negative feedback loops, to the correct region of protein space.

**Question 14**

1 out of 1 points

Which of the following is NOT considered strong evidence for homology?

Correct Answer:  D. Identical function

*Eg: ATP binding  
H<sup>+</sup> pumping ATPase*

**Question 15**

1 out of 1 points

ATP, GTP, NAD, NADP, FMN, and FAD are example of what type of cofactor?

Correct Answer:  A. Nucleotide or modified nucleotide

**Question 16**

1 out of 1 points

Assuming equal frequency of the different building blocks, two random protein sequences are on average \_\_\_\_\_ and nucleotide sequences are on average \_\_\_\_\_?

Correct Answer:  B. 5% identical and 25% identical.

**Question 17**

1 out of 1 points

How are self-splicing introns removed from the mRNA?

Correct Answer:  D. None of the above.

**Question 18**

1 out of 1 points

How does Lysozyme destroy the stability of the bacterial cell wall?

Correct Answer:  Lysozyme cleaves the beta 1-4 glycosidic bond between NAG and N-acetylmuramic acid.

**Question 19**

1 out of 1 points

In the lysozyme structure 1HEW, the enzyme is crystallized together with an NAG trimer. This trimer

Correct Answer:  6) 2 and 4 are correct

**Question 20**

1 out of 1 points

If the murein sacculus of a bacterial cell is weakened, the cells may die

Correct



Answer:

because the cells blow up, because the osmotically driven water influx is no longer balanced by the turgor pressure.

**Question 21**

1 out of 1 points

Transcription denotes the process

Correct Answer:



by which mRNA is synthesized on a DNA template

**Question 22**

4 out of 4 points

Which of the following occur after the primary transcript has been created, and before the the mRNA is translated?

Correct



A.

Answers:

In eukaryotes, the 5' end of the RNA is capped with a modified guanosine



C. Introns are removed through splicing the exons together



D. In eukaryotes for most RNAs a poly A tail is added at the 3' end

Thursday, September 13, 2018 5:40:36 PM EDT

← OK

Else: ATP synthesis & electron transport chains are linked via the electrochemical gradient for protons ( $\Delta pH$  &  $\Delta E$ ) aka proton motive force

⇒ see Wikipedia entry on chemiosmosis