

# Unknown Clone Presentation PSA

## 2014-2015 Guidelines

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### What is an unknown clone presentation and why do we need to do them?

An unknown clone presentation is exactly what you'd think it is--it is a presentation that you give to the class about your unknown clone after you've analyzed it on DSAP. In the presentation, you will describe relevant information about the sequence, such as its function or the overall quality of the sequence. You need to do presentations because sometime in March, the exec board will pick one clone of interest and our school will present that clone at the WSSP poster forum in June. The more presentations we do → the more options we have for the poster forum → the better our poster presentation is in June. **Also note that unknown clone presentations help you stand out and show that you are interested in this class, which will ultimately help when it comes time to apply for next year's exec board.**

### Are presentations mandatory?

Yes, they *are* mandatory (unless otherwise noted in class). Regardless of what kind of clone you have (coding, noncoding, unreadable), you should make a presentation after you've analyzed/completed an unknown clone. **Please note that should you find yourself pressed for time, the priority is that you present East Brunswick clones from the 2014-2015 school year** (clones that follow the 04XX#.14 pattern). However, if you want to present a clone you analyzed that was prepped in another school year or by another school, we won't stop you!

### Steps to Creating a Presentation:

1. **Complete your unknown clone on DSAP.** We recommend you wait until the status is "to be submitted to NCBI" to start making your presentation. That way, you can ensure that what you are presenting is correct.
2. **Determine what type of clone you have.** (Coding, Non-Coding, or Unreadable)
3. **Based on the type of clone you have, make a presentation according to table on the following page.** Here are some tips and comments:
  - Use the sample presentations to your advantage. If you format your presentation like the sample presentations, then you will cover every question on the "things you need to cover" column
  - This will take a long time and may be frustrating if this is your first time. Please be patient and contact BP/ZK if you have any questions.
  - Make sure you know how to screenshot things! You don't want to look ridic!

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| Type of Clone | Things you need to cover  | Sample Presentation Link  |
|---------------|---|---|
| Coding        | <ul style="list-style-type: none"> <li>• How was the quality of your waveform and where did you crop?</li> <li>• What was the overall length of your sequence</li> <li>• What did the BLASTx alignments look like and how strong were the matches?               <ul style="list-style-type: none"> <li>○ Does your sequence code for a full or partial protein?</li> </ul> </li> <li>• What protein does your sequence code for?</li> <li>• What reading frame is your sequence read in and how do you know?</li> <li>• What did the BLASTp alignments look like and how strong were the matches?</li> <li>• What were the conserved domains?</li> <li>• What does the 3D structure of the protein look like (screenshot Cn3D)?</li> <li>• What is the basic function of your protein (provide background information if necessary)</li> <li>• Why is your protein important?</li> <li>• What are the applications of your protein?</li> </ul> | <a href="https://docs.google.com/presentation/d/1nL6POfOYFMfxk8FWSszdd7EXUb2OtS6nzT698wAwCs/edit?usp=sharing">https://docs.google.com/presentation/d/1nL6POfOYFMfxk8FWSszdd7EXUb2OtS6nzT698wAwCs/edit?usp=sharing</a>   |
| Non-Coding    | <ul style="list-style-type: none"> <li>• How was the quality of your waveform and where did you crop?</li> <li>• What was the overall length of your sequence</li> <li>• What did the BLASTn alignments look like and how strong were the matches?               <ul style="list-style-type: none"> <li>○ Include both the nr/nt and est databases</li> </ul> </li> <li>• What did the BLASTx alignments/results look like and how did that lead you to concluding this was a non-coding sequence?</li> <li>• What are the possible functions of this non-coding sequence (just b/c it doesn't code for a protein, doesn't mean that it's "junk")?</li> <li>• Are there any conserved regions in your sequence (regions conserved across other organisms or even just duckweed)?</li> <li>• Are there any repeated sequences?</li> </ul>  | <a href="https://docs.google.com/presentation/d/1UKs8TjCkgTSeKvBXAVJR2iUcZZm-IH9NZwBYuBEajc/edit?usp=sharing">https://docs.google.com/presentation/d/1UKs8TjCkgTSeKvBXAVJR2iUcZZm-IH9NZwBYuBEajc/edit?usp=sharing</a>   |
| Unreadable    | <ul style="list-style-type: none"> <li>• How was the quality of your waveform and why do you think it is unreadable?</li> <li>• How do your gels support your conclusion?</li> <li>• What mistakes did you specifically make in the lab that led to your clone being unreadable?</li> <li>• What can be done now to fix your mistake, or what precautions should be taken in the future to make sure you don't make the same mistake again?</li> </ul>  | <a href="https://docs.google.com/presentation/d/1RFKd9KZaRGsV4mvgPo9u46OmnnKKbsixpbzN43ugDss/edit?usp=sharing">https://docs.google.com/presentation/d/1RFKd9KZaRGsV4mvgPo9u46OmnnKKbsixpbzN43ugDss/edit?usp=sharing</a> |

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4. **Once you finish your presentation, email Zach at [Zach.Kirschenbaum@gmail.com](mailto:Zach.Kirschenbaum@gmail.com)** with the following information, depending on what type presentation you've made:

| Coding   | Non-Coding  | Unreadable   |
|--|---|--|
| <ul style="list-style-type: none"><li>• Clone name</li><li>• Protein name</li><li>• Edited cDNA sequence (find this on the review tab in DSAP)</li><li>• Your presentation powerpoint (if you did it on google drive, share it on drive instead)</li></ul> | <ul style="list-style-type: none"><li>• Clone name</li><li>• Edited cDNA sequence (find this on the review tab in DSAP)</li><li>• Your presentation powerpoint (if you did it on google drive, share it on drive instead)</li></ul> | <ul style="list-style-type: none"><li>• Clone name</li><li>• Your presentation powerpoint (if you did it on google drive, share it on drive instead)</li></ul> |

5. **Practice at home.** You DO NOT need to memorize a speech. Please please please do not memorize a speech--just practice enough so that you can present your information in class and know what you are talking about.
6. **Take a break.** In the words of Donna Meagle, "treat yoself." Making a presentation is a lot of work, especially if this is your first time.
7. **Present in class.** As of right now, we're not making you sign up for a time slot and we aren't allocating formal days for presentations. Instead, you will be able to present whenever we are doing DSAP in class. If you want to present, make sure you let Brooke or Zach know at the beginning of the period!

#### Time Limits:

We have no formal time requirement for presentations. However, we *recommend* that your presentation lasts *5-10 minutes*. Obviously some presentations will be shorter than 5 minutes (i.e. unreadables) and some may lean towards the 10 minute mark. We are more interested in the quality of your presentation--not how long it is.

**Good luck, and contact BP or ZK if you have any questions.**