

Name _____ Date _____ Period _____

Can You Taste That? Predict PTC Tasting Ability among Primates Worksheet



Instructions: Write the answers to your questions on this Student Worksheet, in your lab notebook, or on a separate sheet of paper, as instructed by your teacher. Answer the questions in Section 1 using the information on your primate card. Answer the questions in Section 2 using the bioinformatics program BLAST (Basic Local Alignment Search Tool) and the handout “Predict PTC Tasting Ability among Primates Instructions.” These questions are indicated by a writing pad icon in the Instructions handout.

Section 1: Background Information about Your Non-Human Primate Species

1. Scientific Name: _____
2. Common Name: _____
3. Where is your species found? Is it an Old World primate (from Africa or Asia) or a New World primate (from North or South America)?
4. What type of habitat does your species live in?
5. What is the diet of this species? How does this compare to the diet of most humans?
6. Based on the information above, do you predict that your species will be a PTC / bitter “taster” or “non-taster”? Explain or justify your answer.

Section 2: Using BLAST to Predict Tasting Phenotype

15. Based on your analysis of the TAS2R38 protein sequence from a non-PTC tasting human and your non-human primate species, do you predict that your non-human primate species is a “taster” or a “non-taster”? Explain or justify your answer.

	<u>Amino Acid Position</u>			<u>Explanation of Results:</u>
	<u>49</u>	<u>262</u>	<u>296</u>	
Taster:	P	A	V	
Non-Taster:	A	V	I	
My Species	_____	_____	_____	

Return to Step 16 in the Instructions

17. Does your analysis of the TAS2R38 protein sequence from a PTC tasting human and your non-human primate species support the prediction that you made in step 15? Explain or justify your answer.

	<u>Amino Acid Position</u>			<u>Explanation of Results:</u>
	<u>49</u>	<u>262</u>	<u>296</u>	
Taster:	P	A	V	
Non-Taster:	A	V	I	
My Species	_____	_____	_____	

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25. Scroll through your sequence alignments as you did in step 14 of the instructions and answer the following questions:
- a. Which sequence is your reference sequence [Step 21]? _____

b. Results Summary Table:

Amino Acid Position #	Human Taster Sequence	Number of Non-Human Primates that Match Human Taster Sequence	Percent of Non-Human Primates that Match Human Taster Sequence
49	P		
262	A		
296	V		

- c. Based on the protein sequence data in your BLAST alignment, do you predict that the majority of the non-human primates studied here are PTC tasters or non-tasters? Explain or justify your answer.
- d. Are there any non-human primate species that do not fit into either the “PAV = taster” or “AVI = non-taster” phenotype categories? If so, what sequence do they have at these three key sites? What do you predict their phenotype to be?

	Amino Acid Position			<u>Prediction:</u>
	49	262	296	
Taster:	P	A	V	
Other Sequence:	___	___	___	
My Species	___	___	___	

- e. Find at least three other amino acid sites where the human sequences differ from the majority of the other non-human primate sequences and list them below.

Amino Acid Position #	Human Taster Sequence	Predominant Non-Human Primate Sequence	% of Non-Human Primates with this Sequence

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28. Based on your BLAST results, which three non-human primate sequences are most closely related to the human query sequence? Justify your answer using max score, query coverage, and percent identity.

Species	Max Score	Query Coverage	Percent Identity	Explain what this data means

29. Based on your BLAST results, which three non-human primate sequences are most distantly related to the human query sequence? Justify your answer using max score, query coverage, and percent identity.

Species	Max Score	Query Coverage	Percent Identity	Explain what this data means

Return to Step 16 in the Instructions

32. Experiment with various distance tree parameters until you obtain a tree that you believe is the best visualization of your results. Then, either download the tree as an image file by clicking the “**Download Tree**” link or draw a sketch of your tree below. If you sketch your tree, your tree should include the approximate positions of:
- Your non-human primate species
 - The three closest species neighbors to your sequence [Step 28]
 - The three species most distantly related to your sequence [Step 29]
 - The human taster and non-taster sequences
33. Based on what you have learned in this activity, which do you think is the more ancient or **ancestral** phenotype: being a taster or a non-taster? In other words, do you think that the common ancestor of all of these primates was a taster or a non-taster? Explain or justify your answer.