7.012 Quiz 1 ANSWERS

A≥88 ~32% of test takers!!! (121)
B≥75 ~37% of test takers (139)
C≥60 ~16.6% of test takers (62)
D≥50 ~10.4% of test takers (39)
F<49 ~3.5% of test takers (13)

Regrade requests (with a note attached indicating the problem and part you want reexamined) accepted until Thursday Oct. 13th, 4:30pm, in 68-120.

Monday 10/03/05

Final exam December 16th 1:30 pm

<table>
<thead>
<tr>
<th>Question</th>
<th>Value</th>
<th>Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
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<td></td>
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<td>2</td>
<td>29</td>
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<td>3</td>
<td>21</td>
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<td>4</td>
<td>8</td>
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<tr>
<td>5</td>
<td>20</td>
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Question 1

a) On the molecule represented below, match the circled structure with the name. 4pts

The hypothetical enzyme "Grabase" has a binding pocket for this molecule. The amino acid side chains found in the binding pocket are shown below.

b) For each of the binding pocket amino acids, describe its character and the strongest interaction with the substrate in the following table. 12 pts (graded across in rows-first two columns graded as a unit- (1 point for polar hydrophilic, additional point for determining charge state), third column worth 1 point.)
c) Of the amino acid changes listed below, which one do you predict would abolish the ability of Grabase binding its substrate? .................Put your answer → 3pts

i) Ser22 → Thr  
ii) Asn33 → Gln  
iii) Arg44 → Glu  
iv) Lys55 → Arg

d) Of the amino acid changes listed in c), which one do you predict would increase the likelihood of binding the substrate analogue below? Put your answer → 3pts

\[
\text{\textbf{\textit{STRUCTURES OF AMINO ACIDS at pH 7.0}}}
\]

- ALANINE (ala)  
- ARGinine (arg)  
- ASPARAGINE (asn)  
- ASPARTIC ACID (asp)  
- CYSTEINE (cys)  
- GLUTAMIC ACID (glu)  
- GLUTAMINE (gln)  
- GLYCINE (gly)  
- HISTIDINE (his)  
- Isoleucine (ile)  
- LEucine (leu)  
- LYSINE (lys)  
- METHIONINE (met)  
- PHENYLALANINE (phe)  
- PROLINE (pro)  
- SERINE (ser)  
- THREONINE (thr)  
- TYROSINE (tyr)  
- VALINE (val)
Question 2

A colony of monkeys was found on an island off Cape Cod. Some were hairless and some hairy. As a leading genetics expert, you've been hired to determine the mode of inheritance for hairlessness. You playfully jot down 2 possible inheritances shown below. Fill in the missing genotypes that would correspond using standard notation (HH, hh, Hh).

Mode A 6 points—only 1 point for the F1 cross line. Mode B 8 points. Only 1 point for the F1 cross line. 14 points for page.

Mode A

<table>
<thead>
<tr>
<th></th>
<th>Hairy Monkey</th>
<th>Hairless Monkey</th>
</tr>
</thead>
<tbody>
<tr>
<td>F₀</td>
<td>Hh</td>
<td>hh</td>
</tr>
<tr>
<td>F₁</td>
<td>50 Hairy</td>
<td>50 Hairless</td>
</tr>
<tr>
<td></td>
<td>Monkeys</td>
<td>Monkeys</td>
</tr>
<tr>
<td>F₁</td>
<td>Hairless</td>
<td>F₁ Hairless</td>
</tr>
<tr>
<td></td>
<td>Monkeys</td>
<td>Monkeys</td>
</tr>
<tr>
<td>F₂</td>
<td>100 Hairless</td>
<td></td>
</tr>
</tbody>
</table>

Mode B:

<table>
<thead>
<tr>
<th></th>
<th>Hairy Monkey</th>
<th>Hairless Monkey</th>
</tr>
</thead>
<tbody>
<tr>
<td>F₀</td>
<td>Hh</td>
<td>Hh</td>
</tr>
<tr>
<td>F₁</td>
<td>50 Hairy</td>
<td>50 Hairless</td>
</tr>
<tr>
<td></td>
<td>Monkeys</td>
<td>Monkeys</td>
</tr>
<tr>
<td>F₁</td>
<td>Hairless</td>
<td>F₁ Hairless</td>
</tr>
<tr>
<td></td>
<td>Monkeys</td>
<td>Monkeys</td>
</tr>
<tr>
<td>F₂</td>
<td>75 Hairless</td>
<td>25 Hairy</td>
</tr>
<tr>
<td></td>
<td>Monkey</td>
<td>Monkeys</td>
</tr>
</tbody>
</table>

Mode A: Hairy Monkey_Hh_Hh Hairless Monkey_hh hh

Mode B: Hairy Monkey__Hh_Hh Hairless Monkey_hh_hh

F₀ Hairy Monkey_Hh_Hh Hairless Monkey_hh_hh

F₁ 50 Hairy Monkeys_hh

50 Hairless Monkeys_Hh

F₂ 100 Hairless Monkeys_hh

F₁ Hairless Monkeys_hh _Hh

F₂ 75 Hairless Monkeys_HH, Hh

25 Hairy Monkey_hh
When you actually perform this cross with random island monkeys, you find that all of the monkeys in the F2 generation are hairless.

b) The Hairy phenotype is ...? (Circle one.) 2 points

<table>
<thead>
<tr>
<th></th>
<th>Dominant</th>
<th>Codominant</th>
<th>Recessive</th>
<th>Can’t be determined</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Other hairless monkeys are discovered throughout the world. To determine if these hairless phenotypes are due to the same mutation, you obtain and mate pure-breeding hairless monkeys to each other as well as to a pure-breeding wild type hairy monkey. The results of the matings are listed in the table below.

(+ indicates hairy progeny, - indicates hairless progeny)

<table>
<thead>
<tr>
<th>Place where monkey was found</th>
<th>Arkansas (A)</th>
<th>Boston Common (B)</th>
<th>Cape Cod (C)</th>
<th>Senior House (S)</th>
<th>Wayland (W)</th>
<th>Wildtype (WT)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Arkansas</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>Boston Common</td>
<td></td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Cape Cod</td>
<td></td>
<td></td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>Senior House</td>
<td></td>
<td></td>
<td></td>
<td>-</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Wayland</td>
<td></td>
<td></td>
<td></td>
<td>-</td>
<td></td>
<td>+</td>
</tr>
</tbody>
</table>

c) How many complementation groups have you found? 2 points

d) List the members of each group. (You can use the location abbreviation (A,B,C,S,W.) 2 points each group, -1 for S

ACW

B

e) From the data above, what is the minimum number of genes that you have found involved in determining the hairless phenotype? Circle one. 2 points (Only -1 if matches an incorrect c.).

<table>
<thead>
<tr>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>10</th>
<th>Can’t Tell</th>
</tr>
</thead>
</table>

f) Which monkeys have a recessive mutation? (Circle all that apply.) 4 points

Arkansas (A)  Boston Common (B)  Cape Cod (C)  Senior House (S)  Wayland (W)  None

g) Which monkeys have a dominant mutation? (Circle all that apply.) 1 point

Arkansas (A)  Boston Common (B)  Cape Cod (C)  Senior House (S)  Wayland (W)  None
Question 3

a) True or False. Identify the following as true or false. 16 points/2 each
Do NOT CHANGE a true statement. If the statement is false, circle false, and replace
JUST ONE of the underlined portions so that the statement is true.

Ex.  
T (False)  

OR  

The sky is generally yellow.

T (True)  

The sky is generally yellow.


\[
\begin{array}{|c|c|c|c|c|}
\hline
i & T & F & DNA strands have N and C termini. & \textit{Polypeptides or proteins} \\
\hline
ii & T & F & \textbf{Proteins} have a \textbf{negatively} charged backbone. & \textit{DNA or RNA strands} \\
\hline
iii & T & F & DNA commonly contains the same percentage of G's as A's. & \textit{Cs} \\
\hline
iv & T & F & RNA commonly contains the same percentage of A's as T's. & \textit{DNA} \\
\hline
v & T & F & DNA \textit{is usually found as a parallel double strand.} & \textit{an antiparallel} \\
\hline
vi & T & F & A \textbf{micelle} has a \textbf{phospholipid} bi-layer. & \textit{Vesicle, Cell plasma membrane} \\
\hline
vii & T & F & The lack of a 2' hydroxy \textit{makes DNA more stable than RNA.} \\
\hline
viii & T & F & DNA strands can associate via \textit{hydrogen bonding} to form helices. \\
\hline
\end{array}
\]

b) Check the highest degree of protein organization. 5 points

<table>
<thead>
<tr>
<th>Protein Structure</th>
<th>1°</th>
<th>2°</th>
<th>3°</th>
<th>4°</th>
<th>5°</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beta - Sheet</td>
<td></td>
<td></td>
<td></td>
<td>√</td>
<td></td>
</tr>
<tr>
<td>...Met-His-Arg-Ser-Ala-Cys-Phe...</td>
<td>√</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Alpha - Helix</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>√</td>
</tr>
<tr>
<td>Hemoglobin (composed of 4 polypeptide subunits)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>√</td>
</tr>
</tbody>
</table>
Phospholambin (composed of 5 polypeptide subunits) [✓]
A recent Space mission led to the discovery of a Martian bacterium (haploid) that is able to grow on Red Sand alone. Initial studies indicate that these bacteria are able to convert Red Sand into Glucose. To study this pathway you mutagenize the bacteria and identify 4 different mutants (M1, M2, M3, M4) that can’t grow on Red Sand. You supplement the mutants to observe if the bacteria grow or accumulate pathway intermediates. Results are shown below.

- M1 mutants are able to grow when supplemented with Limestone or Marble.
- M3 mutants accumulate Marble when grown on Granite or Limestone.
- M2, M4 double mutants cannot grow on Granite or Limestone.
- M1, M4 double mutants accumulate Granite when grown on Red Sand.

Circle the biochemical pathway that is consistent with your data.
Note that “Enz 1” denotes the enzyme encoded by the gene mutated in the M1 strain.

8 points for iii (correct answer), 3 points if iv, or 2 points for vi.
Question 5

7.012 prepares you for an illustrious career as a dog breeder. You are contacted by an amateur who asks about a novel trait he has seen in his group of dogs.

Some of his dogs prefer to munch on sneakers rather than their kibbles (food). Since the breeder had a lot of shoes, he only noticed the trait after he had bred several generations of sneaker-snackers. (Note that male dogs are XY and female dogs are XX.)

![Sneaker-Snacking Dog Pedigree Diagram]

a) and b) and c) and d) were graded as a unit. If a) was wrong, -7 points. if a) was correct then b, c, and d were evaluated for correctness and points were removed if incorrect.

a) Given that dogs A, B, C, and D are known to be true breeding non-sneaker-snackers, what is the mode of inheritance of this trait? Circle one. **3 points**

<table>
<thead>
<tr>
<th>Autosomal dominant</th>
<th>Autosomal recessive</th>
<th>X-linked dominant</th>
</tr>
</thead>
<tbody>
<tr>
<td>Y-linked</td>
<td></td>
<td>X-linked recessive</td>
</tr>
</tbody>
</table>

b) If the breeder does **not** wish any more sneaker-snackers, should he breed the dog marked * with another non-sneaker-snacker? (Circle one.) **1 points**

<table>
<thead>
<tr>
<th>YES</th>
<th>NO</th>
<th>Can not be determined</th>
</tr>
</thead>
</table>

c) You notice that the third generation is the result of a brother-sister inbreeding. Is inbreeding responsible for the predominance of the trait in generation 3? (Circle one.) **1 points**
d) Predict, if dogs D and E had another puppy, the likelihood of the puppy being affected.

2 points

if male.

if female.

50%

50%

You observe that some of the dogs have blue tongues and dutifully you draw out the pedigree for this RARE trait.

**Blue Tongue Pedigree**

e) and h) were graded as a unit worth 5 points. If e) was incorrect than 5 points were lost. If e) was correct than h was evaluated for correctness.

f) was graded based on actual answers given by student. Ex.-if two X-linked pedigrees were picked for a) and e) we would accept YES as an answer to f. g) was evaluated for correctness with respect to a correct f).

e) Circle the best mode of inheritance for this blue tongue trait. 3 points

<table>
<thead>
<tr>
<th>Autosomal dominant</th>
<th>Autosomal recessive</th>
<th>X-linked dominant</th>
</tr>
</thead>
<tbody>
<tr>
<td>Y-linked</td>
<td></td>
<td>X-linked recessive</td>
</tr>
</tbody>
</table>

f) Are the genes for blue tongue and sneaker-snacking linked? (Circle one.) 5 point

<table>
<thead>
<tr>
<th>YES</th>
<th>NO</th>
<th>Can’t tell</th>
</tr>
</thead>
</table>

g) In less than 15 words explain your answer from f). 3 points

One is on an autosome. The other is on X chromosome.

h) Predict, if dogs D and E had another puppy, the likelihood of the puppy having a blue tongue...

2 points

if male.

if female.

50%

0%