

DNA sequence editing

Summer School:

„from fungal morphology to genotype”

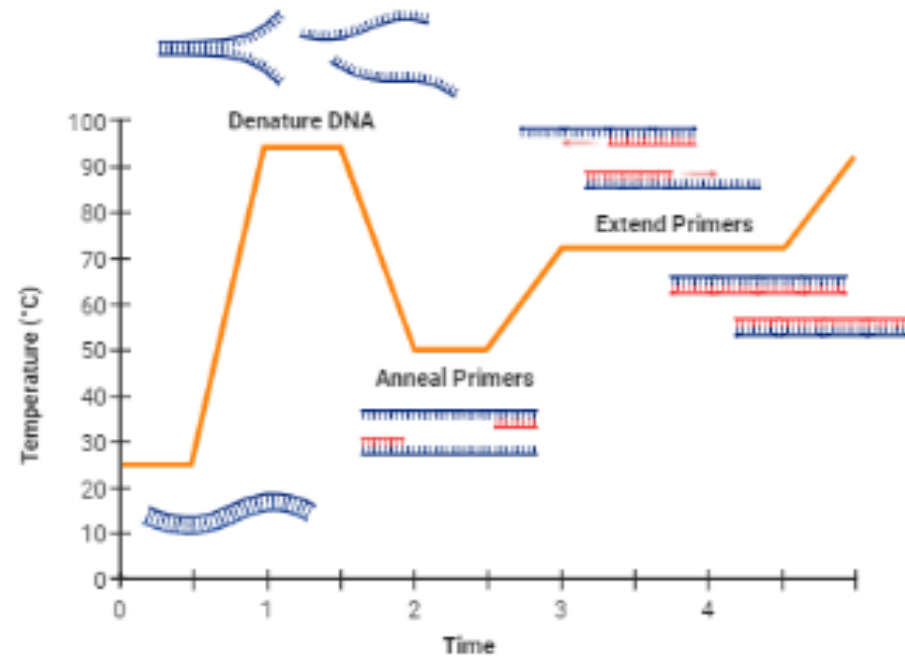
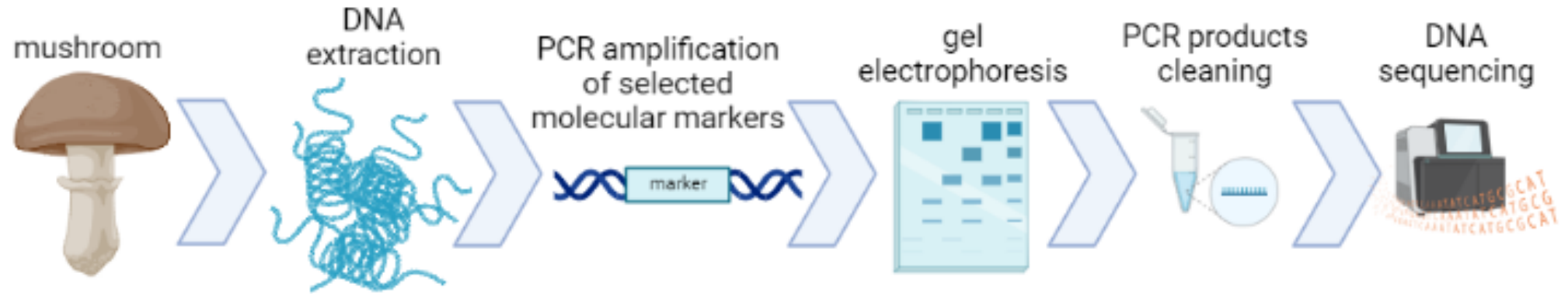


Julia Pawłowska

Univeristy of Warsaw

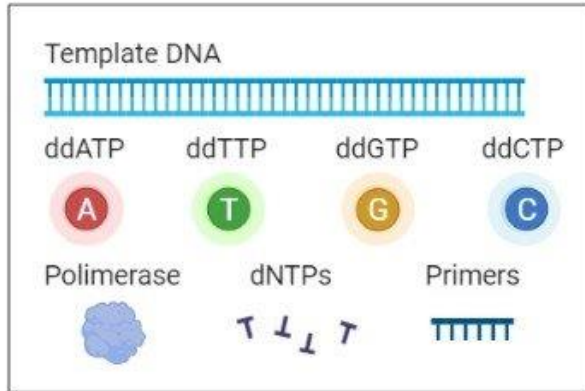
8-9.09.2022

General pipeline

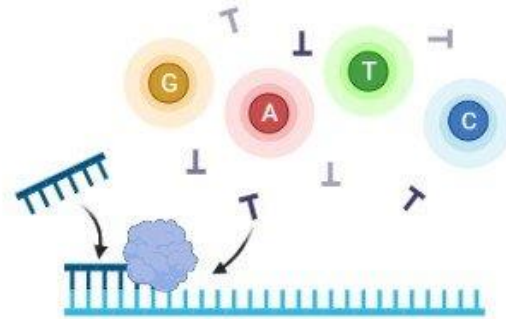


Sanger sequencing results

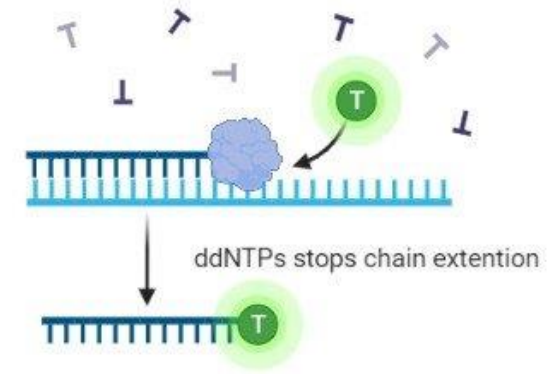
Reagents



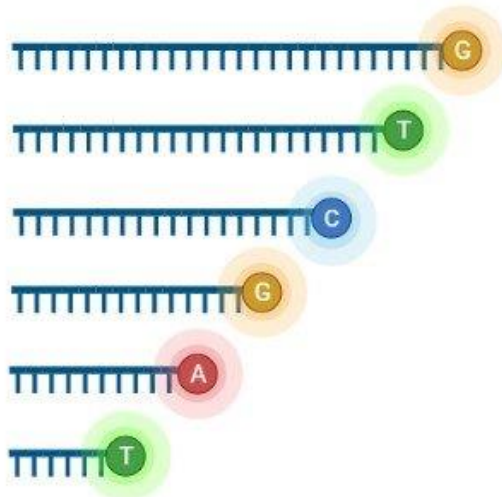
① Primer annealing and chain extension



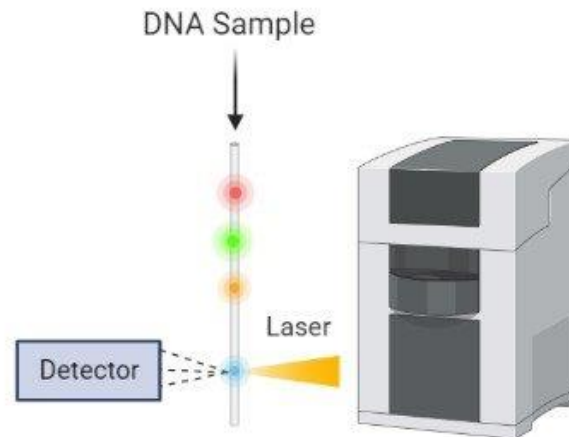
② ddNTP binding and chain termination



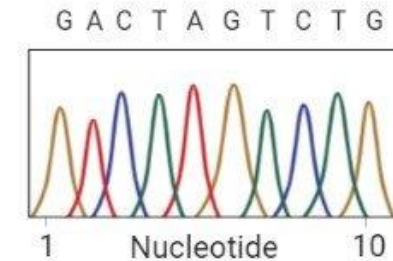
③ Fluorescently labelled DNA sample



④ Capillary gel electrophoresis and fluorescence detection



⑤ Sequence analysis and reconstruction



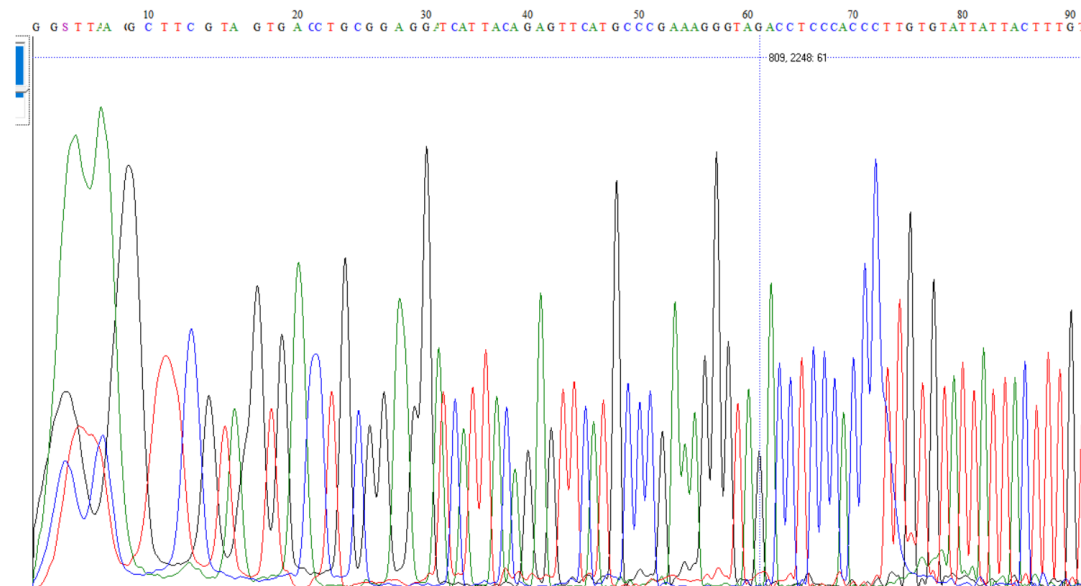
Download the test results

<https://ibe.biol.uw.edu.pl/wp-content/uploads/sites/22/2022/09/test-results.zip>



Nazwa	Data modyfikacji	Typ	Rozmiar
 6_ITS4	07.09.2022 22:35	Plik SEQ	1 KB
 6_ITS1f	07.09.2022 22:35	Plik AB1	244 KB
 6_ITS1f	07.09.2022 22:35	Plik SEQ	1 KB
 6_ITS4	07.09.2022 22:35	Plik AB1	244 KB

ATGGSTGGCWCTACTGATCCGAGGTCACCATAGAAAAATTTGGGTTTTGGCAGAAGCTCACCGAGCACCTGTAACGAGAG
ATATTACTACGTTCAGGACCCAGCGGCGCCGCCACTGATTTTAGAGCCG GCCATTGCTGACATAGACTCAATACCAAGCT
AAGCTTGAGGGTTGAAATGACGCTCGAACAGGCATGCCCCCGGAATACCAAGGGGCGCAATGTGCGTTCAAAGATTCTGA
TGATTCACTGAATTCTGCAATTCACATTACTTATCGCATTTTCGCTGCGTTCTTCATCGATGCCAGAACCAAGAGATCCGT
TGTTGAAAGTTTTAACTATTATATAGTACTCAGACGACAATAATAAAAAGAGTTTTGGTATCCTCTGGCGAGCATAACAAG
GCCCCGAAGGCAGCTCGCCAAAGCAACAAAGTAATAATACACAAGGGTGGGAGGTCTACCCTTTCGGGCATGAACTCTGTA
ATGATCCTTCCGCAGGTTACCTACGGAAACCTTGTTACGACTTTTACTTCCTCTAAWTKGACCAAGAGA



How to see your results?

<https://dnasubway.cyverse.org>

FAST TRACK TO GENE ANNOTATION AND GENOME ANALYSIS

Username:

Password:

Log In

Enter As Guest

Forgot Password?

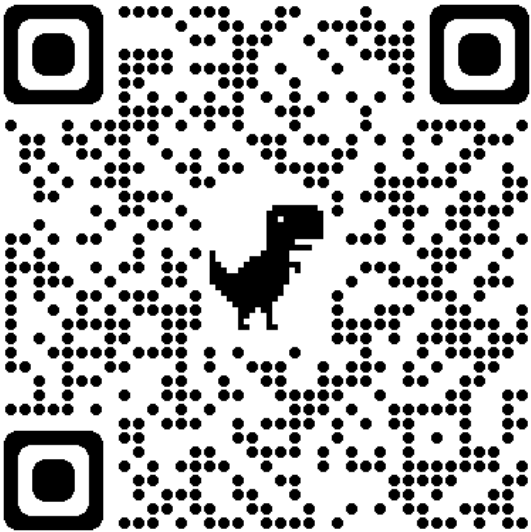
Register

D

N

A

SUBWAY



click



DNA Subway ties together key bioinformatics tools and databases to assemble gene models, investigate genomes, work with phylogenetic trees and analyze DNA barcodes. Roll over the "stations" on the subway map to find out more about the analysis steps. Analyze your own data or sample data provided. To start a project, select one of the "lines" (red, yellow, blue, green, purple). Register and login to be able to save and share your results.

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SUBWAY

Browsers & Transfer

Select Project Type*

Phylogenetics:

- ☒ DNA
- ☐ Protein
- ☐ mtDNA
- ☐ Viral

Barcoding:

- ☐ rbcL
- ☐ COI
- ☐ 16S
- ☐ ITS

Select Sequence Source *

- ☒ Upload **AB1 trace** files or sequences in [FASTA format](#):
(max 150kb)

Wybierz pliki Nie wybrano pliku

- ☐ Enter sequences in [FASTA format](#) (max 150kb):

- ☐ Import trace files from DNALC

- ☐ Select a set of sample sequences:

Name Your Project *

Project title:

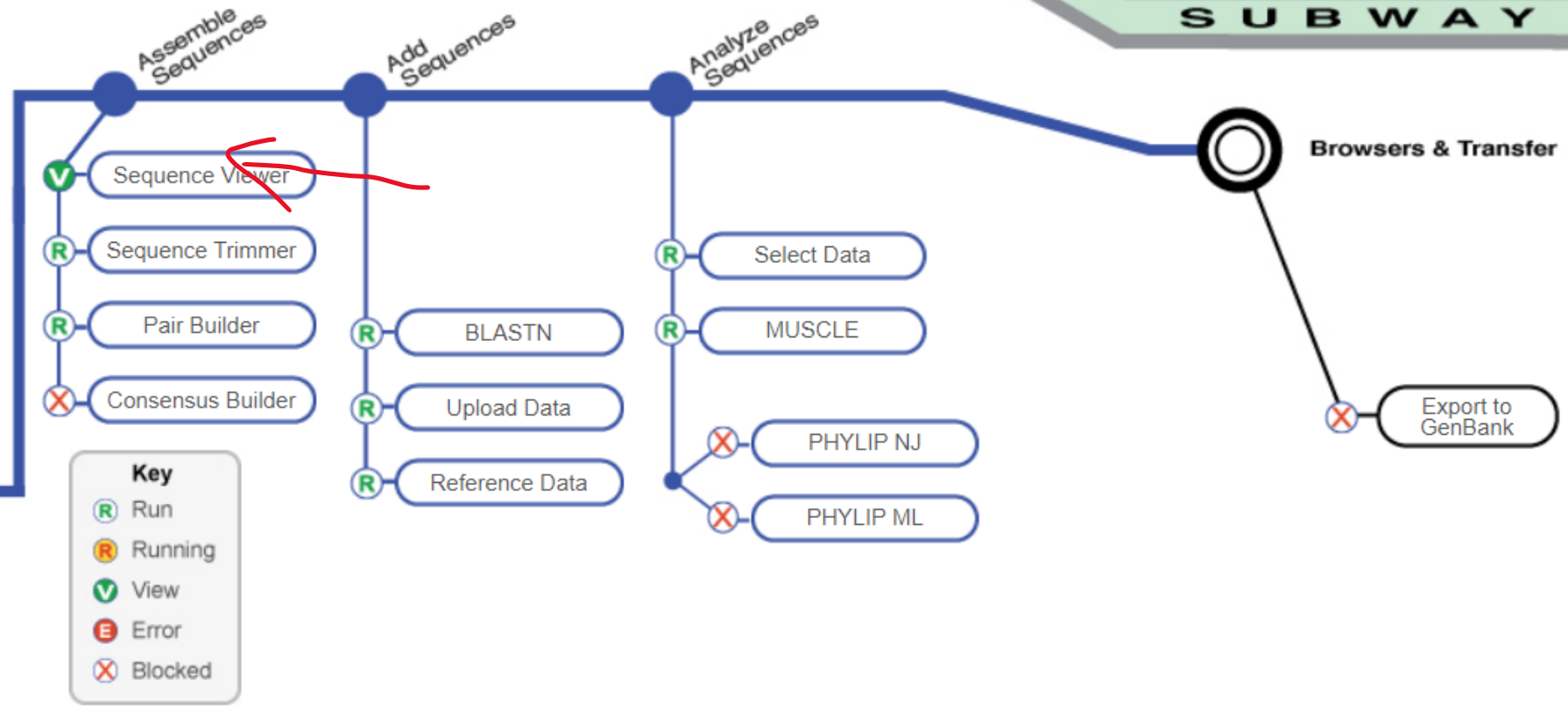
test results

Description

Total characters (max.140): 0

Continue

* Required information

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Project Information

test results

Project ID : 283911
User : Julia Pawłowska
Affiliation : -
Status : ☒ Private ☐ Public

Project type : DNA
Input seqs :
Ref seqs :
Parameters :

Description

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Sequence Trimmer

Pair Builder

Consensus Builder

Key

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- Running
- View
- Error
- Blocked

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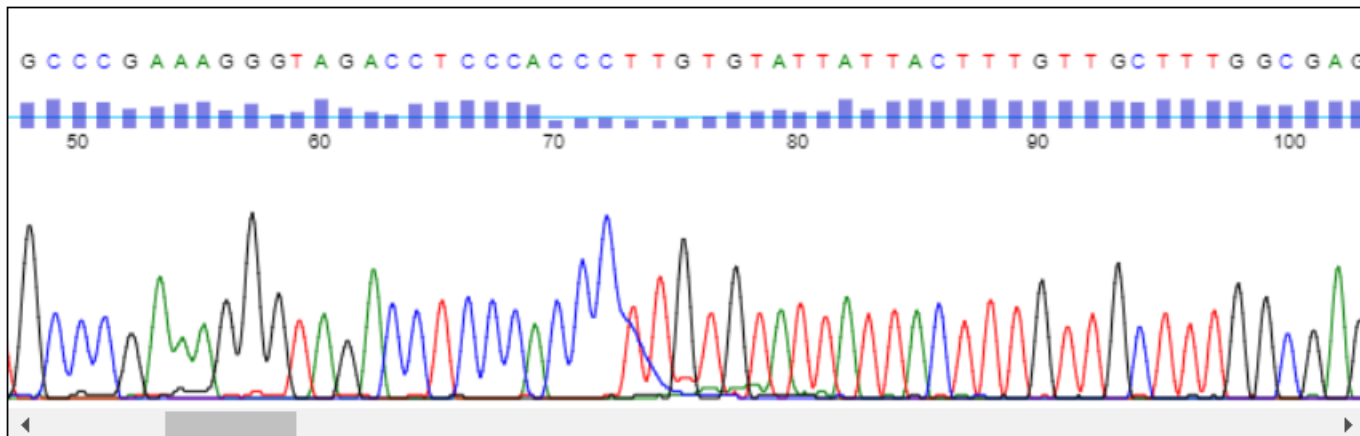
Glossary

Sequence Viewer

6 ITS1f



6 ITS4



Reset

X: + -

Y: + -

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test results

Project ID : 283911
User : Julia Pawłowska
Affiliation : -
Status : ☒ Private ☐ Public

Ref seqs :
Parameters :

Sequence Trimmer

 Your sequences have been trimmed

6 ITS1f



TTCGTAGTGACCTGCGGAGGATCATTACAGAGTTCATGCCCCGAAAGGGTAGACCTCCCACCCTTGTGTATTATTACTTTGTTGCTTTGGC

6 ITS4



TGATCCGAGGTCACCATAGAAAAATTGGGTTTTGGCAGAAGCTCACCGAGCACCTGTAACGAGAGATATTACTACGTTCAGGACCCAGC

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User : Julia Pawłowska
Affiliation : -
Status : ☒ Private ☐ Public

Project type : DNA
Input seqs :
Ref seqs :
Parameters :

Pair Builder

6_ITS1f TTCGTAGTGACCTGCGGAGGATCATTACAGAGTTCATGCCCGAAAGGGTAGACCTCCCACCCTTGTGTA E ☒
6_ITS4 TGATCCGAGGTCACCATAGAAAAATTTGGGTTTGGCAGAAGCTCACCAGACCTGTAACGAGAGATA E ☒

 Auto Pair[Try auto pairing](#) ? Enable Self Pairing[Enable](#) ?

Pair them?

Would you like to pair these
two sequences?

Yes No

click

SAVE

Glossary

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Project Information

test results

Project ID : 283911
User : Julia Pawłowska
Affiliation : -
Status : ☒ Private ☐ Public

Project type : DNA
Input seqs :
Ref seqs :
Parameters :

Consensus Editor

6_ITS

Pair 6_ITS [\[Edit Name\]](#)

```
6_ITS1f : -----TTCGTAG--TGACCTGCGG-AGGATCATTACAGAGTTCATGCCCCGAAAGGC
6_ITS4  : :GTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACAGAGTTCATGCCCCGAAAGGC
Consensus : :GTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACAGAGTTCATGCCCCGAAAGGC
```

[\[Trim Consensus\]](#) ?

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LOG OUT *Julia Pawłowska*

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Assemble Sequences

Add Sequences

Analyze Sequences

Sequence Viewer

Sequence Trimmer

Select Data

Browsers & Transfer

Select Data

☐ Select all

☐ User data

☒ Pair consensus_6_ITS

Save Your Changes

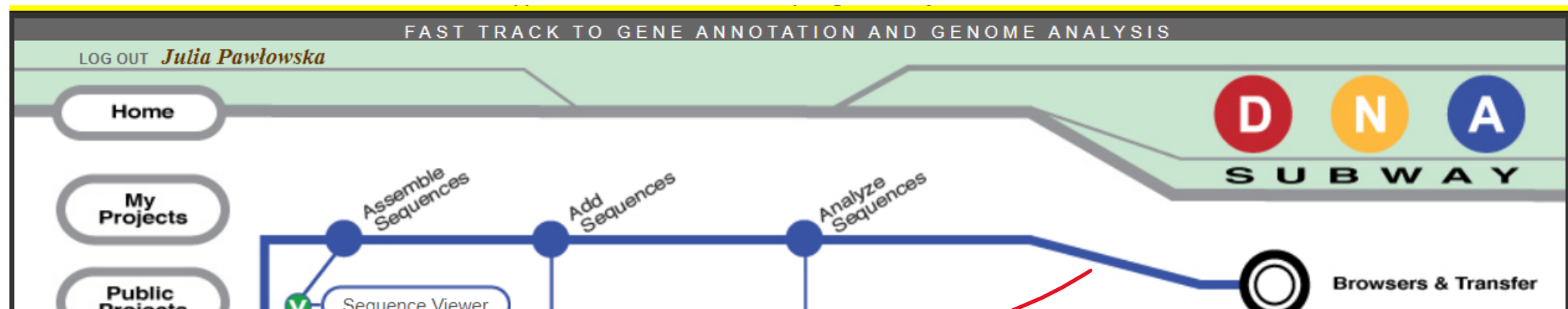
Once you have selected the sequences you wish to align, you must click save below.

Save Selections

Download sequences

Click below to download selected sequences in FASTA format.

Download



selected-seq-283911 — Notatnik

Plik Edytuj Wyświetl

>consensus_6_ITS
TCTCTTGGTCMAWTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACAGAGTTCATGCCCAGAAAGGGTAGACCTCCCACCCTTGTGTATTATTACTTTGTTGCTTTGGCGAGCTGCCTTCGGGCCTTGTATGCTCGCCAGAGGATACCAAACTCTTTT
TTGTCGTCTGAGTACTATATAATAGTTAAAACCTTCAACAACGGATCTCTTGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTGGTATTCCGGGGGGCATGCCTGTTTCGAGCGTCATT
CCTCAAGCTTAGCTTGGTATTGAGTCTATGTCAGCAATGGCCGGCTCTAAAATCAGTGGCGGGCGCCGCTGGGTCTGAACGTAGTAATATCTCTCGTTACAGGTGCTCGGTGAGCTTCTGCCAAAACCAAAATTTTCTATGGTTGACCTCGGATCAGGTAGGGATACCCGCTGAACCTTAAGCAT
TAAGCCGGAGGA

Sequencing

Metabarcoding
Analysis

must click save below.

Save Selections

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selected sequences in FASTA
format.

Download