



Techniques in Molecular Biology: Virtual Edition

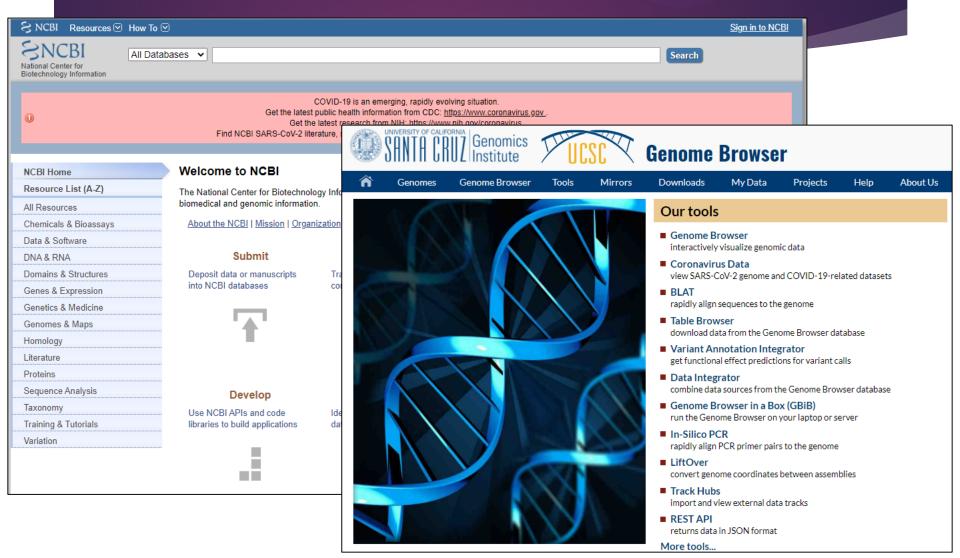
Several labs have been or are being developed as virtual experiences...

In a normal year:

- Dry lab for bioinformatics:
 - Exploring resources of NCBI, UC-Santa Cruz Genome Browser
 - o e.g. NC, NM, NP designators; SNPs database, identify CDS
- Components of molecular cloning completed in silico (SnapGene):
 - Primer design
 - Restriction Enzyme based
 - Gibson Assembly based
- Used bioinformatics and SnapGene in assessment:
 - Cloning question where students locate gene given chromosomal identifier, find corresponding CDS, design primers with compatible restriction enzyme sites for target vector, demonstrate in silico cloning is successful.



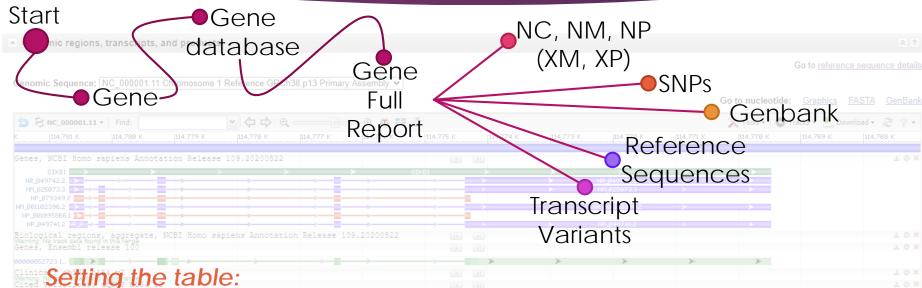
Bioinformatics





Tracks shown: 10/754

Bioinformatics: Examples



- - Give students opportunity to find information that they will need for lab, assessment, project...
 - Layer in information and questions that address fundamental concepts
 - e.g. Define CDS. Show them how to find CDS in multiple places.
 - Compare/Contrast or what is the relationship between NC (chromosomal), NM (mRNA), and CDS

Bioinformatics Ex.

Lactase Persistence lab

- Given 3 SNPs of LCT gene (lactase) design a primer set to amplify a 500 bp region encompassing these 3 SNPs
- Based upon Schultheis & Bowling BMBEd 39:133-140

qPCR lab

 Evaluate TaqMan primer sets for targets

Takehome exams

 Given either gene name or identifier, use information to complete in silico cloning

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Introduction: This lab will introduce you to computational resources related to nucleic acid macromolecules and to software that allows you to view, manipulate, and simulate reactions with nucleic acids.

Throughout the workshop you will be directed to complete tasks. You should record these tasks in LabArchives under the Assignments Tab. Each task should have its own Rich Text Editor entry. As needed, uploaded images with figure leaends.

Step 1: Basic introduction to finding nucleic acid sequences.

Several databases exist that contain the nucleic acid sequences (primarily DNA) of genomes

project (https: as well as indu allow whole g deltocephalin mexicanum [2 as 149,000,000 the role taxpa genomes, the Biotechnology of the Nationa systems for sto genetics; facil community; c internationally information pr molecules." A regarding nuc and access de biological enti your target sys

You will use the

Go to https://

In the layout c primary topics "Popular Reso subset of data

From the window

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Figure 1. Landing page of NCBI.

- Click on the 1st hit and briefly summarize the topics covered in this Full report. Hint: Take note of the section headings.
- 3. How are this entry and <GOI> related?

Under "Genomic regions, transcripts, and product" heading, you will see a window with several tracks of data labels on the left hand side as "Gene," "Biological regions," "dbSNP," and "RNA-seq." For each data track, you will find a download symbol, gear, or red X that allows you to export the data, after its presentation, or remove it from view, respectively. Click on the gear associated with the "Gene" track data. Select "Show All" from the drop-down menu and click apply. (If you want to learn more about the colors and symbols used in this section, the "Track Legend" hyperlink in the Gear menu provides information.) In the "Genes" track data, note the letter and numerical delineators that begin with NC, NM, or NP. These refer to complete genomic, mRNA, or protein sequences, respectively, if "N" is replaced by an "X" this refers to a predicted sequence, lacking experimental validation.

4. How many sequences are available for <GOI>? What are their NM reference numbers? Why does <GOI> have more than one entry? Click on the 1st NM number.

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Advantages:

- LOTS of video tutorial support
- Ease of use

Disadvantages:

- Free Viewer software has limited functionality
- Licenses cost \$\$\$

Some freeware alternatives:

- Serial Cloner
 (http://serialbasics.free.fr/Serial_Cloner.html)
- ApE
 (https://jorgensen.biology.ut ah.edu/wayned/ape/)

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In the remainder of the workshop, you will explore the SnapGeneTM software. <u>This software</u> automates tasks for molecular biologists and can simulate and validate experimental

strategies. As part of your exfrom company websites to a complete requested tasks. \index determine the identity and p tutorial videos noted on the

Step 3: Introduction to Snap! Copy the DNA sequence pe window

Open SnapGene and paste

Highlight the open reading for as a translated feature for the glyoxysomal malate dehydre "Notes" section. Be sure that

This sequence contains the N to the glyoxysome, but this so the mature MDH sequence. the cleavage site to create t

Delete the upstream and do

1. Upload this file to you

Add this feature to common

Modify this file to only contai to reflect this change, "wgM 2. Upload this file to your

Copy the DNA sequence for (http://www.addgene.org/

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"pQE-60"). Place this sequence in a New DNA File in SnapGene. Several features will automatically be annotated. You will need to identify the MCS and add this as a feature.

To sequence this vector, Qiagen suggests the following two sequences for regions surrounding the MCS: 5'-CCCGAAAAGTGCCACCTG-3' for sequencing the antisense strand and 5'-GTTCTGAGGTCATTACTGG-3' for sequencing the sense strand. Add features to the vector that denote these sequencing primers. Name the antisense strand primer "pQE60.FQR" and the sense strand primer "pQE60.FQR". Save this file as pQE60.dna.

3. Upload this file to your LabArchives assignments page.

<u>Step 4: Using SnapGene to explore a plasmid and assess DNA sequencing results</u>

Open the pQE60_wgMDH_mature.dna file (Google Drive shared folder

CHEM330_Student_Resources/DNA_Sequences_F19/). Evaluate the map and sequence.

4. What restriction enzyme cloning strategy was used to insert the wgMDH mature sequence into the pQE60 vector? Could this have been completed with chromosomal DNA from watermelons? Explain.

Simulate an agarose gel with the 1Kb Plus DNA Ladder as your standard and 4 restriction enzyme digest reactions of the pQE60_wgMDH_mature plasmid with Bgll, HindIll, and Scal as either single digests or the triple digest. Adjust percentage of agarose to obtain best separation of bands. Export a PNG image of your gel. HINT: Explore the "Tools" menu.

 Upload an image and Figure legend denoting agarose percentage and lane contents

Complete an alignment of the pQE60_wgMDH_mature.dna with the pQE60_forward_primer.ab1 and pQE60_reverse_primer.ab1. Typical DNA sequencing results using traditional methods are limited to 700-800 bp reads (the length of sequence that is confidently identified, commonly referred to as base calling). Identify for each sequence that you analyzed where you think the signal from the sequencing reaction is no longer reliable. Save the file with alignment as pQE60_wgMDH_mature_confirmed.dna

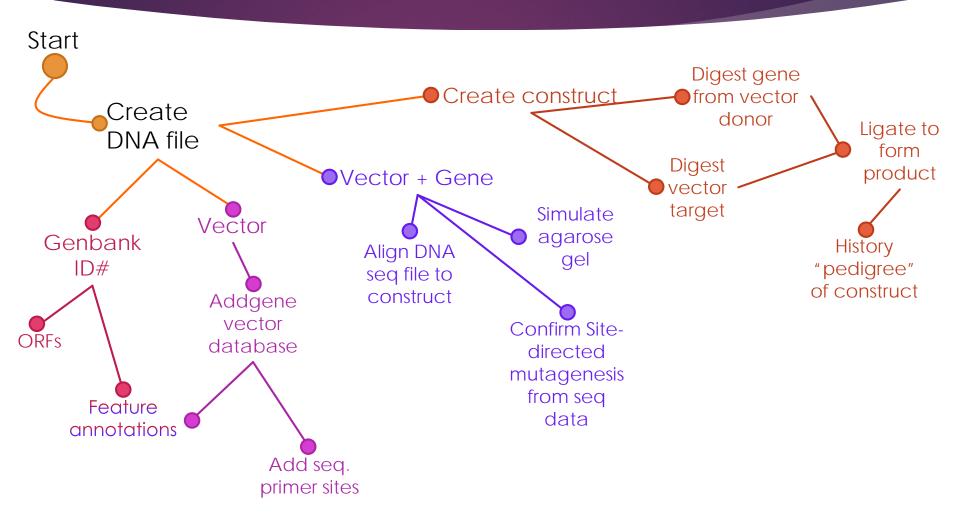
 Upload this file to your LabArchives assignments page and your answer to the region of the data that is reliable for each DNA sequence file.

Starting with the pQE60_wgMDH_mature.dna, complete two independent sequence alignments with the DNA sequencing results assigned to you – see table at right and Google Drive folder. You should identify the mutation confirmed by the sequencing results. Identify for each sequence that you will analyze where you think the signal from the sequencing reaction is no longer reliable. Name your files as follows

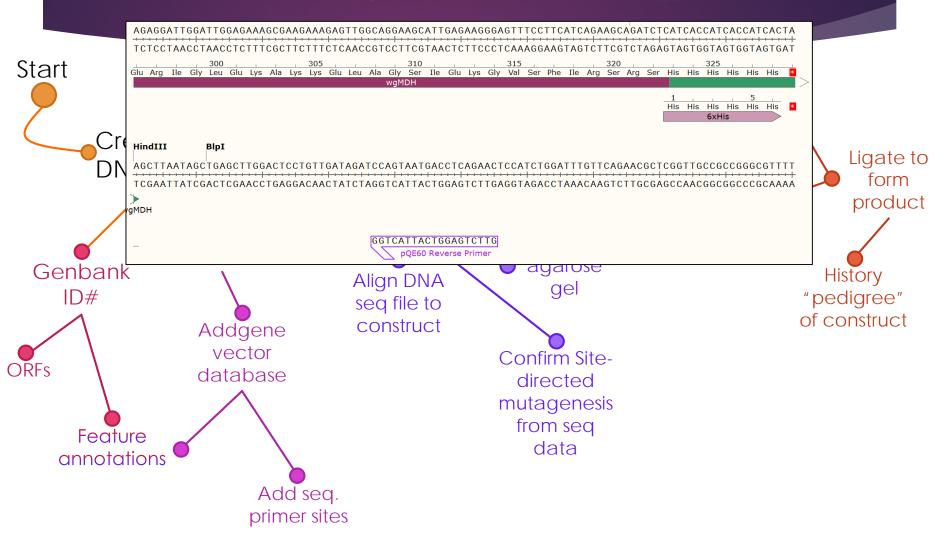
	DNA Sequence file
Name	starting with
Student 1	12
Student 2	13
Student 3	14
Student 4	15
Student 5	16
Student 6	17
Student 7	18
Student 8	10
Student 9	9
Student 10	8
Student 11	7
Student 12	6
Student 13	11
Student 14	1
Student 15	2
Student 16	3
Student 17	4
Student 18	5

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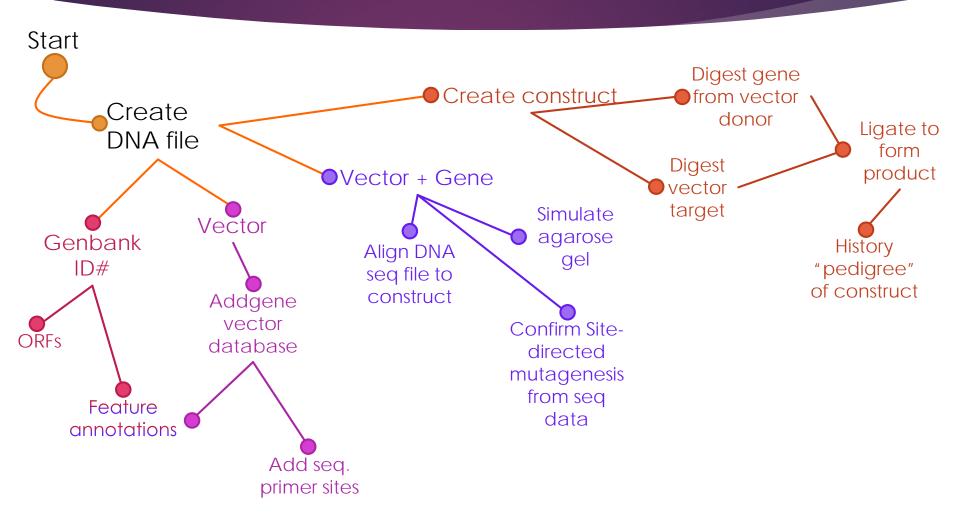




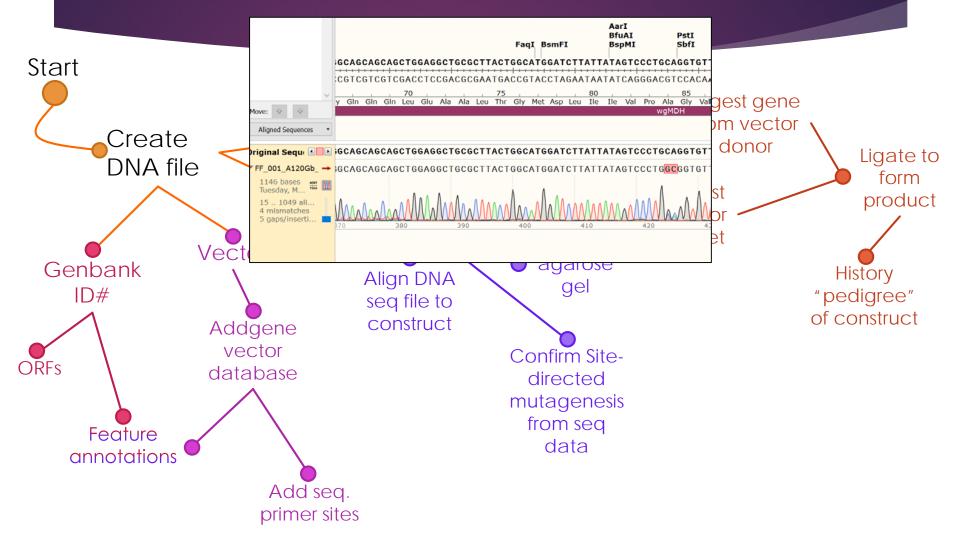






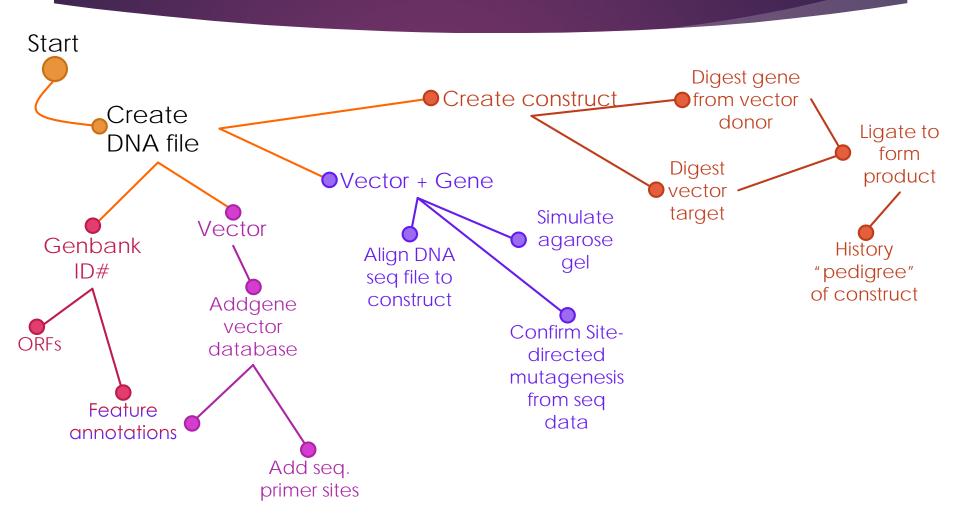




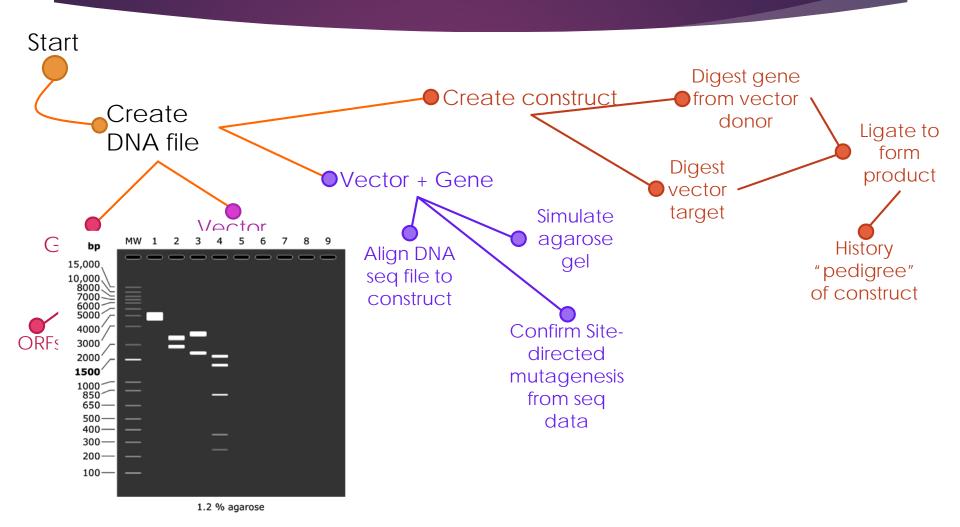


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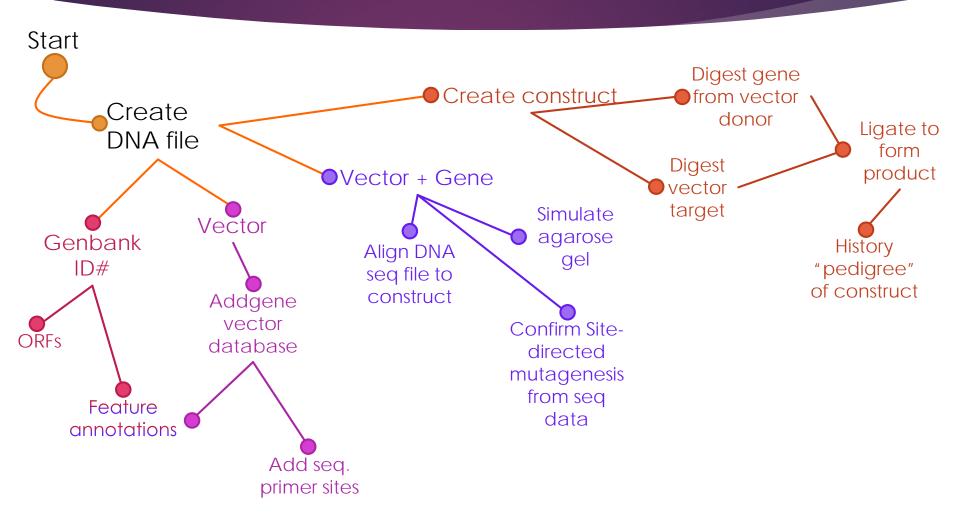




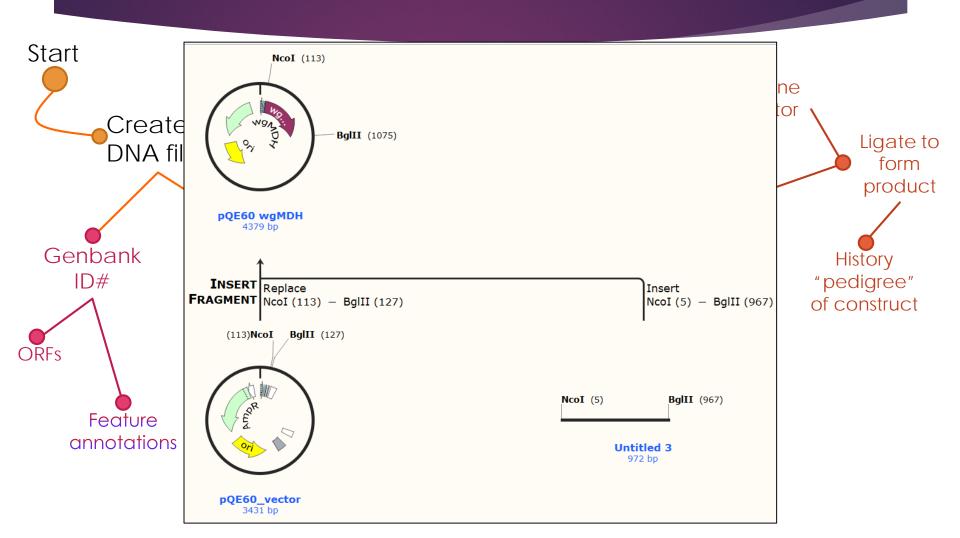












USD Schedule for Hybrid Techniques in Molecular Biology **Basic** Tentative Schedule Section 01 - Tuesday Lab: The schedule is tentative and may change based on the pace of the class. Be prepared to adjust depo ojects proceed! **Skills** Lecture - Monday 8 - 9:30 am Block Activity Description Assign. NB Project Exam Adv Introduction, Safety, ELNs, Solns, Lab Math, Sterile & Bacteriological techniques 8/17 **PCR** Bacterial Transformation, Plasmid & components 8/24 Restriction enzymes, Intro to cloning and subcloning 8/31 **Basic** Restriction enzymes, Intro to cloning and subcloning **Adv Nucleic Nucleic Acid** Basic PCR 9/14 Acid Basic PCR 9/21 Manipulation 9/28 Manipulation Sequencing Adv PCR 10/5 Adv PCR 10/12 Independent CRISPR systems Basic CRISPR systems 10/26 **Projects** Wrap-up, Review 11/2 **PCR** Project Presentations 11/9 Laboratory - Tuesdays 8 am - 11:50 am Group 1 In Person Virtual Pipetting, Sterile/streak/culture technique, Transformation 8/18 1 Standard Operating Procedure 8/25 2 2 9/8 Plasmid DNA Purification 9/1 Bioinformatics/SnapGene Intro 3 9/15 3 Primer design - Lactase Expt. 9/22 Restriction Digest/Agarose gel 4 9/29 4 Adv. Primer design; RNASeq and/or CHIPSeq 10/6 Lactase expt. 5 **aPCR** 10/13 5 Project Design 10/20 COVID-19 Exploration of Mol. Tech Applications 10/27 6 11/3 Project Group 2 In-Person Virtual 1 Pipetting, Sterile/streak/culture technique, Transformation 8/25 1 Standard Operating Procedure 8/18 2 2 9/1 Plasmid DNA Purification 9/8 Bioinformatics/SnapGene Intro 3 Restriction Digest/Agarose gel 9/22 3 Primer design – Lactase Expt. 9/15 Adv. Primer design; RNASeq and/or CHIPSeq 4 Lactase expt. 10/6 4 9/29 5 5 qPCR 10/20 10/13 Project Design 6 11/3 6 COVID-19 Exploration of Mol. Tech Applications 10/27 Project 7 Data Analyses; Wrap-up projects 11/10 Final oral exam: 15 min interview, 11/16 8 am - 10 am; 11/17 8 am - 1 pm



Acknowledgements

USD

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My students for being fabulous beta testers!

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