Translation 3 Questionnaire Responses

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| test |
| Adithya Balu |
| Ryan Duong |
| Jared Mann |
| Bethany Yachuw |
| Kevin Limlengco |
| E, alqaffas |
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| Summary |
| Yes |
| Yes, the how to write a summary page was very helpful. I am just having trouble deciding which article to summarize an experiment from, but I will have to consult my mentor. Could you speak on hte BNFO300 summary blog? What is it and how to submit? |
| Yes! all clear! |
| Yes |
| Yes! |
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| All clear |

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| Crick1961 |
| No |
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| Nope |
| None |
| I'm confused on the process as to why adding acridines during replication forces an insertion etc. |
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| PS5 |
| No |
| Could we talk about the last question. I used the advice you gave to assign an arbitrary amino acid for a codon and then figure out all the codons that must also be the same amino acid, but I found myself having to assign a new one often and getting possible overlaps where a codon could possibly encode two amino acids. |
| Nein |
| None |
| will turn it in late. Sorry |
| In Q3, I've chosen the primer rules and picked the two primers. What I don't get is that, since it is not a real sequence, how its possible to ensure that enzyme will not do any other function, or have the same strength? when picking the primers, why don't we just go always to the terminals  and chose the first few sequences that fits the critera? |
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| ResProposal |
| Sent another email just asking for response from Dr. Swati Deb. |
| Going well! |
| Nein |
| None |
| Just recently met with a mentor (Dupree) I hope to come up with a specific research topic within the week possibly concerning Nox1 on Microglials. |
| yes, I feel overwhelmed to say the least, where I am right now, shows a medium understanding of the articles at best. however, this is not an overall reaction, it's more about the experiment section. I how can I anticipate a result without testing it in real life. |
| I met with my mentor again last Friday and was given suggestions on good protein modeling programs to look into referencing in the proposal. We also talked through some protein structures and their usefulness to the proposal. |

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| CrickSimExtent |
| Not completed the attempt |
| Having technical difficulties, so I will be using a desktop in the library to access tomorrow. |
| I have not started the simulation yet but I look forward to running through it. I should have it done by Wednesday. |
| Started it. |
| 3b |
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| Unfortunately my computer is very spotty when it comes to running Java apps which I was reminded of when attempting the program. They run, but they appear very small and I have yet to find a way to make them larger. So I plan to borrow a computer or drop by the library to actually do it. |

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| CrickSim problems |
| Something keeps failing when trying to separate suppressor mutations in strains from FC0 mutations by using the CROSS function. |
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| No, it works. |
| None |
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| From what I could see, the simulation looked fairly straight forward. |

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| JonesExtent |
| Trying to understand the instructions for the alien one and just started the Jones & Nirenberg |
| Done with companion. Yet to start Alien genetic code. |
| SQ1 |
| Started it. |
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| I'm currently playing the alien game. |
| SQ9.   I have not yet begun the Alien Genetic Code, but I'm looking forward to it! |

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| Jones |
| Not yet |
| I'm having trouble understanding the role of PNP in the experiment. If it is usually involved in RNA degradation intra cellularly, how could it be used to synthesize RNA extra cellularly? Also, regarding SQ13, I cant see why the numbers might be regarded as suspicious. The control must be the amino acid frequency of the cell itself while the data is the difference from control and exogenous RNA.  ***[March 23]*** |
| Nein |
| None |
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| Where can I find the alien genetic code? or should I make some up? |
| I am comfortable with the work of Nirenberg.   I have read the instructions for Alien Genetic Code, and I feel like I won't have many problems getting set up. |

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| Misc |
| none |
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| See you in class tomorrow |
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| the aline story is fun to say the least, my question is, why did you chose this method of figuring out the nature of coding its DNA gene? why can we just use some of our own ribosomes to produce their ribosomes...this sounds silly but even if we produce a somewhat nonfunctional ribosome out of their sequence we can learn more by failing. |
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