

Designer Genes C - Designer Genes C - Rickards Invitational Div. C - 12-05-2020



2021 Rickards Designer Genes C Exam

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Hi everyone! Welcome to the **Rickards Designer Genes C exam**! I just have a few quick tips and information/instructions for you before you get started.

Information & Instructions:

- You get **50 minutes** to take this test.
- The topics on this exam include **Nationals** topics.
- For fill-in-the-blank questions, capitalization does not affect your score, but incorrect spelling **does affect your score**. Most fill-in-the-blank questions will prompt you to avoid misunderstanding.
- Pay **VERY** close attention to instructions about how to format your answers, especially for questions involving X-linked genes or DNA sequences. Fill-in-the-blank does not award partial credit!
- You can contact me for questions through email: ambermath99@gmail.com or through Discord [@Silverleaf1#5370](#) after the exam.

One more general tip: this test is pretty long, and it's meant to be difficult. Don't worry about leaving questions blank or skipping sections - it's a good idea to snatch the easy points (there are many!) and attempt the hard points later. Most importantly, this test is meant to be fun, so have fun! :3

Chi Square Table:

Percentage Points of the Chi-Square Distribution

Degrees of Freedom	Probability of a larger value of χ^2								
	0.99	0.95	0.90	0.75	0.50	0.25	0.10	0.05	0.01
1	0.000	0.004	0.016	0.102	0.455	1.32	2.71	3.84	6.63
2	0.020	0.103	0.211	0.575	1.386	2.77	4.61	5.99	9.21
3	0.115	0.352	0.584	1.212	2.366	4.11	6.25	7.81	11.34
4	0.297	0.711	1.064	1.923	3.357	5.39	7.78	9.49	13.28
5	0.554	1.145	1.610	2.675	4.351	6.63	9.24	11.07	15.09
6	0.872	1.635	2.204	3.455	5.348	7.84	10.64	12.59	16.81
7	1.239	2.167	2.833	4.255	6.346	9.04	12.02	14.07	18.48
8	1.647	2.733	3.490	5.071	7.344	10.22	13.36	15.51	20.09
9	2.088	3.325	4.168	5.899	8.343	11.39	14.68	16.92	21.67
10	2.558	3.940	4.865	6.737	9.342	12.55	15.99	18.31	23.21
11	3.053	4.575	5.578	7.584	10.341	13.70	17.28	19.68	24.72
12	3.571	5.226	6.304	8.438	11.340	14.85	18.55	21.03	26.22
13	4.107	5.892	7.042	9.299	12.340	15.98	19.81	22.36	27.69
14	4.660	6.571	7.790	10.165	13.339	17.12	21.06	23.68	29.14
15	5.229	7.261	8.547	11.037	14.339	18.25	22.31	25.00	30.58
16	5.812	7.962	9.312	11.912	15.338	19.37	23.54	26.30	32.00
17	6.408	8.672	10.085	12.792	16.338	20.49	24.77	27.59	33.41
18	7.015	9.390	10.865	13.675	17.338	21.60	25.99	28.87	34.80
19	7.633	10.117	11.651	14.562	18.338	22.72	27.20	30.14	36.19
20	8.260	10.851	12.443	15.452	19.337	23.83	28.41	31.41	37.57
22	9.542	12.338	14.041	17.240	21.337	26.04	30.81	33.92	40.29
24	10.856	13.848	15.659	19.037	23.337	28.24	33.20	36.42	42.98
26	12.198	15.379	17.292	20.843	25.336	30.43	35.56	38.89	45.64
28	13.565	16.928	18.939	22.657	27.336	32.62	37.92	41.34	48.28
30	14.953	18.493	20.599	24.478	29.336	34.80	40.26	43.77	50.89
40	22.164	26.509	29.051	33.660	39.335	45.62	51.80	55.76	63.69
50	27.707	34.764	37.689	42.942	49.335	56.33	63.17	67.50	76.15
60	37.485	43.188	46.459	52.294	59.335	66.98	74.40	79.08	88.38

Section 1: Eukaryotic Genetic Analysis

IMPORTANT INSTRUCTIONS FOR THIS SECTION:

- All organisms are assumed to be diploid unless otherwise stated.
- Express epistatic alleles as e+ for non-epistatic allele and e for epistatic allele. Assume that epistatic alleles are recessive unless otherwise stated.
- Pay close attention to instructions about how to format your answer.
- This is probably the hardest section on the test, but many points are awarded here. If you are struggling, a good idea would be to visit the other sections and return here later.

*Backpack Brothers***1. (2.00 pts)**

Neull Mayta was going through his brother's backpack and found two packets of seeds. One was labeled "Recessive Mutation A" and the other "Recessive Mutation B"; when he planted the seeds, both sprouted into plants with bright blue leaves. When Neull crossed plants within packets (e.g. a plant from packet A with another plant from packet A), the phenotype remained unchanged. Then, he had the brilliant idea to cross a plant from packet A with a plant from packet B, expecting to obtain the recessive phenotype. Instead, he obtained a wild type plant with green leaves.

Let the two genes controlling leaf color be called gene A and gene B, where a+ & b+ represent wild type alleles and a & b represent recessive mutated alleles.

What is the genotype of a plant from packet A (first blank)? Packet B (second blank)?

 2. (3.00 pts)

Neull Mayta decides to cross two plants from the F1 generation together. What is the expected phenotypic ratio of green plants to blue plants? Express your answer as x:y. For example, if the calculated phenotypic ratio is 3 green plants to 1 blue plant, enter 3:1.

3. (1.00 pts) What is this phenomenon called?**4. (1.00 pts)**

Neull has a bad feeling that he didn't search his brother's backpack thoroughly enough (he's really invasive). He searches his brother's backpack again, and sure enough, there's a third unlabeled packet of seeds. When he crosses them with each other, he observes that they always produce white stems. A little scared, he decides to cross these strange plants with plants from the F1 generation and gets a phenotypic ratio of 3 green plants : 5 blue plants. Why didn't he get any plants with white stems?

5. (5.00 pts) What are the two possible genotypes of the seeds from the unlabeled plant packet? Hint: You should include three loci in your answer.**6. (2.00 pts)** Which of the following scenarios is most similar to the one that Neull is facing with seed packets A and B with regards to the expression of the wild type phenotype?

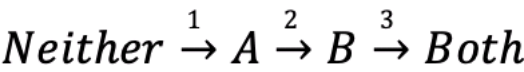
- ☐ A) An elevator has an up and a down button.

- ☐ B) Two people are working on a task; only one person needs to complete it for the task to be completed.
- ☐ C) In the game Among Us, the radiator requires two people pressing on it simultaneously in order for the task to be completed.
- ☐ D) In the science competition called Science Olympiad, even if one partner does all the work and another does no work, a medal is won.

Jennie the Superstar

7. (1.00 pts)

Jennie Kim is investigating the *SUPERSTAR* gene. The ultimate product of this gene gives people the ability to both sing and rap proficiently (Jennie expresses this gene product). Jennie knows that the *SUPERSTAR* gene is constitutively expressed in all people, including those who can't sing or rap, those who can sing but can't rap, and those who can rap but can't sing. *SUPERSTAR* depends on the actions of enzymes W, X, and Y to synthesize the final gene product. The incomplete pathway for the *SUPERSTAR* gene is listed below for your reference; Jennie is missing several crucial pieces of information.



A and B represent the phenotype **can sing but can't rap** and **can rap but can't sing**; Jennie doesn't know which phenotype corresponds to which letter.

1, 2, and 3 represent enzymes **W, X, and Y, in some order**; Jennie doesn't know what order the enzymes act in the pathway.

Clearly, Jennie needs your help. She conducted a large-scale observational study with people of known genotypes and obtained the following data:

WwXXYY and wwXXYY	200 neither 200 both
WwXxYy and wwXxyy	200 neither 50 rap only 75 sing only 75 both

What is A? (Choices: can sing but can't rap OR can rap but can't sing).

8. (4.00 pts)

What is the order of the enzymes W, X, and Y? Fill in the first blank with the enzyme corresponding to 1, the second with the enzyme corresponding to 2, and the third with the enzyme corresponding to 3.

9. (6.00 pts)

[TB] Rose can sing but she can't rap, and J-Hope can rap and sing. Although we don't promote shipping K-Pop idols, for our purposes, Rose and J-Hope have 8 children. Assume that this is a perfect world and there is no statistical variation; all ratios are exactly as they should be. Of the children:

2 can't sing or rap

0 can rap but can't sing

3 can sing but can't rap

3 can sing and rap.

w+, x+, and y+ represent wild type alleles while w, x, and y represent recessive nonfunctional alleles. In the first blank, provide Rose's genotype and in the second blank, J-Hope's.

10. (3.00 pts)

All done! Jennie kicks back and relaxes... then notices something strange. There appear to be five or so of the 4200 people that have the genotype $W_X_Y_$ (where $_$ denotes a wild type or recessive allele) but can't sing or rap proficiently. Provide three reasons for why this might be.

Dr. Aluk's Fruit Flies

11. (2.00 pts)

The var gene in fruit flies is responsible for non-variegated (var+) or variegated (var) eye color, and the shr gene is responsible for normal wings (shr+) or shriveled wings (shr). Assume that var and shr are **unlinked**. Dr. Aluk crosses a fly that is heterozygous for both alleles with a fly that is homozygous recessive for both alleles. What is the expected phenotypic ratio? Your answer should be in the form A:B:C:D, where:

A = var+ shr+

B = var shr+

C = var+ shr

D = var shr

Make sure your ratio is fully reduced whole numbers.

12. (3.00 pts)

Dr. Aluk is a little skeptical about her intern's claim that the genes are unlinked. She decides to cross a lot of flies and gets the following results:

418 non-variegated eyes and normal wings

94 variegated eyes and normal wings

103 non-variegated eyes and shriveled wings

385 variegated eyes and shriveled wings

Conduct a chi-squared test with 3 degrees of freedom. What is the chi-squared value (blank 1, round to the nearest **whole number**), and do you accept or reject the null hypothesis (blank 2, accept or reject)?

13. (2.00 pts)

Unfortunately, things are never this easy when it comes to genetics. Dr. Aluk finds out that the genes are actually spaced 20 cM apart on the same chromosome. What is the expected phenotypic ratio now?

14. (3.00 pts)

Conduct the chi-squared test with your new null hypothesis. What is your chi-squared value (first blank; **two decimal places**) and do you accept or reject your null hypothesis (second blank; accept or reject)?

15. (2.00 pts)
Dr. Aluk crosses a var+ var shr shr fly and a var+ var shr+ shr fly. What is the probability of obtaining the phenotype var shr? Express your answer as a fully simplified fraction.

Charizard Crossing

16. (2.00 pts)
Mr. Tam has a farm of Charizards, which differ in three loci: wing shape, horn length, and fear of Stealth Rock.

Wing shape: t+ (rounded), t (triangular)

Horn length: s+ (long), s (short)

Fear of Stealth Rock: f+ (no fear), f (fear)

Mr. Tam knows that the three loci are located on the same chromosome and are linked, but he doesn't know what order they're in. He crosses two Charizards and obtains 1000 offspring (these Charizards are very fertile):

Round wing, long horn, fear of Stealth Rock (t+ s+ f)	368
Triangular wing, short horn, no fear of Stealth Rock (t s f+)	395
Round wing, short horn, no fear of Stealth Rock (t+ s f+)	64
Triangular wing, long horn, fear of Stealth Rock (t s+ f)	61
Triangular wing, long horn, no fear of Stealth Rock (t s+ f+)	54
Round wing, short horn, fear of Stealth Rock (t+ s f)	46
Round wing, long horn, no fear of Stealth Rock (t+ s+ f+)	5
Triangular wing, short horn, fear of Stealth Rock (t s f)	7

What is the order of the genes on the chromosome?

- ☐ A) tsf
- ☐ B) fts
- ☐ C) tfs

17. (6.00 pts) Calculate the distance between the genes in centimorgans, rounded to **one decimal place**. Present your answer as [gene] [distance] [gene] [distance] [gene].
For example:
t 13 s 19 f
The order of the genes around the center does not matter; t s f and f s t will be graded the same.

18. (3.00 pts)
Mr. Tam has recently been watching Star Wars x Pokemon crossovers, and he realized that he wanted to look for double crossovers in his Charizard crosses too! What is the expected number of double crossovers between these loci that Mr. Tam will observe in his 1000 Charizards, using the map distances you calculated in the previous problem? Round to one decimal place.

Note: This question is graded for consistency with your previous answer; therefore, even if you get the previous question wrong, you can still get this one right if you calculate correctly using **your calculated values**.

19. (2.00 pts) Mr. Tam thinks he's been scammed and that he should have more double crossovers. Calculate the interference, I , and interpret it. Round to two decimal places.

$I = 1 - \text{observed number of double crossovers/expected number of double crossovers}$.

Section 2: Prokaryotic Genetic Analysis

20. (1.00 pts) What are the three ways in which bacteria can accept foreign DNA? Present them in alphabetical order.

21. (1.00 pts) Which plasmid allows bacteria to exchange genetic information?

- ☐ A) A plasmid
- ☐ B) C plasmid
- ☐ C) F plasmid
- ☐ D) K plasmid
- ☐ E) R plasmid

22. (2.00 pts) Which of the following are differences between eukaryotic and prokaryotic cells?

(Mark **ALL** correct answers)

- ☐ A) Eukaryotic cells have linear chromosomes while prokaryotic cells have circular chromosomes.
- ☐ B) Eukaryotic cells have longer Okazaki fragments than prokaryotic cells.
- ☐ C) Eukaryotic cells have polycistronic genes while prokaryotic cells don't.
- ☐ D) Eukaryotic cells have introns while prokaryotic cells don't.
- ☐ E) Prokaryotic cells have Shine-Dalgarno sequences while eukaryotic cells don't.

23. (2.00 pts) Eukaryotic cells produce telomerase to lengthen the ends of their chromosomes, which shorten over time. Do prokaryotes produce this enzyme? Why not?

24. (2.00 pts) Place the following steps concerning genetic recombination in bacteria in order:

A: Bacteria is treated with CaCl_2 .

B: cDNA is created from mRNA using reverse transcriptase and restriction enzyme sites are added on either side.

C: Bacteria is shocked with heat.

D: cDNA and bacterial plasmid are treated with the same restriction enzyme.

E: Bacterial colonies are screened to select for recombination.

F: cDNA is introduced into the bacterium.

G: cDNA is ligated into plasmid.

- ☐ A) B, D, F, A, C, G, E
- ☐ B) A, C, B, D, F, G, E
- ☐ C) B, G, D, A, C, F, E
- ☐ D) B, G, A, D, C, F, E
- ☐ E) B, D, A, C, F, G, E

25. (2.00 pts)

Lederberg and Tatum conducted a famous experiment in which they mixed a *met+ bio+ thr- leu- thi-* E. coli strain with a *met- bio- thr+ leu+ thi+* strain and plated them together on a minimal medium lacking amino acids, biotin, and thiamine. They observed 10 bacterial colonies. Why is this surprising?

26. (1.00 pts)

Davis expanded on this experiment by showing that the two strains of bacteria had to make physical contact in order to transfer genetic material. Given this information, what bacteria process is occurring? When this process occurs, the two bacteria exchange genetic material through a tube called a [blank].

27. (1.00 pts)

Carolyn sequenced a prokaryotic plasmid and found the order of genes to be:

A E B oriT F C D

During conjugation, which gene will be transferred first?

- ☐ A) B
- ☐ B) F
- ☐ C) C
- ☐ D) E
- ☐ E) D
- ☐ F) Not enough information

28. (2.00 pts)

Which of the following transfers of DNA are possible?

(Mark **ALL** correct answers)

- ☐ A) F+ to F-
- ☐ B) F- to F+
- ☐ C) Hfr to F-

- ☐ D) F- to F-
- ☐ E) F' to F-

29. (1.00 pts) Of these transfers of DNA, which two have the potential to transfer genomic DNA from one bacterial cell to the other to form recombinant chromosomes?

(Mark **ALL** correct answers)

- ☐ A) F+ to F-
- ☐ B) F- to F+
- ☐ C) Hfr to F-
- ☐ D) F- to F-
- ☐ E) F' to F-

Colony Conundrum

30. (1.00 pts)

Sydney is investigating horizontal gene transfer in E. coli. She has one Hfr strain of E. coli that is his+ leu+ thr+ val+, and one F- strain of E. coli that is his- leu- thr- val-, where + indicates that the bacteria can synthesize the indicated amino acid while - indicates that the bacteria cannot, and requires this amino acid in its medium to survive and reproduce. She mixes the bacteria together and interrupts them at certain time intervals with a blender. After she interrupts them, she plates the bacteria on medium with a single amino acid as the carbon source and records the percentage of surviving colonies. She wants to find the order of the genes on the plasmid in relation to the origin of transfer.

Here is her data:

Minutes before interruption	his only	leu only	thr only	val only
5	0	0	100	30
10	20	3	100	82
15	72	31	100	98
20	81	74	100	100

Each column represents the percentage of surviving colonies when plated with medium containing only a certain amino acid.

What process is Sydney interrupting (one word)?

31. (2.00 pts) [TB] Which of the following are possible orders of the genes on the plasmid?

(Mark **ALL** correct answers)

- ☐ A) oriT thr val his leu
- ☐ B) oriT val his leu thr
- ☐ C) oriT thr his leu val
- ☐ D) oriT leu his val thr

Section 3: DNA Process - Replication, Transcription, and Translation

32. (1.00 pts)

In Meselson and Stahl's experiment, all cell DNA was initially labeled with ¹⁵N, a heavy isotope of nitrogen. These cells were transferred to a ¹⁴N medium and grown for several generations, then ultracentrifuged and density bands were observed. For example, in the 0th generation, one band was observed near the bottom of the density gradient because all DNA was labeled with heavy isotopes. After the first DNA replication, one intermediate band of DNA is observed. Which model(s) of DNA replication is this consistent with?

(Mark **ALL** correct answers)

- ☐ A) Dispersive
- ☐ B) Conservative
- ☐ C) Semiconservative

33. (2.00 pts)

According to the semiconservative model of DNA replication, which of the following bands should be observed in the third generation (after three rounds of DNA replication; 8 strands of DNA)?

Pick one answer.

(Mark **ALL** correct answers)

- ☐ A) One light band and one intermediate band, light band 3x thicker
- ☐ B) One light band and one intermediate band of same thickness
- ☐ C) One intermediate band
- ☐ D) One light band and one intermediate band, light band 2x thicker
- ☐ E) One heavy band and one light band, light band 2x thicker

34. (1.00 pts)

During DNA replication, DNA polymerase can only add nucleotides to the [blank] end of a DNA strand because it requires a [blank; write out the functional group] group to form a [blank] bond between the two nucleotides.

35. (1.00 pts) Match the enzymes to their functions:

1: Helicase

2: Topoisomerase

3: DNA ligase

4: DNA primase

A: Creates transient breaks in DNA to relieve tension from supercoiling

B: Catalyzes formation of phosphodiester bonds between Okazaki fragments

C: Breaks hydrogen bonds between nucleotide bases and unwinds the DNA double strand

D: Lays down short RNA sequences for DNA polymerase to extend

☐ A) 1: A

2: B

3: D

4: C

☐ B) 1: C

2: A

3: B

4: D

☐ C) 1: C

2: A

3: D

4: B

- ☐ D) 1: A
2: C
3: B
4: D

36. (2.00 pts) Which of the following are true about DNA Polymerase I? It:

(Mark **ALL** correct answers)

- ☐ A) Removes RNA primers
☐ B) Extends the leading strand of DNA
☐ C) Has 5'-3' polymerase activity
☐ D) Has 3'-5' exonuclease activity
☐ E) Has 5'-3' exonuclease activity
☐ F) Has 3'-5' polymerase activity

37. (1.00 pts)

DNA polymerase III synthesizes [towards or away] from the replication fork on the leading strand and [towards or away] from the replication fork on the lagging strand.

38. (2.00 pts)

Explain how DNA replication on the lagging strand works. Include the following terms in your answer: 5', 3', replication fork, DNA primase, Okazaki fragment, DNA Polymerase I, DNA ligase

39. (2.00 pts) Which of the following are true about telomerase? Telomerase:

(Mark **ALL** correct answers)

- ☐ A) Uses a RNA template to synthesize DNA
☐ B) Extends centromeres
☐ C) Is expressed in all cells
☐ D) Acts on the lagging strand
☐ E) Extends the 3' strand of DNA

40. (4.00 pts)

[TB] Suppose the repeat sequence of telomeres is 5'-TTAGGC-3'. The complementary region between the RNA template of telomerase and the DNA strand is 5 bases and the first five bases of the RNA template are: 3'-GAAUC-5'. If you know that the RNA template of telomerase is 12 bases long, provide the entire RNA template for telomerase, indicating 3' and 5' directionality. Express your answer as:

A'-NNNNNNNNNNNNN-B'

where N is any nucleotide letter and A and B are 5 and 3 in some order.

Hint: The sequence of telomeres **repeats**; the RNA template must be complementary! You just need to find the starting point on the DNA strand using the information about the first five bases.

41. (0.50 pts) I lied about the sequence of telomeres in the last question. What is the actual sequence of telomeres in humans? Indicate directionality.

Transcription

42. (1.50 pts) Prokaryotes require a bacterial transcription factor called a [blank] that binds with RNA polymerase to form the RNA polymerase [blank] to begin DNA transcription.

43. (1.50 pts) Which of the following are true about the TATA box? It:

(Mark **ALL** correct answers)

- ☐ A) Defines the direction of transcription
- ☐ B) Indicates the DNA strand to be read
- ☐ C) Is present in the promoter of all genes
- ☐ D) Has a bacterial homolog called the Pribnow box
- ☐ E) Is also known as the Goldberg-Hogness Box

44. (0.50 pts) Which transcription factor recognizes the TATA box?

- ☐ A) TFIIB
- ☐ B) TFIID
- ☐ C) TFIIF
- ☐ D) TFIIIE
- ☐ E) TFIIH

45. (0.50 pts) Which RNA polymerase transcribes all protein-coding genes in eukaryotes?

- ☐ A) I
- ☐ B) II
- ☐ C) III

46. (0.50 pts) Which RNA polymerase transcribes 5.8S, 18S, and 28S rRNA genes?

- ☐ A) I
- ☐ B) II
- ☐ C) III

47. (0.50 pts) Which RNA polymerase transcribes miRNA and siRNA?

- ☐ A) I
- ☐ B) II
- ☐ C) III

48. (0.50 pts) Which RNA polymerase transcribes tRNA?

- ☐ A) I
- ☐ B) II
- ☐ C) III

49. (0.50 pts) Which eukaryotic RNA polymerase is most similar to bacterial RNA polymerase?

- ☐ A) I
- ☐ B) II
- ☐ C) III

50. (1.00 pts) In prokaryotes, transcription and termination occur simultaneously. Why is this not possible in eukaryotes?

51. (0.50 pts) RNA polymerase II requires a helicase to help unwind DNA.

- ☐ True ☐ False

52. (2.00 pts) RNA Polymerase II requires which of the following to begin transcription:

(Mark **ALL** correct answers)

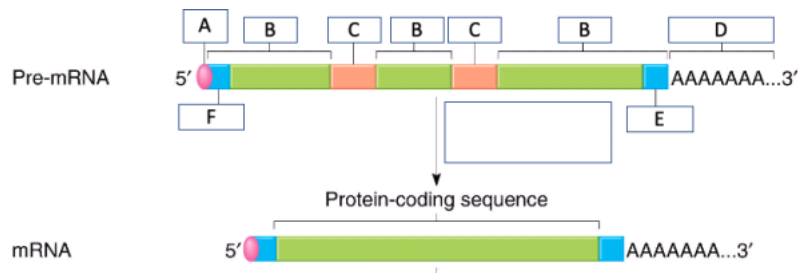
- ☐ A) General transcription factors
- ☐ B) Specific transcription factors
- ☐ C) Chromatin remodeling complexes
- ☐ D) Mediator

53. (1.00 pts) In eukaryotes, the [blank] signal, with sequence [blank; indicate directionality], catalyzes the formation of the poly-[blank] tail.

To indicate directionality, your answer should be in the form:

A'-NN...NN-B'

The RNA polymerase has finished transcribing the length of DNA, and the following diagram shows the remaining steps to be taken.



54. (0.50 pts) A (one number with a punctuation mark and one word):

55. (0.50 pts) B (singular):

56. (0.50 pts) C (singular):

57. (0.50 pts) D (two words):

58. (0.50 pts) E (one number with a punctuation mark and one acronym):

59. (0.50 pts) F (one number with a punctuation mark and one acronym):

60. (1.00 pts)

What is it called when the red sections of RNA are removed and the green sections can be rearranged to form **several different** mRNA transcripts? Enter two words.

61. (1.00 pts)

Structure A is a modified [adenine, cytosine, guanine, or thymine] nucleotide methylated on position [blank; write out the number] and is connected to mRNA via a 5' to [blank] triphosphate linkage.

62. (2.00 pts) Which of the following are functions of structure E?

(Mark **ALL** correct answers)

- ☐ A) Binding site for miRNA
- ☐ B) Silencer regions that bind repressor proteins
- ☐ C) Repository for pseudogenes
- ☐ D) Alternative polyadenylation

63. (3.00 pts)

Rebecca and Neal wanted to insert a human gene into a bacterium, so using their robust Designer Genes knowledge, they took the entire human gene, promoter and all, and inserted it into the bacterial plasmid. However, when they cultured the bacteria, no colonies produced the gene product! What a disaster! Name 3 reasons why no gene product is being made.

Translation Time!

64. (1.00 pts) Which choice correctly identifies where the ribosome binds?

- ☐ A) Eukaryote: Shine-Dalgarno sequence. Prokaryotes: TATA box
- ☐ B) Eukaryote: TATA box. Prokaryotes: Shine-Dalgarno sequence
- ☐ C) Eukaryote: 5' cap. Prokaryotes: Shine-Dalgarno sequence
- ☐ D) Eukaryote: 5' cap. Prokaryotes: TATA box
- ☐ E) Eukaryote: 3' tail. Prokaryotes: Shine-Dalgarno sequence

65. (0.50 pts) Which enzyme catalyzes the bond between tRNA and the amino acid?

- ☐ A) Peptidyl transferase
- ☐ B) Aminoacyl tRNA synthetase
- ☐ C) Aminoacyl tRNA-ase
- ☐ D) Aminoacyl transferase

66. (1.00 pts)

Provide the name of the three ribosomal sites, in the chronological order that a tRNA passes through them. 3 words, 3 words, 2 words. Watch your spelling and punctuation!

67. (3.00 pts)

Explain the process of RNA translation, starting with a met-tRNA_i in the P site and empty A and E sites. Include the following terms in your answer: anticodon, GTP, release factor, polypeptide.

68. (0.50 pts) The small subunit of ribosomes binds before the large subunit.

☐ True ☐ False

69. (0.50 pts)
Ribosomes are made of proteins and rRNA. [rRNA or proteins] catalyze reactions in the ribosome, and molecules of this kind that possess catalytic activity are known as [blank].

70. (1.00 pts)
After ribosomal subunits bind to the mRNA and begin translation, they scan for the first 5'-AUG-3' sequence. Sometimes, the first AUG codon is ignored and ribosomes skip to subsequent AUG codons to begin translation. What is this phenomenon known as?

71. (3.00 pts)
Suppose a protein exists in two forms: secreted form and retained-in-the-cytoplasm form. Explain how the previous process could enable this protein to exist in two forms.

72. (1.00 pts) An mRNA that encodes several functionally distinct proteins is [blank]. These mRNA are only found in [prokaryotes or eukaryotes].

73. (2.00 pts) An pre-mRNA is 2541 base pairs long.

5' UTR	300 bp
Signal sequence	15 bp
Intron 1	420 bp
Exon 1	90 bp
Intron 2	840 bp
Exon 2	66 bp
3' UTR	810

How many amino acids are in the polypeptide before it completely enters the lumen of the ER?

74. (2.00 pts) [TB] How many amino acids are in the secreted protein, assuming the quaternary structure is the same as the tertiary structure?

--

Rames Jickards sequenced the *RSO* gene:

5'-CTATT³**ATG**CACTACCGA¹TGA²AAGACTCCAGT⁵AGTGGATT⁴GAACT-3'
3'-GATAATACGTGATGGCTACTTCTGAGGTCATCACCTAACCTTTGA-5'
7└───┘6└───┘

Start codons are bolded and stop codons are underlined (you're welcome).

Note: A piece of paper might be helpful for these questions. Hopefully you already have one out.

75. (0.50 pts) Identify the template strand. Is it the strand on the top or the bottom (one word)?

--

76. (1.00 pts) Write out the sequence of the 5' UTR **on the mRNA**, indicating directionality.

--

77. (1.00 pts) Write out the sequence of the 3' UTR **on the mRNA** when the mRNA is sequenced using the first start codon, indicating directionality.

--

78. (1.50 pts) What is the amino acid sequence of the polypeptide? Use three letter abbreviations, and link each amino acid to the next with a -. Do not write the stop codon.

For example: Leu-Thr-Cys-Met

79. (1.00 pts) What is the region of DNA between the start codon and stop codon known as (three words)?

80. (1.00 pts) What characteristic of these regions makes them useful for the detection of new protein-coding genes?

The RSO gene has been provided again to make your life easier.

17/30

☐ B) Shorter

85. (1.00 pts) A mutation occurred at site 5:

5' -CTATTATGCACTACCGATGAAAGACTCCAGTAGTGGATTGAACT-3'
5' -CTATTATGCACTACCGATGAAAGACACCAGTAGTGGATTGAACT-3'

Using the first start codon, which of the following describes this mutation?

(Mark **ALL** correct answers)

- ☐ A) Transversion
☐ B) Transition
☐ C) Missense
☐ D) Nonsense
☐ E) Silent

86. (1.00 pts) Suppose the same mutation occurred at site 5, but the second start codon was used. Which of the following describes this mutation?

(Mark **ALL** correct answers)

- ☐ A) Point
☐ B) Insertion
☐ C) Missense
☐ D) Nonsense
☐ E) Silent

87. (1.50 pts) Oh, poop!

5' -CTATTATGCACTACCGATGAAAGACTCCAGTAGTGGATTGAACT-3'
3' -GATAATACGTGATGGCTACTTCTGAGGTCATCACCTAACTTTGA-5'

What is this called (two words) and how is it repaired (three words)?

88. (0.50 pts) What is the most likely cause of this (two words)?

89. (2.00 pts) Which of the following enzymes function in this mode of repair?

(Mark **ALL** correct answers)

- ☐ A) DNA Polymerase III
☐ B) DNA Polymerase I
☐ C) UV endonuclease
☐ D) DNA ligase
☐ E) DNA primase
☐ F) Glycosylases

90. (0.50 pts) In this mode of repair, the DNA backbone is cut.

☐ True ☐ False

91. (1.00 pts) This type of mutation can be repaired in an even more energy-saving manner. What is this method called (one word)?

92. (1.00 pts) Which enzymes function in this mode of repair?

(Mark **ALL** correct answers)

- ☐ A) DNA polymerase III
- ☐ B) DNA polymerase I
- ☐ C) Photolyase
- ☐ D) Glycosylase
- ☐ E) DNA ligase
- ☐ F) AP endonuclease

93. (0.50 pts) Ummm...

5' -CTATT**ATG**CACTACCG**ATGA**AAGACTCCAGTAGTGGATTGAACT-3'
3' -GATAATACGTGATGGCTACTTCTGAGGTCAT**U**ACCTAACTTTGA-5'

A(n) [blank] group was removed from the cytosine.

94. (0.50 pts) This is repaired by [blank; three words].

95. (2.00 pts) In this form of repair, the uracil nucleotide is excised by [blank, two words], leaving a(n) [blank, one word] site that is recognized and cleaved by [blank, two words].

96. (2.00 pts) Which of the following are true about NHEJ and HDR?

(Mark **ALL** correct answers)

- ☐ A) HDR requires a homologous template
- ☐ B) HDR usually occurs during DNA replication, but it can happen in meiosis too, in which case it can create crossovers
- ☐ C) NHEJ is more accurate than HDR
- ☐ D) NHEJ requires a homologous template
- ☐ E) NHEJ is the most common method of repairing double stranded breaks

INSTRUCTIONS:

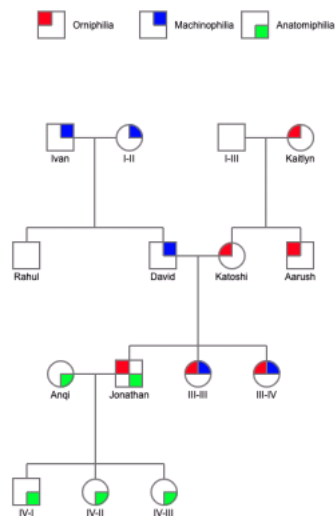
- To enter an X-linked genotype, write the X next to the letter denoting the disease and put a space between the two alleles. For example, a carrier of an X linked disease should be typed as: Xa+ Xa, where a varies depending on the letter assigned to the gene.
- Do NOT use AA, Aa, and aa to denote autosomal genotypes in fill-in-the-blank problems! These questions not case sensitive. Use a+ to denote wild type and a to denote mutated.
- If the wording of any questions is confusing, please don't hesitate to ask the event supervisor.

97. (2.00 pts) Katoshi Gleenus has the rare disease that makes her want to do Ornithology for Science Olympiad (ew!). Let's call this disease **Orniphilia (o)**.

Her more fortunate husband, David, has the disease that makes him want to do Machines for Science Olympiad. Let's call this disease **Machinophilia (m)**.

One of Katoshi and David's children, Jonathan, has the disease that him want to do Anatomy for Science Olympiad (yes!). Let's call this disease **Anatomiphilia (a)**.

Here's a pedigree of her family:



What mode(s) of inheritance could **machinophilia** exhibit?

(Mark **ALL** correct answers)

- ☐ A) Autosomal recessive
- ☐ B) Autosomal dominant
- ☐ C) X-linked recessive
- ☐ D) X-linked dominant
- ☐ E) Mitochondrial

98. (2.00 pts) Which mode(s) of inheritance could **anatomiphilia** exhibit?

(Mark **ALL** correct answers)

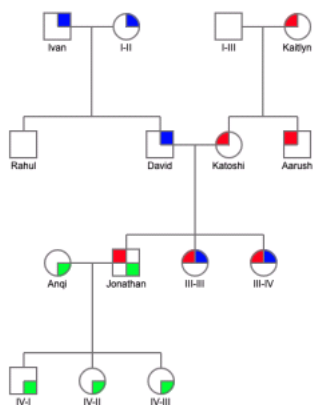
- ☐ A) Autosomal recessive
- ☐ B) Autosomal dominant
- ☐ C) X-linked recessive
- ☐ D) X-linked dominant
- ☐ E) Mitochondrial

99. (1.00 pts) Which mode of inheritance does orniphilia **most likely** exhibit?

- ☐ A) Autosomal recessive

- ☐ B) Autosomal dominant
☐ C) X-linked recessive
☐ D) X-linked dominant
☐ E) Mitochondrial


 Orniphilia Machinophilia Anatomiphilia



100. (2.00 pts) [TB] Given that Ivan is not a carrier of machinophilia, what is the genotype of I-II with regards to machinophilia?

Note: Given this information about Ivan, you should be able to eliminate all inheritance patterns of machinophilia but one.

101. (1.00 pts)

I-II has a child with someone who is a machinophiliac. What is the probability of having a heterozygous machinophiliac child? Express your answer as a fully simplified fraction.

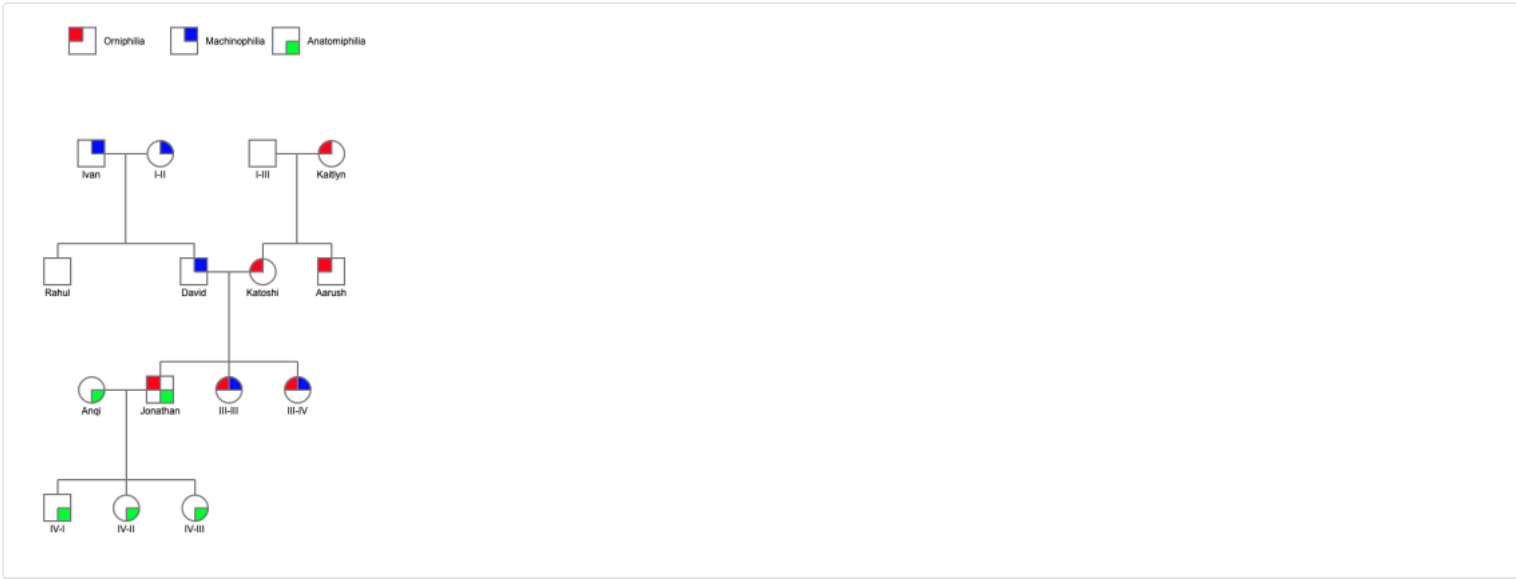
102. (2.00 pts)

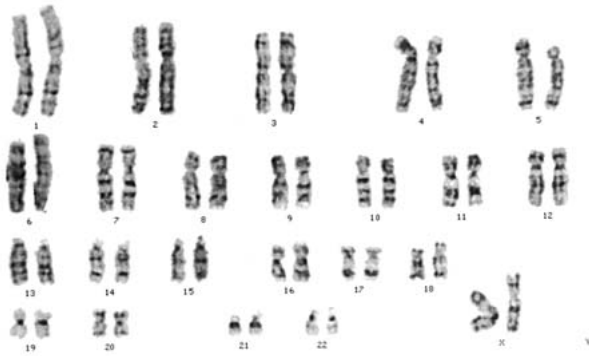
David is not a carrier for anatomiphilia. What does this tell us about Katoshi's genotype? Note: Given this information about David, you should be able to eliminate all inheritance patterns of anatomiphilia but one.

Refer to the instructions at the beginning of this section to enter your answer.

Katoshi's genotype for anatomiphilia must be:

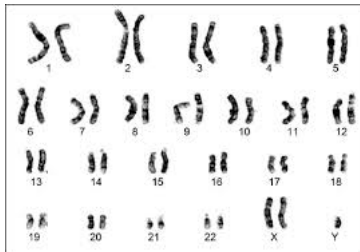
103. (1.00 pts) Knowing this information about Katoshi's genotype, what do we know about Kaitlyn's genotype for anatomiphilia? It must be:





109. (0.50 pts) What is the sex of the individual (male or female)?

110. (0.50 pts) What disease is this?



- ☐ A) Patau
- ☐ B) Klinefelter
- ☐ C) Down
- ☐ D) Turner

111. (2.00 pts) Which of the following could cause this disease?

(Mark **ALL** correct answers)

- ☐ A) Nondisjunction in meiosis I of female
- ☐ B) Nondisjunction in meiosis II of female
- ☐ C) Nondisjunction in meiosis I of male
- ☐ D) Nondisjunction in meiosis II of male

112. (2.00 pts) If the two X chromosomes have the exact same genetic sequence, which of the following could have occurred?

(Mark **ALL** correct answers)

- ☐ A) Nondisjunction in meiosis I of female
- ☐ B) Nondisjunction in meiosis II of female
- ☐ C) Nondisjunction in meiosis I of male

☐ D) Nondisjunction in meiosis II of male

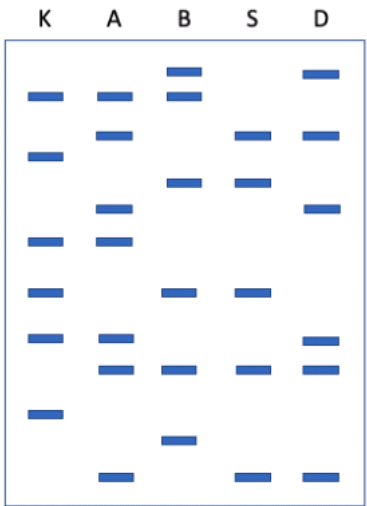
113. (0.50 pts) How many Barr bodies will someone with the genotype XXXXXY have? Type out the number in **letters**.

Section 6: Genetic Technologies

114. (0.50 pts)

If you recall the pedigree, Kaitlyn's husband was unnamed! This is because Kaitlyn had a bout of amnesia and forgot the name of her husband. To make matters worse, when she posted an advertisement searching for her husband, three men (Bob, Sunny, and Day) responded! Lucky for her, she has two children (Katoshi and Aarush) and she plans to use RFLP to find out who her husband is. What does RFLP stand for?

115. (0.50 pts) Here are the results of her RFLP gel electrophoresis:



K: Kaitlyn

A: Aarush

B: Bob

S: Sunny

D: Day

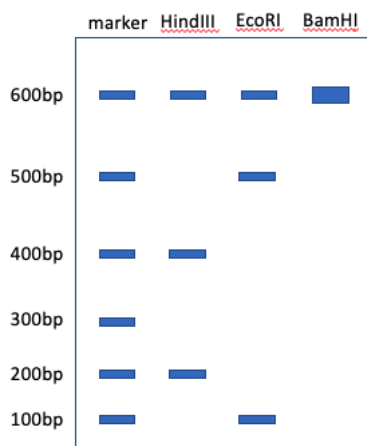
DNA is [positively, negatively, neutrally] charged, so the far end of the gel has a [positively, negatively, neutrally] charged electrode.

116. (2.00 pts) Who is the father?

- ☐ A) Bob
- ☐ B) Sunny
- ☐ C) Day

117. (1.00 pts) Name two other genetic techniques she could have used to find out who the father was.

118. (1.00 pts) Sophia isolated a gene from a eukaryotic chromosome and digested it with four restriction enzymes.



How many base pairs is the gene? Don't include units in your answer.

119. (1.00 pts) How many BamHI sites are there on this gene? Write out the number.

120. (1.00 pts) How many HindIII sites?

121. (1.00 pts)

Jean wants to insert a gene into this plasmid and select colonies using blue-white screening. After digesting the plasmid and gene with the same restriction enzyme, Jean introduces the gene into the bacterial cell. Now, she wants to select for the colonies that accepted plasmids containing foreign DNA. What substrate does she need to add?

- ☐ A) A-gal
- ☐ B) B-gal
- ☐ C) Y-gal
- ☐ D) X-gal
- ☐ E) Z-gal

122. (1.00 pts) Before adding _-gal, Jean adds ampicillin to the bacterial colonies. Why does she do this?

123. (2.00 pts) Jean adds _gal. Some colonies are blue and others are white. If a colony is blue, which of the following may have occurred?

(Mark **ALL** correct answers)

- ☐ A) The bacteria took up the plasmid, but the gene was inserted in the wrong spot.
- ☐ B) The bacteria took up the plasmid, and the gene was inserted correctly.
- ☐ C) The bacteria took up the plasmid, but the gene was not inserted.
- ☐ D) The bacteria did not take up the plasmid.

124. (1.50 pts) Rames wants to amplify the *RSO* gene so he can bathe in its glory. Place the following steps of PCR in order.

A: DNA is cooled

B: DNA is heated to separate the strands

C: Primers anneal

D: Taq polymerase and dNTPs are added

E: DNA is heated to allow for elongation

- ☐ A) B, C, A, D, E
- ☐ B) B, A, C, D, E
- ☐ C) D, B, A, C, E
- ☐ D) D, B, C, E, A
- ☐ E) D, B, A, E, C

125. (3.00 pts) 5' -CTATTATGCACTACCGATGAAGACTCCAGTAATGGATTGAACT-3'
3' -GATAATACGTGATGGCTACTTCTGAGGTCATUACCTAACTTTGA-5'

Which pair of primers can Rames use to amplify the DNA using PCR?

- ☐ A) 5'-CTATTATGC-3'
3'-GATAATACG-5'
- ☐ B) 3'-GATAATACG-5'
3'-TCAAAGTTA-5'
- ☐ C) 3'-GATAATACG-5'
5'-CTATTATGC-3'
- ☐ D) 5'-CTATTATCAC-3'
5'-AGTTTCAAT-3'

126. (1.00 pts) Which of the following are required for Sanger sequencing?

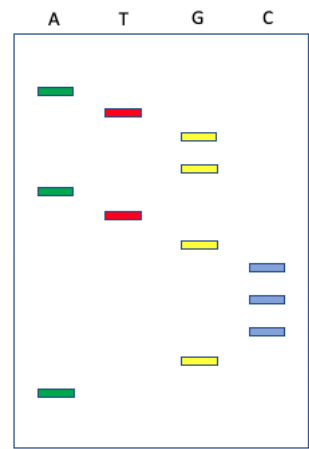
(Mark **ALL** correct answers)

- ☐ A) DNA polymerase
- ☐ B) ddNTP

- ☐ C) NTP
- ☐ D) dNTP
- ☐ E) Primers
- ☐ F) DNA ligase

127. (4.00 pts)

Sahana and Kate want to sequence the gene that's responsible for anatomiphilia. They know the first six bases of the coding strand, so they use that for the primer, whose sequence is 5'-AGGCAT-3'. They conduct Sanger sequencing and run the fragments on a gel.



What is the TEMPLATE strand of the gene? Include the sequence used for the primer and indicate directionality, starting with the 3' end.

128. (2.00 pts)

Hannah and Sammi are investigating gene expression in breast cancer for their sophomore InSTAR project. They collect DNA samples and want to conduct a microarray analysis. Put the following steps in order.

- A: Use reverse transcriptase on mRNA
- B: Fluorescently label cDNA
- C: Place DNA oligomers in wells on glass bead
- D: Wash with SDS and SSC
- E: Apply light to excite fluorescent tags
- F: Add cDNA to microarray and allow to hybridize

- ☐ A) C, D, A, B, F, E
- ☐ B) C, A, B, F, E, D
- ☐ C) C, A, B, F, D, E
- ☐ D) C, A, F, B, D, E
- ☐ E) C, A, F, B, E, D

129. (3.00 pts) Here are several genes that Hannah and Sammi observed. They conventionally labeled the cDNA of the cancer patients (red for cancer, green for no cancer).

Gene A	Green
Gene B	Yellow
Gene C	Red

Which of the following could gene C be?

- (Mark **ALL** correct answers)
- ☐ A) Mitogen (enhances cell division)
 - ☐ B) p53
 - ☐ C) Ras (GTPase that enhances progression of the cell cycle)
 - ☐ D) Apoptosis inhibitor
 - ☐ E) CKI (cyclin-dependent kinase inhibitor)
 - ☐ F) Telomerase

130. (2.00 pts) Would you be surprised if gene A turned out to be p53? Why or why not?

Section 7: Population genetics and phylogeny

131. (1.00 pts)
Alex is observing a large population of people at Hardy-Weinberg equilibrium. The *Blackpink* (bp) gene makes somebody a fan of Blackpink (Blink). Somebody who is heterozygous for the bp gene (bp+ bp) somewhat likes Blackpink. Here are the counts that he obtains:

Blink (bp+ bp+)	360
Somewhat likes Blackpink (bp+ bp)	480
Does not like Blackpink (bp bp)	160

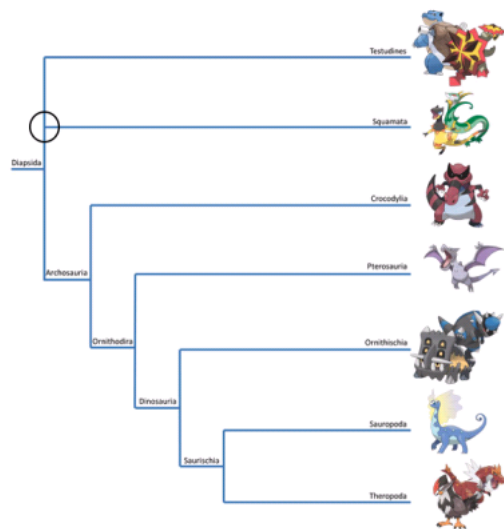
What is the allelic frequency of bp+? bp? Express your answer as a decimal WITHOUT a leading zero.

132. (2.00 pts) After three generations (just pretend like this is possible please), Alex observes the following phenotypes:

Blink	680
Somewhat likes Blackpink	300
Does not like Blackpink	20

Conduct a chi-squared test with two degrees of freedom. Express your answer to two decimal places and do you accept or reject your hypothesis?

133. (1.00 pts) Last question set - let's end with some Pokemon!



What is the circled point called?

134. (1.00 pts) Which of the following forms a sister clade?

- ☐ A) Ornithischia and sauropoda
- ☐ B) Squamata and Testudines
- ☐ C) Sauropoda and theropoda
- ☐ D) Pterosauria, ornithischia, and theropodia

135. (2.00 pts) Which of the following are paraphyletic?

(Mark **ALL** correct answers)

- ☐ A) Sauropoda and theropoda
- ☐ B) Ornithischia and sauropoda
- ☐ C) Crocodylia, pterosauria, ornithischia, and theropoda
- ☐ D) Pterosauria and theropoda

136. (1.00 pts) Which species is/are the outgroup?

(Mark **ALL** correct answers)

- ☐ A) Crocodylia
- ☐ B) Testudines
- ☐ C) Squamata
- ☐ D) Sauropoda
- ☐ E) Theropoda

Phew, you made it! Congratulations. Please let me know what you thought of the test and email any questions/complaints to ambermath99@gmail.com or contact me through Discord [@Silverleaf1#5370](#).

