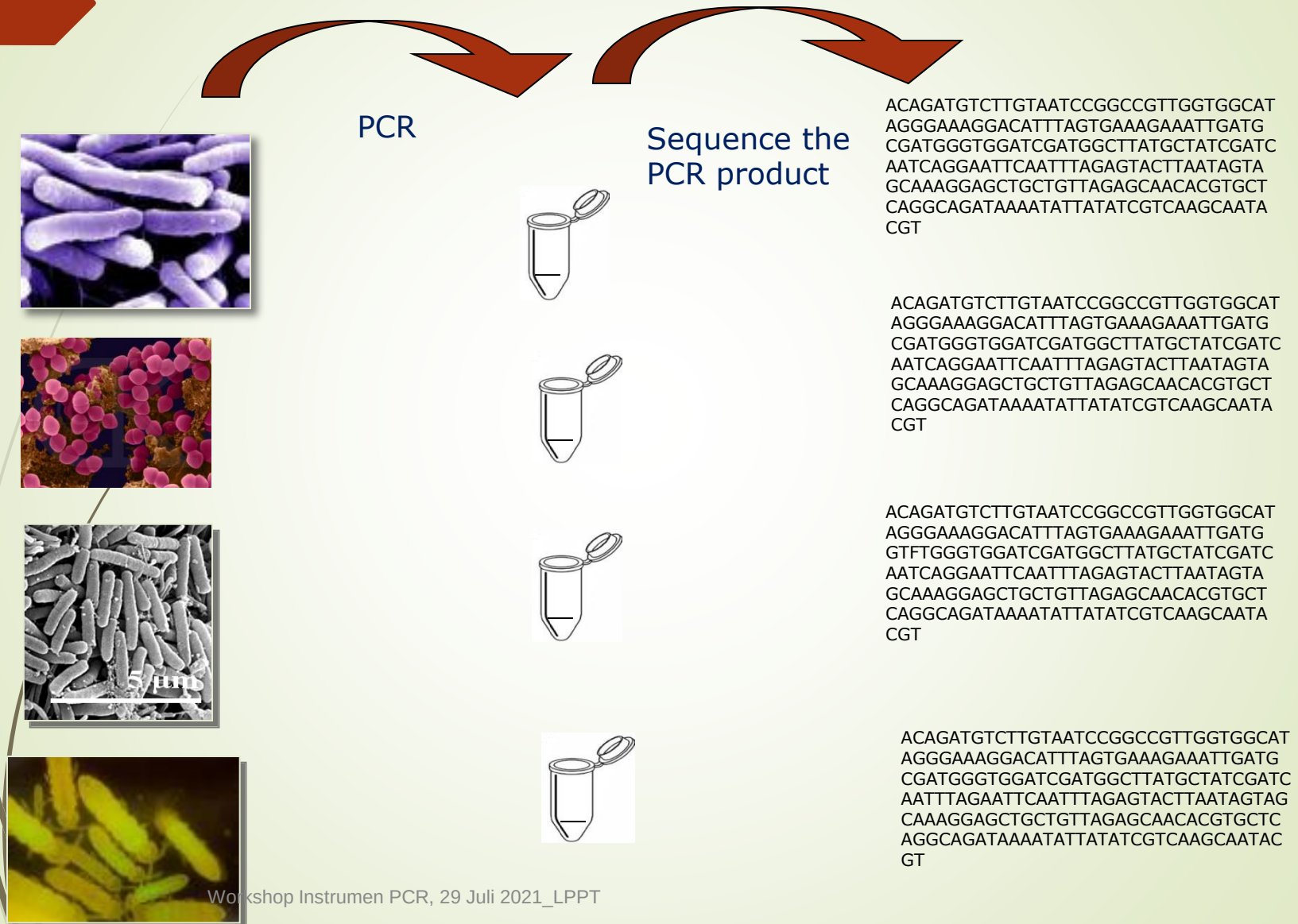


Pembuatan Pohon Filogenetik

RINI WIDAYANTI

2. Amplify and Sequence this region across isolates....





ANALISIS DATA SEKUEN DNA

- ➡ On line: NCBI (BLAST)
- ➡ Off line: MEGA



BLAST

(Basic Local Alignment Search Tool)

Browser window showing the NCBI (National Center for Biotechnology Information) website. The address bar displays <https://www.ncbi.nlm.nih.gov>.

The page features a navigation bar with links to **NCBI**, **Resources**, and **How To**. A search bar is present with a dropdown menu set to "All Databases" and a "Search" button. A "Sign in to NCBI" link is also visible.

A prominent banner for **COVID-19 Information** is displayed, including links to [Public health information \(CDC\)](#), [Research information \(NIH\)](#), [SARS-CoV-2 data \(NCBI\)](#), [Prevention and treatment information \(HHS\)](#), and [Español](#).

Below the banner, a section titled **UNITE** (A new NIH initiative to end structural racism and achieve racial equity in the biomedical research enterprise) is shown, with a "LEARN MORE" link.

The main content area is titled **Welcome to NCBI** and describes the center's mission: "The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information." It includes links to [About the NCBI](#), [Mission](#), [Organization](#), and [NCBI News & Blog](#).

Three primary actions are highlighted:

- Submit**: Deposit data or manuscripts into NCBI databases.
- Download**: Transfer NCBI data to your computer.
- Learn**: Find help documents, attend a class or watch a tutorial.

A sidebar on the left lists various resources, including **NCBI Home**, **Resource List (A-Z)**, and categories like **All Resources**, **Chemicals & Bioassays**, **Data & Software**, **DNA & RNA**, **Domains & Structures**, and **Genes & Expression**.

On the right, a **Popular Resources** section lists:

- PubMed
- Bookshelf
- PubMed Central
- BLAST** (highlighted with a red arrow)
- Nucleotide
- Genome
- SNP
- Gene

The Windows taskbar at the bottom shows the search bar, several open applications (including Chrome and PowerPoint), and system information: 27°C, Berawan, 20:24, 26/07/2021.

BLAST®

Home Recent Results Saved Strategies Help

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)

NEWS

BLAST+ 2.12.0 is here!
We have made some improvements to how BLAST multi-threads and the amount of memory required by makeblastdb.
Tue, 13 Jul 2021 12:00:00 EST [More BLAST news...](#)

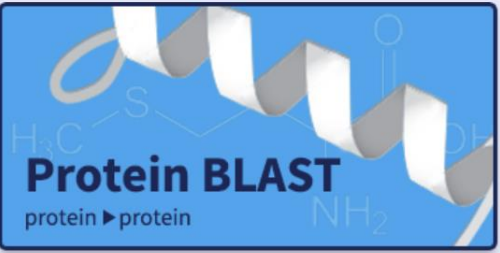
Web BLAST



Nucleotide BLAST
nucleotide ► nucleotide

blastx
translated nucleotide ► protein

tblastn
protein ► translated nucleotide



Protein BLAST
protein ► protein

https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome

Nucleotide BLAST: S... x

blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&BLAST_PROGRAMS=megaBlast&PAGE_TYPE=BlastSearch&SHOW_DEFAULTS=on&LINK_LOC=blastn

BLAST® Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

My NCBI [Sign In] [Register]

NCBI/ BLAST/ blastn suite

Standard Nucleotide BLAST

blastn blastp blastx tblastn tblastx

BLASTn programs search nucleotide databases using a nucleotide query. [more...](#) [Reset page](#) [Bookmark](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) [Query subrange](#)

From

To

Or, upload file No file chosen [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Choose Search Set

Database ☒ Human genomic + transcript ☐ Mouse genomic + transcript ☒ Others (nr etc.):
Human genomic plus transcript (Human G+T) [?](#)

Exclude Optional ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Entrez Query Optional

Enter an Entrez query to limit search [?](#)

Program Selection

Optimize for ☒ Highly similar sequences (megablast) ☐ More dissimilar sequences (discontiguous megablast) ☐ Somewhat similar sequences (blastn) [Choose a BLAST algorithm](#)

18:53 09/05/2012

Nucleotide BLAST: S... x

blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&BLAST_PROGRAMS=megaBlast&PAGE_TYPE=BlastSearch&SHOW_DEFAULTS=on&LINK_LOC=blastn

Enter accession number(s), gi(s), or FASTA sequence(s)

ATGCCCAACTAAATACATCAACATGATTATTACCCCTCTATCTATAACACTAACACCT
TTATCCTATTTCACACTGAACATTTCAAACTGACTTATCCTCTCAATCTAAACCTAAAAA
TATTAATACAGAATCATTAAACTCCCTGAGAACTAAATGAACGAAACCTATTGCGCT
CTTTCATTACCCCAAA

Clear Query subrange

From

To

Or, upload file No file chosen

Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database ☐ Human genomic + transcript ☐ Mouse genomic + transcript ☒ Others (nr etc.):

Nucleotide collection (nr/nt)

Organism

Optional ☐ Exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude

Optional ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Entrez Query

Optional

Program Selection

Optimize for ☒ Highly similar sequences (megablast)

☐ More dissimilar sequences (discontiguous megablast)

☐ Somewhat similar sequences (blastn)

Choose a BLAST algorithm

BLAST

Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window

NCBI Blast:Nucleotide Sequence X

https://blast.ncbi.nlm.nih.gov/Blast.cgi

U.S. National Library of Medicine
National Center for Biotechnology Information

Log in

BLAST® » blastn suite » results for RID-VGF6YRSX014

Home Recent Results Saved Strategies Help

[Edit Search](#) Save Search Search Summary ▾

[How to read this report?](#) [BLAST Help Videos](#) [Back to Traditional Results Page](#)

Job Title Nucleotide Sequence

RID [VGF6YRSX014](#) Search expires on 10-30 21:21 pm [Download All](#) ▾

Program BLASTN [Citation](#) ▾

Database nt [See details](#) ▾

Query ID lcl|Query_47789

Description None

Molecule type dna

Query Length 952

Other reports [Distance tree of results](#) [MSA viewer](#) [?](#)

Filter Results

Organism only top 20 will appear ☐ exclude

Type common name, binomial, taxid or group name

[Add organism](#)

Percent Identity to

E value to

Query Coverage to

[Filter](#) [Reset](#)

Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download ▾ Manage Columns ▾ Show 100 ▾ [?](#)

☐ select all 0 sequences selected

[GenBank](#) [Graphics](#) [Distance tree](#)

Waiting for www.ncbi.nlm.nih.gov...

Feedback

8:22 PM 10/29/2019

NCBI Blast:Nucleotide Sequence

https://blast.ncbi.nlm.nih.gov/Blast.cgi

Other reports [Distance tree of results](#) [MSA viewer](#) [Filter](#) [Reset](#)

Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download Manage Columns Show 100

☒ select all 100 sequences selected

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
☒	Hemibagrus nemurus mitochondrion, complete genome	1736	1736	100%	0.0	99.58%	NC_044863.1
☒	Hemibagrus wyckioides mitochondrion, complete genome	1736	1736	100%	0.0	99.58%	KJ624624.1
☒	Hemibagrus nemurus mitochondrion, complete genome	1736	1736	100%	0.0	99.58%	KJ573466.1
☒	Hemibagrus sp. RCH-2015 mitochondrion, complete genome	1676	1676	100%	0.0	98.43%	KM507291.1
☒	Hemibagrus spilopterus mitochondrion, complete genome	1676	1676	100%	0.0	98.43%	JQ343983.1
☒	Hemibagrus sp. SWH mitochondrion, complete genome	1386	1386	99%	0.0	93.00%	KM577633.1
☒	Sperata seenghala mitochondrial DNA, complete genome	1375	1375	99%	0.0	92.78%	AB907556.1
☒	Phractocephalus hemiolepis mitochondrion, complete genome	1367	1367	99%	0.0	92.69%	NC_037886.1
☒	Hemibagrus wyckii voucher INHS 93682 12S ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and 16S ribosomal RNA	1356	1356	98%	0.0	92.80%	JX899747.1
☒	Mystus cavasius mitochondrion, complete genome	1317	1317	100%	0.0	91.72%	KU870465.1
☒	Mystus rhegma mitochondrion, complete genome	1314	1314	100%	0.0	91.63%	JQ343984.1
☒	Tachysurus vachellii isolate male mitochondrion, complete genome	1303	1303	100%	0.0	91.43%	MK104137.1
☒	Tachysurus vachellii mitochondrion, complete genome	1303	1303	100%	0.0	91.43%	KT202282.1
☒	Pelteobagrus eupogon mitochondrion, complete genome	1297	1297	100%	0.0	91.32%	

[Feedback](#)

NCBI Blast:Nucleotide Sequence

https://blast.ncbi.nlm.nih.gov/Blast.cgi

Other reports [Distance tree of results](#) [MSA viewer](#) [?](#)

Filter Reset

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise ☐ CDS feature [?](#) Download

100 sequences selected [?](#)

[Download](#) [GenBank](#) [Graphics](#) [Next](#) [Previous](#) [Descriptions](#)

Hemibagrus nemurus mitochondrion, complete genome

Sequence ID: [NC_044863.1](#) Length: 16526 Number of Matches: 1

[See 1 more title\(s\)](#)

Range 1: 75 to 1026 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1736 bits(940)	0.0	948/952(99%)	0/952(0%)	Plus/Plus

Query 1 GGGTTGGTCCTGACTTTACTATCAGCTTTAACTCCATTATACATGCAAGTATCCGCACC 60
 Sbjct 75 GGGTTGGTCCTGACTTTACTATCAGCTTTAACTCCATTATACATGCAAGTATCCGCACC 134

Query 61 CCTGTGAGAATGCCCTTAATCCTCTACCCGAGGACGAGGAGCAGGTATCAGGCACAATTA 120
 Sbjct 135 CCTGTGAGAATGCCCTTAATCCTCTACCCGAGGACGAGGAGCAGGTATCAGGCACAATTA 194

Query 121 ACATTGGCCCATGACGCCTTGCTACGCCACACCCCAAGGGACTTCAGCAGTAATAAATA 180
 Sbjct 195 ACATTGGCCCATGACGCCTTGCTACGCCACACCCCAAGGGACTTCAGCAGTAATAAATA 254

Query 181 TTAAGCCATAAGTGAAAACCTGACTTAGTCAGAGTTAAAAGGGCCGGTAAAATTCGTGCC 240
 Sbjct 255 TTAAGCCATAAGTGAAAACCTGACTTAGTCAGAGTTAAAAGGGCCGGTAAAATTCGTGCC 314

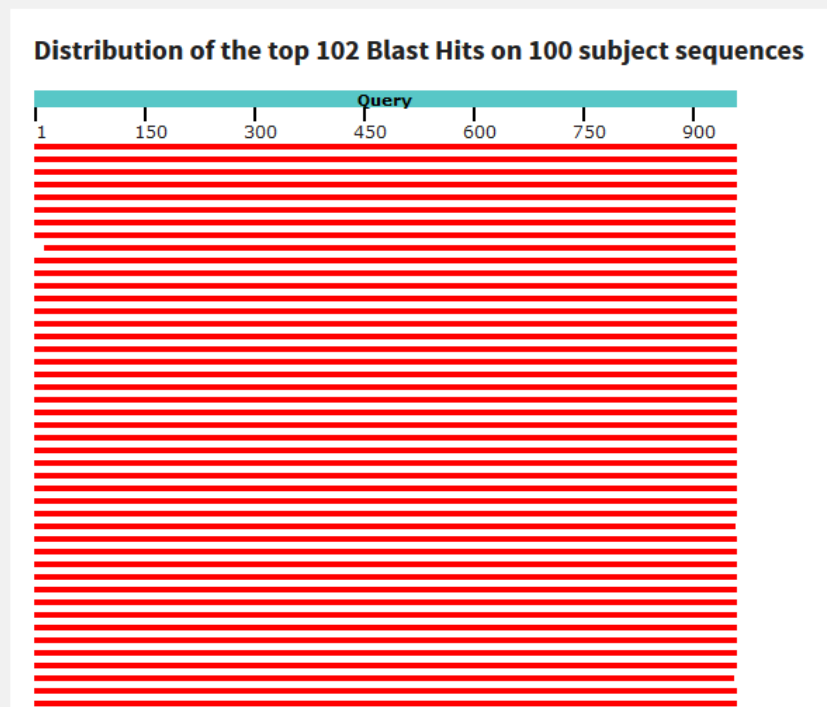
[Feedback](#)

Descriptions **Graphic Summary** Alignments Taxonomy

hover to see the title click to show alignments

Alignment Scores < 40 40 - 50 50 - 80 80 - 200 >= 200 ?

100 sequences selected ?



Feedback

Alignment view Pairwise CDS feature ? Download

100 sequences selected ?

Download GenBank Graphics Next Previous Descriptions

Hemibagrus nemurus mitochondrion, complete genome

Sequence ID: [NC_044863.1](#) Length: 16526 Number of Matches: 1

[See 1 more title\(s\)](#)

Range 1: 75 to 1026 GenBank Graphics

Next Match Previous Match

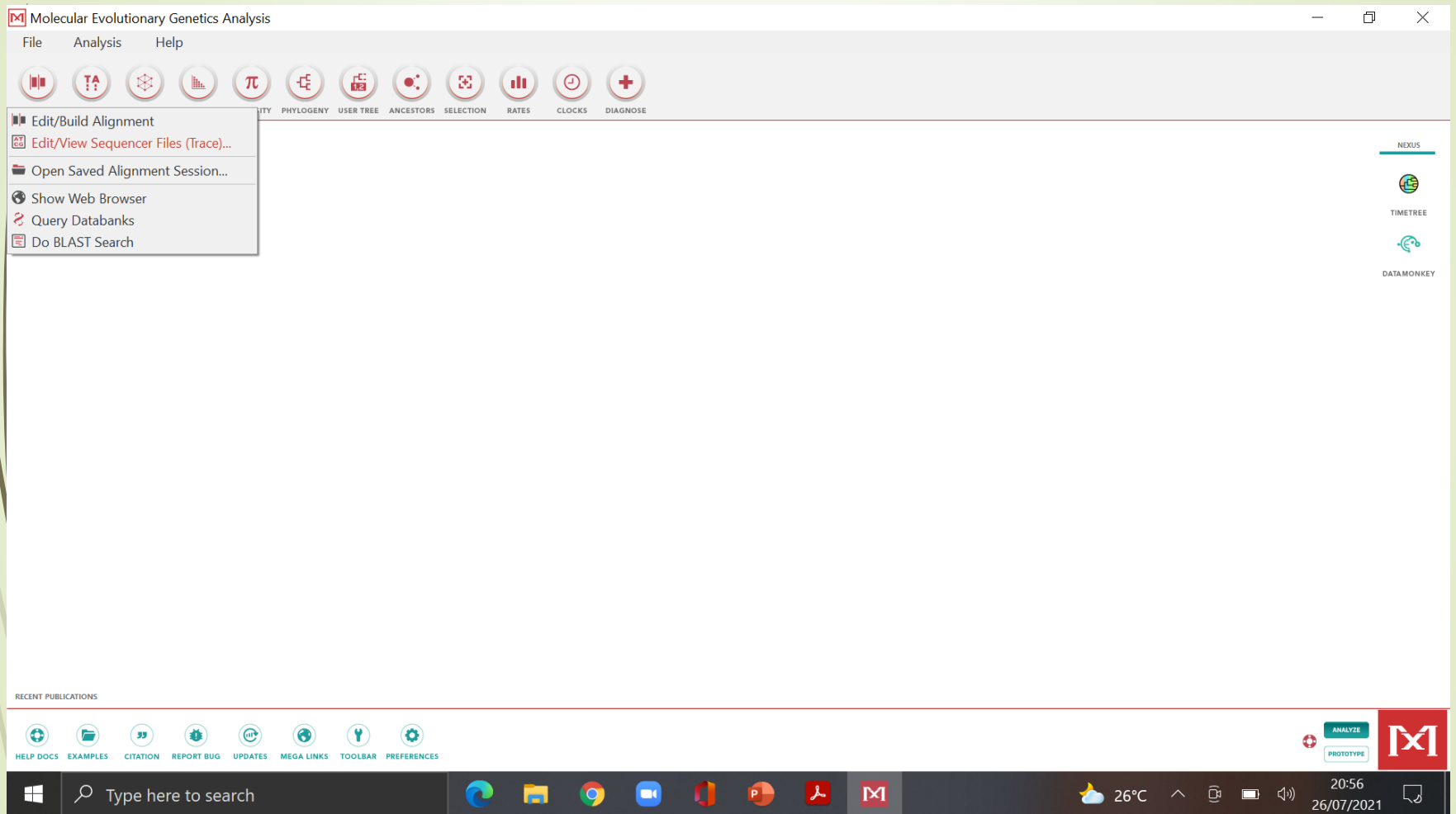
Score	Expect	Identities	Gaps	Strand
1736 bits(940)	0.0	948/952(99%)	0/952(0%)	Plus/Plus
Query 1	GGTTTGGTCCTGACTTTACTATCAGCTTTAACTCCATTATACATGCAAGTATCCGCACC	60		
Sbjct 75	GGTTTGGTCCTGACTTTACTATCAGCTTTAACTCCATTATACATGCAAGTATCCGCACC	134		
Query 61	CCTGTGAGAATGCCCTTAATCCTCTACCCGAGGACGAGGAGCAGGTATCAGGCACAATTA	120		
Sbjct 135	CCTGTGAGAATGCCCTTAATCCTCTACCCGAGGACGAGGAGCAGGTATCAGGCACAATTA	194		
Query 121	ACATTTGCCCATGACGCCTTGCTACGCCACACCCCAAGGGACTTCAGCAGTAATAAATA	180		
Sbjct 195	ACATTTGCCCATGACGCCTTGCTACGCCACACCCCAAGGGACTTCAGCAGTAATAAATA	254		
Query 181	TTAAGCCATAAGTGAAAACCTTGACTTAGTCAGAGTTAAAAGGGCCGGTAAAATTCGTGCC	240		
Sbjct 255	TTAAGCCATAAGTGAAAACCTTGACTTAGTCAGAGTTAAAAGGGCCGGTAAAATTCGTGCC	314		
Query 241	AGCCACCGCGGTTATACGAAAGACCCAGTTGATAGGTGCGGCGTAAAGGGTGTTATGG	300		
Sbjct 315	AGCCACCGCGGTTATACGAAAGACCCAGTTGATAGGTGCGGCGTAAAGGGTGTTATGG	374		
Query 301	aaaaaaaaTAAATAAAGCTAAAGACCCTCCAAGTCGTCATACGCATTCTGAGGACACGAAG	360		

Feedback



MEGA (Molecular Evolutionary Genetics Analysis)

- Alignment/ multiple alignment
- Komposisi nukleotida, asam amino
- Perbedaan nukleotida
- Jarak genetik/ distance
- Phylogenetic tree



Molecular Evolutionary Genetics Analysis

File Analysis Help

ALIGN DATA MODELS DISTANCE

AT CG

Open existing file

« Penelitian De... » sekuensing

Search sekuensing

Organize New folder

This PC

3D Objects

Desktop

Documents

Downloads

Music

Pictures

Videos

Acer (C:)

New Volume

Network

Name	Date modified
1st_BASE_4181661_BO1_F.ab1	06/05/2021 20:31
1st_BASE_4181662_BO1_R.ab1	06/05/2021 20:31
1st_BASE_4181663_BO2_F.ab1	06/05/2021 20:31
1st_BASE_4181664_BO2_R.ab1	06/05/2021 20:31
1st_BASE_4181665_BO3_F.ab1	06/05/2021 20:31
1st_BASE_4181666_BO3_R.ab1	06/05/2021 20:31
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1st_BASE_4181668_X1_R.ab1	06/05/2021 20:31
1st_BASE_4181669_X2_F.ab1	06/05/2021 20:31
1st_BASE_4181670_X2_R.ab1	06/05/2021 20:31
1st_BASE_4181671_KM1_F.ab1	06/05/2021 20:31
1st_BASE_4181672_KM1_R.ab1	06/05/2021 20:31

File name: 1st_BASE_4181661_BO1_F.ab1

ABI File (*.abi, *.ab1)

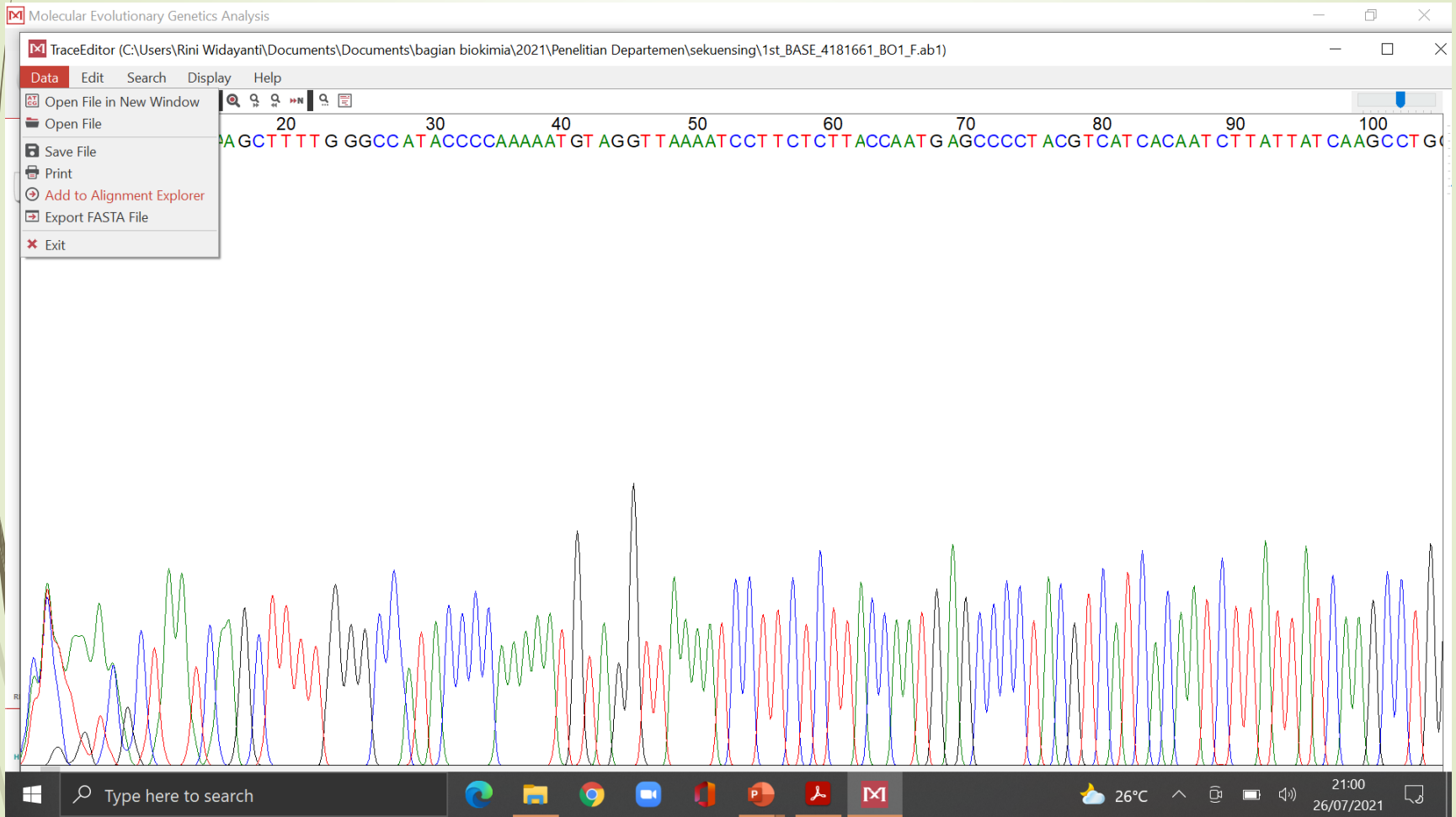
Open Cancel

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ANALYZE PROTOTYPE

20:57 26/07/2021



Recycle Bin AquaKeyFast

Today is July 26, 2021 Monday

MX: Alignment Explorer

Data Edit Search Alignment Web Sequencer Display Help

DNA Sequences Translated Protein Sequences

Species/Abbrv	
1. 4181661_BO1_F	CACAAACGCTAATCAAGCTTTTGGGCCATACCCCAAAATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCTACGTCATCAATCTTATTATCAAGCCTGGGCCGAGCCTTAACATTCAAGCTCCCA

Type here to search

26°C 21:02 26/07/2021

Teori Pembuatan Primer dan Pohon Filogenetik_Workshop Instrumen PCR_290721_LPPT_2 - PowerPoint

File Home Insert Draw Design Transitions Animations Slide Show Review View Recording Help

Picture Tools Rini Widayanti RW

Format Tell me what you want to do Share

MX: Alignment Explorer

Data Edit Search Alignment Web Sequencer Display Help

Open existing file

« Penelitian De... > sekuensing

Search sekuensing

Organize New folder

Name	Date modified
1st_BASE_4181661_BO1_F.ab1	06/05/2021 20:31
☒ 1st_BASE_4181662_BO1_R.ab1	06/05/2021 20:31
☒ 1st_BASE_4181663_BO2_F.ab1	06/05/2021 20:31
☒ 1st_BASE_4181664_BO2_R.ab1	06/05/2021 20:31
☒ 1st_BASE_4181665_BO3_F.ab1	06/05/2021 20:31
☒ 1st_BASE_4181666_BO3_R.ab1	06/05/2021 20:31
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☒ 1st_BASE_4181668_X1_R.ab1	06/05/2021 20:31
☒ 1st_BASE_4181669_X2_F.ab1	06/05/2021 20:31
☒ 1st_BASE_4181670_X2_R.ab1	06/05/2021 20:31
☒ 1st_BASE_4181671_KM1_F.ab1	06/05/2021 20:31
☒ 1st_BASE_4181672_KM1_R.ab1	06/05/2021 20:31

File name: "1st_BASE_4181672_KM1_R.ab1" "1st_E" ABI (*.abi;*.ab1)

Open Cancel

*****TACCAATGAGCCCTACGTCATCACAACTTATTATCAAGCCTGGGCTGGGCACAGCCTTAACATTCATAAGCTCCCA*****

Type here to search

26°C 21:04 26/07/2021

MX: Alignment Explorer

DataEditSearchAlignmentWebSequencerDisplayHelp

DNA SequencesTranslated Protein Sequences

Species/Abbrv	
1. 4181712_BJ3_R	CTGTTAGTGTCTGAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
2. 4181711_BJ3_F	ATTAAAGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGAAACAACCCCTAACATTCATAAGCTCCCCAC
3. 4181710_BJ2_R	GNTAAGTGTCTGAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGT
4. 4181709_BJ2_F	ATTANAGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGAAACAACCCCTAACATTCATAAGCTCCCCAC
5. 4181708_BJ1_R	TGTATAAGTGTCTGAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
6. 4181707_BJ1_F	TTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGAAACAACCCCTAACATTCATAAGCTCCCCAC
7. 4181706_B_R	CTGNTAAAGTGGTCTGAAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
8. 4181705_B_F	AATTAANAGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGTAACAACCCCTAACATTCATAAGCTCCCC
9. 4181704_A_R	CCGTTTAAGTGGTCTGAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
10. 4181703_A_F	ATTAAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGTAACAACCCCTAACATTCATAAGCTCCCCAC
11. 4181702_F_R	TAAAGTGGTCTGAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGT
12. 4181701_F_F	TTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGAAACAACCCCTAACATTCATAAGCTCCCCAC
13. 4181700_E_R	CCGTGTTAAGGCTCTGAAGTTGCTTTCAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
14. 4181699_E_F	ATTAAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGAAACAACCCCTAACATTCATAAGCTCCCCAC
15. 4181698_D_R	CTGTTTAAGTGGTCTGAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
16. 4181697_D_F	AATTANCGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGAAACAACCCCTAACATTCATAAGCTCCCCAC
17. 4181696_34_R	NTTTAAGTGTCTGAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
18. 4181695_34_F	AATTAANCGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGAAACAACCCCTAACATTCATAAGCTCCCC
19. 4181694_24_R	TANAAGTGGTCTGAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAG
20. 4181693_24_F	AATTAACNCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGAAACAACCCCTAACATTCATAAGCTCCCCAC
21. 4181692_14_R	GTNTAAGTGGTCTGAAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
22. 4181691_14_F	ATTTAANCGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGAAACAACCCCTAACATTCATAAGCTCCCC
23. 4181690_B3_R	CTGNTTAGTGTCTGAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
24. 4181689_B3_F	TAGNAGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGAAACAACCCCTAACATTCATAAGCTCCCCAC
25. 4181688_B2_R	GTNTAAGTGGTCTGAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
26. 4181687_B2_F	TTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGAAACAACCCCTAACATTCATAAGCTCCCCAC
27. 4181686_B1_R	TTAAGTGGTCTGAGTTGCATTGAGAGATGTTGGGATAGAGTCCGCAAGTCTTAGTTAGAGACTAGGAGATTTTCACTCCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
28. 4181685_B1_F	TTTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCCTTACAACTCTTACTATCAAGTTTAGGCCTAGGTAACAACCCCTAACATTCATAAGCTCCCCAC

Site #1

☒ with☐ w/o gaps

Selected genetic code: Vertebrate Mitochondrial

Windows Taskbar

Workshop Instrumen PCR, 29 Juli 2021_LPPT

MX: Alignment Explorer

Data Edit Search Alignment Web Sequencer Display Help

UUC L F

DNA Sequences Translated Protein Sequences

Species/Abbrv	Sequence
1. 4181712_BJ3_R	CTGTTTAGTGTCTGAGTTGATTTCAGAAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
2. 4181710_BJ2_R	GNTAAGTGTCTGAGTTGCAATTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
3. 4181708_BJ1_R	TGTATAAGTGTCTGAGTTGCAATTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAC
4. 4181706_B_R	CTGNTAAGTGGTCTGAAGTTGCATTTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
5. 4181704_A_R	CCGTTTAAGTGGTCTGAGTTGCATTTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
6. 4181700_E_R	CCTGTTTAAGGGTCTGAAGTTGCATTTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
7. 4181702_F_R	TAAGTGGTCTGAGTTGCATTTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
8. 4181698_D_R	CTGTTTAAGTGGTCTGAGTTGCATTTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
9. 4181696_34_R	NTTTAAGTGTCTGAGTTGCAATTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
10. 4181694_24_R	TANAAGTGGTCTGAGTTGCATTTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
11. 4181692_14_R	GTNTAAGTGGTCTGAAGTTGCATTTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
12. 4181690_B3_R	CTGNTTAGTGTCTGAGTTGCAATTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
13. 4181688_B2_R	GTNTAAGTGGTCTGAGTTGCAATTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
14. 4181686_B1_R	TTAAGTGGTCTGAGTTGCATTTCAGAAGATGTGGGATAGAGTCTGCAAGTCTTAGTTTCAGAGACTAGGAGATTTTCACCTCTACTTAAAGCTTTGAAGGCTTTTGGTCTGATGTTATCCTAAGTCTCTAGCTTATTAGTCT
15. 4181711_BJ3_F	ATTAAAGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCCAC
16. 4181709_BJ2_F	ATTANAGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCCAC
17. 4181707_BJ1_F	TTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCCAC
18. 4181705_B_F	AATTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCCAC
19. 4181703_A_F	ATTAAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCCAC
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22. 4181697_D_F	AATTANCGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCCAC
23. 4181695_34_F	AATTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCCAC
24. 4181693_24_F	AATTAACNCCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCCAC
25. 4181691_14_F	ATTTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCCAC
26. 4181689_B3_F	TAGNAGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCCAC
27. 4181687_B2_F	TTANNGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCCAC
28. 4181685_B1_F	TTTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCCACGTCCTTACCAATCTTACTATCAAGTTTAGGCCCTAGGTTACCAACCCCTAACATTTCATAAGCTCCCCAC

Site # 20

Selected genetic code: Vertebrate Mitochondrial

21:11 26/07/2021

MX: Alignment Explorer

Data Edit Search Alignment Web Sequencer Display Help

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Phylogenetic Analysis

Save Session
 Export Alignment

DNA Sequences
 Protein Sequences

Translate/Untranslate
 Genetic Code

Reverse Complement
 Reverse
 Complement

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tein Sequences

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Site # 20 ☐ with ☐ w/o gaps

Selected genetic code: Vertebrate Mitochondrial

MX: Alignment Explorer

Data Edit Search Alignment Web Sequencer Display Help

Align by ClustalW
Align by ClustalW (Codons)
Align by MUSCLE
Align by MUSCLE (Codons)
Mark/Unmark Site
Align Marked Sites
Unmark All Sites
Delete Gap-Only Sites
Auto-Fill Gaps

DNA Sequences Translated Protein

Species/Abbrv

1. 4181712_BJ3_R	T	GTAAATCCTCTCTTACCAATGAGCCCTAAGTCCTTACAATCTTACTTTCAAGTTTAGGCCTAGGAACAACCCCTTACATTCATAAGCTNCCACTGACTATTAGCTTGAATAGC
2. 4181710_BJ2_R	C	AGAAAATCAGTAAATAGTCTTTGGGCCATACCCAAAAGTAGGTAAATCCTTCNTACCAATGAGCCCTAAGTCCTTACAATTTTACTATCAAGTTTAGGCCTAGGAAAACCTT
3. 4181708_BJ1_R	T	AAAGTAGGTAAAACTTTTCTACCATGAGCCCTAAGTCCTACAATCTTANTATCAAGTTTAGGCCTAGGACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTGAATAG
4. 4181706_B_R	T	ATTAGCTTGAATAGCTCTTTGAAATTAATACACTAGCAATTTTACCATTAAATAGCACACAACACCACCCCGTGCAGTAGAAGCCACCACCAATCTTTTAGCCCAAGCTGC
5. 4181704_A_R	T	CTAGGGACAACCCCTAACATTTCATAAGCTNCCCTGACTATTAGCTTGAATAGGTTCTGAAATTAATCNCCTAGCAATTTTACCATTATAGNCAACACCCCAACCCCGTGCAGC
6. 4181700_E_R	G	TGGAAATTTACNCACTAGGCAATTTTNCCTAATAGGCAACACCACCAACCCCGGGGCGAGTAGAAGGCCACCCCAAACTTTCTTAGCCCAAGCTGCAGCAGCAGCA
7. 4181702_F_R	A	AATTCATAAGTTCCACTGACTATTAGCTGGAAGAGGCTTGAATTAACACACTAGCAATTTTACCATTAAATAGCCCAACACCAACACCCCGGGGCGAGTAGAAGCCACCCCA
8. 4181698_D_R	A	AGCCCAACAGCAACACCCCGGGGCGAGTAGAAGGCCACCAACCAATCTTCTAGCCCAAGCTGCAGCAGCAGCAACCATTTTATTGGCAAGCACTATTAAAGCCTGAGCAACAG
9. 4181696_34_R		CAACCTAACATTTCATAAGTTCCCACTGACTATTAGCTTGAATAGGCTTGAATTAACACACTAGCAATTTTACCATTATAGCCCAACACCATCATCCCGGCGAGTAGAAGGCCACCCCAAACTTTCTTAGCCCAAGCT
10. 4181694_24_R		CAAAGGTTTTGAAATTAACCACTAGCAATTTTACCATTATAGGCAACAGCATCATCCCGGGGCGAGTAGAAGGCCACCCCAAACTAGTTCTTAGCCCAAGCTGCAGCAGCAGCAACCATTTTATTTCGCAAGCATTATTAG
11. 4181692_14_R		AGTTCGCCCTAGGCNNNTTAGCCTGAATAAGGTTTNTGGAAATAACCCCATTTGGCAATTTTCCATTAAATAGGCCCTACCCCATCTTTCCCGGGGCGAGTAGAAGGCCACCCCAAACTTTTCTTAGCCCAAGGTCG
12. 4181690_B3_R		ACCCCAAAAAATNAGGTTAAATCCTTTCTTACCAATGAGCCCTNACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTTCCACTGACTATTAGCTTGAATAGGCTCTTGA
13. 4181688_B2_R		CTTCCCAAGTTTAGGCCTAGGAACAACCCCTTAACATTTTAAGTTCCTCCCGNACTATTAAGCTGGAATAGGTTCTGAAATTAACACAATAGCAATTTTACCATTATAGCACAAACCCCAACCCCGGCGAGTTGAAG
14. 4181686_B1_R		TTAAGTGGCTGAGTTGCATTGAGAAGATGTTGGATAGAGTCTCGCAAGCTTAGTTCTAGAGACTAGGAGATCTCTACTCTACTTAAAGCTTTGAGGCTTTTGGTCTGATGTTATCCTAAGCTCTAGCTTATTAATC
15. 4181711_BJ3_F		ATTAAAGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
16. 4181709_BJ2_F		ATTANAGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
17. 4181707_BJ1_F		TTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
18. 4181705_B_F		AATTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
19. 4181703_A_F		ATTAAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGTAACAACCCCTAACATTTCATAAGCTCCCAC
20. 4181701_F_F		TTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
21. 4181699_E_F		ATTAAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
22. 4181697_D_F		AATTANCGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
23. 4181695_34_F		AATTANCGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
24. 4181693_24_F		AATTAAACNCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
25. 4181691_14_F		ATTTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
26. 4181689_B3_F		TAGNAGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
27. 4181687_B2_F		TTANNGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGAACAACCCCTAACATTTCATAAGCTCCCAC
28. 4181685_B1_F		TTTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAAATGTAGGTTAAAAATCCTTCTCTTACCAATGAGCCCTACGTCCTTACAATCTTACTATCAAGTTTAGGCCTAGGTACAACCCCTAACATTTCATAAGCTCCCAC

Site # 40

with w/o gaps

Selected genetic code: Vertebrate Mitochondrial



DNA Sequences Translated Protein Sequences

Species/Abbrv	
1. 4181712_BJ3_R	TTGGGCCCCAACCCCAAAAAAGTAGGTAAATCCTCTC
2. 4181710_BJ2_R	CCAAGGTTTCCACAATACCATTTTGTAGAAAATCAGTAA
3. 4181708_BJ1_R	TAAATAAGTTTGGGCCCAACCCCAAAAAAGTAGGTAAAT
4. 4181706_B_R	TAAACATTCATAAGGTCCACGGCACTATTAGCTTGAATA
5. 4181704_A_R	TAAAAATCCCACCTATCAAGTTTAGGCCCTAGGGACAACCC
6. 4181700_E_R	GGACTATTAGGTTTGAATAGGTTCTGGAAAAATTTACN
7. 4181702_F_R	AGTTTAGGCCCTAGGAACAACCCCTTAAATTCATAAGTTG
8. 4181698_D_R	AACCATTAGCAATTTTACCATTATATAGCCCAACAGCA
9. 4181696_34_R	CAACCTAACATTCATAAGTTCCCACTGACTATTAGCTT
10. 4181694_24_R	CAAGGTTTGTAAATTAACCACCTAGCAATTTTACCAT
11. 4181692_14_R	AGTTCCCCCTAGGCNNNTTAGCCTGAATAAGGTTNTGG
12. 4181690_B3_R	ACCCCAAAAAATNAGGTTAAATCCNTTTTCTTACCAA
13. 4181688_B2_R	CTTCCCAAGTTTGGCCCTAGGAACAACCCCTTAACATTT
14. 4181686_B1_R	TTAAGTGGTCTGAGTTGCATTCAGAAAGATGTGGGATAG
15. 4181711_BJ3_F	ATTAAAGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
16. 4181709_BJ2_F	ATTANAGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
17. 4181707_BJ1_F	TTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
18. 4181705_B_F	AATTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
19. 4181703_A_F	ATTAAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
20. 4181701_F_F	TTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
21. 4181699_E_F	ATTAAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
22. 4181697_D_F	AATTANCGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
23. 4181695_34_F	AATTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
24. 4181693_24_F	AATTAACNCTAATTAAGCTTTTGGGCCATACCCCAAAAA
25. 4181691_14_F	ATTTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
26. 4181689_B3_F	TAGNAGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
27. 4181687_B2_F	TTANNGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
28. 4181685_B1_F	TTTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA

ClustalW Options

Alignment

Pairwise Alignment

Gap Opening Penalty 15,00

Gap Extension Penalty 6,66

Multiple Alignment

Gap Opening Penalty 15,00

Gap Extension Penalty 6,66

Matrix

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Site # 40

☒ with ☐ w/o gaps

Selected genetic code: Vertebrate Mitochondrial

MX: Alignment Explorer

Data Edit Search Alignment Web Sequencer Display Help

DNA Sequences Translated Protein Sequences

Species/Abbrv

Species/Abbrv	Sequence
1. 4181712_BJ3_R	TTGGGCCCCAAACCCCAAAAAAGTAGGTAATAATCCTCTCTTACCAATGAGCCCTTAAGTCCTTACAATCTTACTTTCAAGTTTAGGCCTAGGAACAACCCCTTACATTTCATAAGCTNCCACTGACTATTAGCTTGAATAGC
2. 4181710_BJ2_R	CCAAGGTTTCCACAATACCATTTTTAGAAAAATCAGTAAATTAAGTTTGGGCCATACCCAAAAAGTAGGTAAATCCTTTCNTACCAATGAGCCCTTAAGTCCTTACAATTTTACTATCAAGTTTAGGCCTAGGAACCCCT
3. 4181708_BJ1_R	TAAATAAGTTTGGGCCCCAACCCCAAAAAAGTAGGTAATAATCCTTCTTACCCTAGAGCCCTTAAGTCCTTACAATCTTANTATCAAGTTTAGGCCTAGGACAACCCCTAACATTCATAAGCTCCCAGTACTATTAGCTGAATAC
4. 4181706_B_R	TAAACATTTCATAAGGTTCCACGGGACTATTAGCTTGAATAGCTCTTGAAATTAATACACTAGCAATTTTACCATTAAATAGCACAACAACACCCCGTGCAGTAGAAGCCACCACCAATACTTTTAGCCCCAAGCTGC
5. 4181704_A_R	TAAAATCCCACTATCAAGTTTAGGCCTAGGACACACCCCTTAATTAATCNCCTAGCAATTTTACCATTATAGNCAACACCCCCACCCCGTGCAGCT
6. 4181700_E_R	GGACTATTAGGTTTGAATAAGGTTCTGGGAAAATTACNA
7. 4181702_F_R	AGTTTAGGCCTAGGAACAACCCCTTAAATTCATAAGTTG
8. 4181698_D_R	AACCATTAGCAATTTTACCATTATAGCCCCAACAGCAAA
9. 4181696_34_R	CAACCTAACATTCATAAGTTCCTCACTGACTATTAGCTT
10. 4181694_24_R	CAAAAGTTTGAATAACCACTAGCAATTTTACCATT
11. 4181692_14_R	AGTTCCCCCTAGGCNNNTTAGCCTGAATAAGGTTNTGG
12. 4181690_B3_R	ACCCCAAAAAATNAGGTTAAATCCNTTTTCTTACCAAT
13. 4181688_B2_R	CTTCCCAAGTTTAGGCCTAGGAACAACCCCTTAACATT
14. 4181686_B1_R	TAAAGTGGTCTGAGTTGCATTGAGAAGATGTGGGATAG
15. 4181711_BJ3_F	ATTAAAGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
16. 4181709_BJ2_F	ATTANAGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
17. 4181707_BJ1_F	TAAAGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
18. 4181705_B_F	AATTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
19. 4181703_A_F	ATTAAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
20. 4181701_F_F	TTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
21. 4181699_E_F	ATTANAGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
22. 4181697_D_F	AATTANCGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
23. 4181695_34_F	AATTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
24. 4181693_24_F	AATTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
25. 4181691_14_F	ATTAAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
26. 4181689_B3_F	TAGNAGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
27. 4181687_B2_F	TTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA
28. 4181685_B1_F	TTAANGCTAATTAAGCTTTTGGGCCATACCCCAAAAA

ClustalW Progress

ALIGNMENT BY CLUSTALW (00:00:49)

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MULTIPLE ALIGNMENT

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Site # 40

Selected genetic code: Vertebrate Mitochondrial

26°C 21:14 26/07/2021

MX: Alignment Explorer

Data Edit Search Alignment Web Sequencer Display Help



DNA Sequences Translated Protein Sequences

Species/Abbrv	
1. 4181712_BJ3_R	AAAAGTAGGTAAGTAAATCCTCTCTTACCAATGAGCCCCFAA-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
2. 4181710_BJ2_R	AAAAGTAGGTAAGTAAATCCTTTTCNT-ACCAATGAGCCCC-TAA-GTCCCTTACAATTTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
3. 4181708_BJ1_R	AAAAGTAGGTAAGTAAATCCTTTTCNT-ACCAATGAGCCCC-TAA-GTCCCTTACAATTTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
4. 4181706_B_J	-----TAAAAATCCCACATATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
5. 4181704_A_R	-----TAAAAATCCCACATATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
6. 4181700_E_R	-----TAAAAATCCCACATATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
7. 4181702_F_R	-----TAAAAATCCCACATATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
8. 4181698_D_R	-----TAAAAATCCCACATATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
9. 4181696_34_R	-----TAAAAATCCCACATATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
10. 4181694_24_R	-----TAAAAATCCCACATATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
11. 4181692_14_R	-----TAAAAATCCCACATATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
12. 4181690_B3_R	ATNAGGTTAAATCCTTTTCCTTACCAATGAGCCCCCTNAGTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
13. 4181688_B2_R	-----TAAAAATCCCACATATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
14. 4181711_BJ3_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
15. 4181709_BJ2_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
16. 4181707_BJ1_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
17. 4181705_B_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
18. 4181703_A_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
19. 4181701_F_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
20. 4181699_E_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
21. 4181697_D_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
22. 4181695_34_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
23. 4181693_24_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
24. 4181691_14_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
25. 4181689_B3_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
26. 4181687_B2_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-
27. 4181685_B1_F	AATGTAGGTTAAATCCTTCTCTTACCAATGAGCCCCCTAC-GTCCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAACAACCCCTTA-CATTTCATAAGCTNCCACTG-CTG-ACT-ATTA-GC-TTGAATAG-GTCTTGAAAT-

Site # 226

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Selected genetic code: Vertebrate Mitochondrial

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MX: Alignment Explorer

Data
Edit
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DNA Sequences

Translated Protein Sequences

Species/Abbrv	Sequence
1. 4181712_BJ3_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
2. 4181710_BJ2_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
3. 4181708_BJ1_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
4. 4181706_B_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGCTACTATCAGT
5. 4181704_A_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGGCTACTATCAGT
6. 4181700_E_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
7. 4181702_F_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
8. 4181698_D_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
9. 4181696_34_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
10. 4181694_24_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
11. 4181692_14_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
12. 4181690_B3_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
13. 4181688_B2_R	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
14. 4181711_BJ3_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
15. 4181709_BJ2_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
16. 4181707_BJ1_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
17. 4181705_B_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGGCTACTATCAGT
18. 4181703_A_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGGCTACTATCAGT
19. 4181701_F_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
20. 4181699_E_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
21. 4181697_D_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
22. 4181695_34_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
23. 4181693_24_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
24. 4181691_14_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
25. 4181689_B3_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
26. 4181687_B2_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGATTACTATCAGT
27. 4181685_B1_F	CCGCCCCGCATACAAGGCTTAGACTTAAACCACCGGGCTAATCATGGCTACTTGACAAAAATTAGCACCATTGCACTAATTATCCAAGTTGCCCTTACACACACCCCACTATTAAACCGCACTAGGGCTACTATCAGT

Site # 226

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☐ w/o gaps

Selected genetic code: Vertebrate Mitochondrial

MX: Alignment Explorer

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DNA Sequences Translated Protein Sequences

Species/Abbrv	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
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2. 4181710_BJ2_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGA-CA-CTTANC																						
3. 4181708_BJ1_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGA-CA-CTTATACA																						
4. 4181706_B_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANACAG																						
5. 4181704_A_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTAAACGG																						
6. 4181700_E_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTAAACAGG																						
7. 4181702_F_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTAA																						
8. 4181698_D_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTAAACAG																						
9. 4181696_34_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTAAAN																						
10. 4181694_24_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTNTA																						
11. 4181692_14_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
12. 4181690_B3_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGA-CA-CTANACAG																						
13. 4181688_B2_R	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
14. 4181711_BJ3_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
15. 4181709_BJ2_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
16. 4181707_BJ1_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
17. 4181705_B_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
18. 4181703_A_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
19. 4181701_F_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
20. 4181699_E_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
21. 4181697_D_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
22. 4181695_34_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
23. 4181693_24_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
24. 4181691_14_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
25. 4181689_B3_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
26. 4181687_B2_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						
27. 4181685_B1_F	TAGAGACTTAGGATAACATC	AGACCAA	AAGCCTTCAAAGCTTTAAGTAGGAGTGAAAAATCTCCTAGTCTCTGAACTAAGACTTGCAGGACT	CTATCCCACATCTTCTGAAATGCAACT	CAGACCACTTANAC																						

Site # 226 with w/o gaps Selected genetic code: Vertebrate Mitochondrial

MX: Alignment Explorer (ALIGNMENT nd2 BAUNG TAMABH GENBANK POTONG.mas)

Data Edit Search Alignment Web Sequencer Display Help

DNA Sequences Translated Protein Sequences

Species/Abbrv	Sequence
27. <i>Mystus cavasius</i> KU870465.1	ATGAGCCCCACGTCCTTATAAATCTAGTATCAAGCTTAGGCCCTAGGCACAAACCCTAACATTTCATAAGCTCCCACTGACTACTAGCCCTGAATAGGCCCTTGAATTAATACCCCTAGCAATTC
28. <i>Arius maculatus</i> NC_045222.1	ATGAGCCCCATATTTCTAAACAATCTTCTATCAAGCTTAGGCCCTAGGCACAGCCCTAACATTTCATAAGCTCCCACTGACTCTAGCCCTGAATAGGCCCTTGAATTAATACCACTAGCAATTC
29. <i>Arius dispar</i> NC_048969.1	ATGAGCCCCATATTTCTAAACAATCTTCTATCAAGCTTAGGCCCTAGGCACAGCCCTAACATTTCATAAGCTCCCACTGACTCTAGCCCTGAATAGGCCCTTGAATTAATACCACTAGCAATTC
30. <i>Arius arius</i> KX211965.1	ATGAGCCCCATATTTCTAAACAATCTTCTATCAAGCTTAGGCCCTAGGCACAGCCCTAACATTTCATAAGCTCCCACTGACTCTAGCCCTGAATAGGCCCTTGAATTAATACCACTAGCAATTC
31. 4181697_D_F	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
32. 4181699_E_F	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
33. <i>Pangasius pangasius</i> KC572135.1	ATGAGCCCCACGTCATCACAATTTTATTATCAAGTCTAGGCCCTGGGCACAGCCCTGACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
34. <i>Mystus vittatus</i> KX177968.1	ATGAGCCCCACGTCCTTATAAATTTTAGTATCGAGCTTGGGCCCTAGGCACAAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAATACCCCTAGCAATTC
35. <i>Mystus rhegma</i> JQ343984.1	ATGAGCCCCACGTCCTTATAAATTTTAGTATCAAGCTTGGGCCCTAGGCACAAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAATACCACTAGCAATTC
36. <i>H. wyckioides</i> KJ624624.1	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
37. <i>H. spilopterus</i> JQ343983.1	ATGAGCCCCACGTCCTTACAATTTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
38. 4181701_F	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
39. 4181692_14_R	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
40. 4181694_24_R	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
41. 4181696_34_R	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
42. 4181691_14_F	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
43. 4181693_24_F	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
44. 4181695_34_F	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAACACACTAGCAATTC
45. 4181672_KM1_R	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAATACACTAGCAATTC
46. 4181674_KM2_R	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAATACACTAGCAATTC
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48. 4181671_KM1_F	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAATACACTAGCAATTC
49. 4181673_KM2_F	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAATACACTAGCAATTC
50. 4181675_KM3_F	ATGAGCCCCACGTCCTTACAATCTTACTATCAAGTTTAGGCCCTAGGAAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTCTTGAATTAATACACTAGCAATTC
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61. 4181661_BO1_F	ATGAGCCCCACGTCATCACAATCTTATTATCAAGCTTGGGCCCTGGGCACAGCCCTAACATTTCATAAGCTCCCACTGACTACTTGGCTGAATAGGCCCTTGAATTAATACATTAGCAATTC
62. 4181663_BO2_F	ATGAGCCCCACGTCATCACAATCTTATTATCAAGCTTGGGCCCTGGGCACAGCCCTAACATTTCATAAGCTCCCACTGACTACTTGGCTGAATAGGCCCTTGAATTAATACATTAGCAATTC
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Workshop Instrumen PCR, 29 Juli 2021_LPPT



DNA Sequences Translated Protein Sequences

Species/Abbrv	
27. <i>Mystus cavasius</i> KU870465.1	ATGAGCCCCACGTCCTTAATAATCTAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTCTTAGCCCTGAATAGGCCCTTGAAATTAATACCCCTAGCAATCC
28. <i>Arius maculatus</i> NC_045222.1	ATGAGCCCCATATTTCTAACAATCCTGCTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTCTTAGCCCTGAATAGGCCCTTGAAATCAACACACTAGCAATTC
29. <i>Arius dispar</i> NC_048969.1	ATGAGCCCCATATTTCTAAATAATCCTGCTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTCTTAGCCCTGAATAGGCCCTTGAAATCAACACACTAGCAATTC
30. <i>Arius arius</i> KX211965.1	ATGAGCCCCATATTTCTAACAATCCTGCTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTCTTAGCCCTGAATAGGCCCTTGAAATCAACACACTAGCAATTC
31. 4181697_D_F	ATGAGCCCCACGTCCTTCAATCTTACTATCAAGCTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAACACACTAGCAATTT
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33. <i>Pangasius pangasius</i> KC572135.1	ATGAGCCCCACGTCATCAACAATTTTATTATCAAGCTTAGGCCCTGGGCACACGCCCTGACATTTCATAAGCTCCCACTGATTACTTGCCTGAATAGGCCCTTGAAATTAACACACTAGCAATTC
34. <i>Mystus vittatus</i> KX177968.1	ATGAGCCCCACGTCCTTCAATTTTATAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTGTTAGCTTGAATAGGCCCTTGAAATTAATACCCCTAGCAATTT
35. <i>Mystus rhegma</i> JQ343984.1	ATGAGCCCCACGTCCTTCAATTTTATAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATCAACACACTAGCAATTC
36. <i>H. wyckioides</i> KJ624624.1	ATGAGCCCCACGTCCTTCAATTTTATAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAACACACTAGCAATTT
37. <i>H. spilopterus</i> JQ343983.1	ATGAGCCCCACGTCCTTCAATTTTATAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAACACACTAGCAATTT
38. 4181701_F_F	ATGAGCCCCACGTCCTTCAATTTTATAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAACACACTAGCAATTT
39. 4181692_14_R	ATGAGCCCCACGTCCTTCAATTTTATAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAACACACTAGCAATTT
40. 4181694_24_R	ATGAGCCCCACGTCCTTCAATTTTATAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAACACACTAGCAATTT
41. 4181696_34_R	ATGAGCCCCACGTCCTTCAATTTTATAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAACACACTAGCAATTT
42. 4181691_14_F	ATGAGCCCCACGTCCTTCAATTTTATAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAACACACTAGCAATTT
43. 4181693_24_F	ATGAGCCCCACGTCCTTCAATTTTATAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAACACACTAGCAATTT
44. 4181695_34_F	ATGAGCCCCACGTCCTTCAATTTTATAGTATCAAGCTTAGGCCCTAGGCACACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAACACACTAGCAATTT
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47. 4181676_KM3_R	ATGAGCCCCACGTCCTTCAATCTTACTATCAAGCTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAATACACTAGCAATTT
48. 4181671_KM1_F	ATGAGCCCCACGTCCTTCAATCTTACTATCAAGCTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAATACACTAGCAATTT
49. 4181673_KM2_F	ATGAGCCCCACGTCCTTCAATCTTACTATCAAGCTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAATACACTAGCAATTT
50. 4181675_KM3_F	ATGAGCCCCACGTCCTTCAATCTTACTATCAAGCTTAGGCCCTAGGAACAACCCCTAACATTTCATAAGCTCCCACTGACTATTAGCTTGAATAGGCTTTGAAATTAATACACTAGCAATTT
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52. 4181682_PA3_R	ATGAGCCCCACATCTTAATAATTTTACTATCAAGCTTAGGCCCTAGGCACACGCTCTAACATTTCATAAGTTCTCACTGACTCTTGGCCCTGAATAGGCTTTGAAATTAACACACTAGCAATTC
53. 4181684_PA4_R	ATGAGCCCCACATCTTAATAATTTTACTATCAAGCTTAGGCCCTAGGCACACGCTCTAACATTTCATAAGTTCTCACTGACTCTTGGCCCTGAATAGGCTTTGAAATTAACACACTAGCAATTC
54. 4181679_PA2_F	ATGAGCCCCACATCTTAATAATTTTACTATCAAGCTTAGGCCCTAGGCACACGCTCTAACATTTCATAAGTTCTCACTGACTCTTGGCCCTGAATAGGCTTTGAAATTAACACACTAGCAATTC
55. 4181681_PA3_F	ATGAGCCCCACATCTTAATAATTTTACTATCAAGCTTAGGCCCTAGGCACACGCTCTAACATTTCATAAGTTCTCACTGACTCTTGGCCCTGAATAGGCTTTGAAATTAACACACTAGCAATTC
56. 4181683_PA4_F	ATGAGCCCCACATCTTAATAATTTTACTATCAAGCTTAGGCCCTAGGCACACGCTCTAACATTTCATAAGTTCTCACTGACTCTTGGCCCTGAATAGGCTTTGAAATTAACACACTAGCAATTC
57. 4181668_X1_R	ATGAGTCCCTATGTCCTCATAAATTTCTACTATCAAGCTTAGGCCCTAGGTAACCTTACATTTCATAAGTTCTCACTGACTCTTGGCCCTGAATAGGCTTTGAAATTAATACCCCTCGCAATTC
58. 4181670_X2_R	ATGAGTCCCTATGTCCTCATAAATTTCTACTATCAAGCTTAGGCCCTAGGTAACCTTACATTTCATAAGTTCTCACTGACTCTTGGCCCTGAATAGGCTTTGAAATTAATACCCCTCGCAATTC
59. 4181667_X1_F	ATGAGTCCCTATGTCCTCATAAATTTCTACTATCAAGCTTAGGCCCTAGGTAACCTTACATTTCATAAGTTCTCACTGACTCTTGGCCCTGAATAGGCTTTGAAATTAATACCCCTCGCAATTC
60. 4181669_X2_F	ATGAGTCCCTATGTCCTCATAAATTTCTACTATCAAGCTTAGGCCCTAGGTAACCTTACATTTCATAAGTTCTCACTGACTCTTGGCCCTGAATAGGCTTTGAAATTAATACCCCTCGCAATTC
61. 4181661_BO1_F	ATGAGCCCCACGTCATCAACAATCTTATTATCAAGCTTAGGCCCTGGGCACACGCTTAACTTCATAAGCTCCCACTGACTACTTGGCTTGAATAGGCCCTTGAAATTAATACATTAGCAATTC
62. 4181663_BO2_F	ATGAGCCCCACGTCATCAACAATCTTATTATCAAGCTTAGGCCCTGGGCACACGCTTAACTTCATAAGCTCCCACTGACTACTTGGCTTGAATAGGCCCTTGAAATTAATACATTAGCAATTC
63. 4181665_BO3_F	ATGAGCCCCACGTCATCAACAATCTTATTATCAAGCTTAGGCCCTGGGCACACGCTTAACTTCATAAGCTCCCACTGACTACTTGGCTTGAATAGGCCCTTGAAATTAATACATTAGCAATTC
64. 4181662_BO1_R	ATGAGCCCCACGTCATCAACAATCTTATTATCAAGCTTAGGCCCTGGGCACACGCTTAACTTCATAAGCTCCCACTGACTACTTGGCTTGAATAGGCCCTTGAAATTAATACATTAGCAATTC

Confirmation



Protein-coding nucleotide sequence data?

Yes

No

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Monday

Tuesday

Wednesday

Thursday

Friday

Saturday

Sunday

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26°C



21:20

26/07/2021

MX: Sequence Data Explorer (PhyloAnalysis.meg)

Menu: Data | Display | Search | Groups | Highlight | Statistics | Help

Save Session | Export Data... | Translate Sequences | Select Code Table... | Select & Edit Genes/&Domains... | Select & Edit Taxa/&Groups... | Add Labels By Site Number | Quit Data Explorer

8. 4181708 BJ1 R
 9. 4181707 BJ1 F
 10. 4181710 BJ2 R
 11. 4181712 BJ3 R
 12. 4181709 BJ2 F
 13. 4181711 BJ3 F
 14. 4181704 A R
 15. 4181703 A F
 16. 4181706 B R
 17. 4181705 B F
 18. 4181698 D R
 19. 4181700 E R
 20. 4181702 F R
 21. Pangasius sanitwongsei MN809630.1
 22. Pangasius larnaudii AP012018.1
 23. Pangasius bocourti NC 046590.1
 24. Pangasianodon hypophthalmus KC846907.1
 25. Pangasianodon gigas AY762971.1
 26. Netuma thalassina MG587041.1
 27. Mystus cavasius KU870465.1
 28. Arius maculatus NC 045222.1
 29. Arius dispar NC 048969.1

Sequence alignment view showing nucleotide positions (A, T, G, C) for 66 taxa selected. The alignment is displayed in a grid format with columns for each site and rows for each taxon.

Site# 1 /1045 Highlighted: None 66 taxa selected Data

Windows taskbar: Type here to search, 26°C, 21:22, 26/07/2021

MX: Sequence Data Explorer (PhyloAnalysis.meg)

Data Display Search Groups Highlight Statistics Help

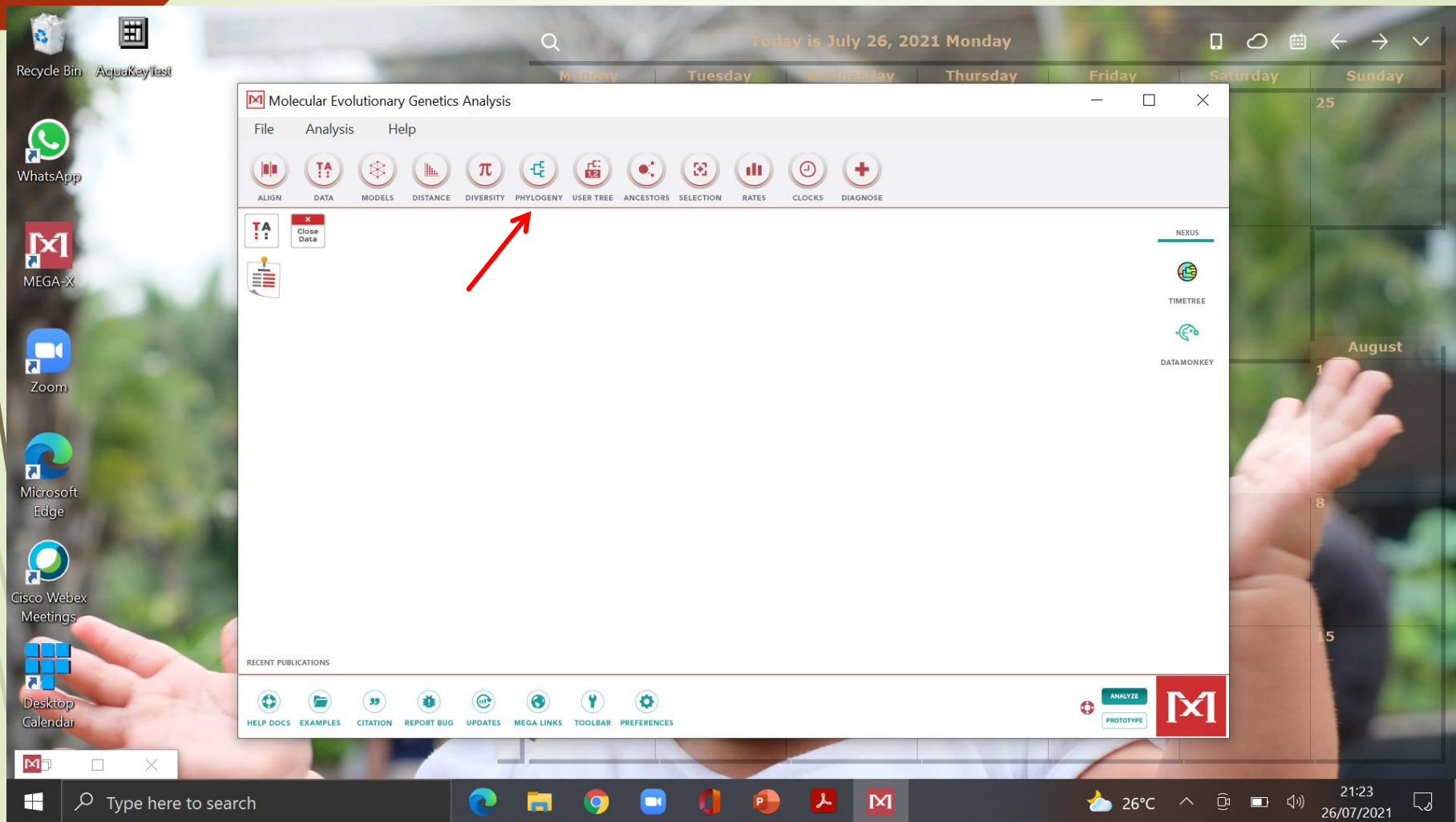
☐ Name
 ☐ 7. 4181688 B2 R
 ☐ 8. 4181708 BJ1 R
 ☒ 9. 4181707 BJ1 F
 ☐ 10. 4181710 BJ2 R
 ☐ 11. 4181712 BJ3 R
 ☒ 12. 4181709 BJ2 F
 ☒ 13. 4181711 BJ3 F
 ☐ 14. 4181704 A R
 ☒ 15. 4181703 A F
 ☒ 16. 4181705 B F
 ☐ 17. 4181698 D R
 ☐ 18. 4181706 B R
 ☐ 19. 4181700 E R
 ☐ 20. Pangasius sanitwongsei MN809630.1
 ☐ 21. Pangasius larnaudii AP012018.1
 ☐ 22. Pangasius bocourti NC 046590.1
 ☒ 23. Pangasianodon hypophthalmus KC846907.1
 ☒ 24. Pangasianodon gigas AY762971.1
 ☒ 25. Netuma thalassina MG587041.1
 ☒ 26. Mystus cavasius KU870465.1
 ☒ 27. Arius maculatus NC 045222.1
 ☐ 28. Arius dispar NC 048969.1
 ☒ 29. Arius arius KX211965.1
 ☒ 30. 4181697 D F
 ☒ 31. 4181699 E F
 ☒ 32. Pangasius pangasius KC572135.1
 ☒ 33. Mystus vittatus KX177968.1
 ☒ 34. Mystus rhegma JQ343984.1
 ☒ 35. H. workinides K1624624.1

M (MET)

A T G A G C C C T A C G T C C T T A C A A T C T T A C T A T C A A G T T T A G G C C T A G G A A C A A C C C T A A C / ^

Site# 1 /1045 Highlighted: None 40 taxa selected Data

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Construct/Test Neighbor-Joining Tree...
Construct/Test Minimum-Evolution Tree...
Construct/Test UPGMA Tree...
Construct/Test Maximum Parsimony Tree(s)
Open Tree Session

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☐ Remember to reuse currently active data.

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MX: Analysis Preferences

Phylogeny Reconstruction

Option	Setting
ANALYSIS	
Scope	→ All Selected Taxa
Statistical Method	→ Neighbor-joining
PHYLOGENY TEST	
Test of Phylogeny	→ Bootstrap method
No. of Bootstrap Replications	→ 1000
SUBSTITUTION MODEL	
Substitutions Type	→ Nucleotide
Genetic Code Table	→ Not Applicable
Model/Method	→ Kimura 2-parameter model
Fixed Transition/Transversion Ratio	→ Not Applicable
Substitutions to Include	→ d: Transitions + Transversions
RATES AND PATTERNS	
Rates among Sites	→ Uniform Rates
Gamma Parameter	→ Not Applicable
Pattern among Lineages	→ Same (Homogeneous)
DATA SUBSET TO USE	
Gaps/Missing Data Treatment	→ Pairwise deletion
Site Coverage Cutoff (%)	→ Not Applicable
Select Codon Positions	→ ☒ 1st ☒ 2nd ☒ 3rd ☒
SYSTEM RESOURCE USAGE	
Number of Threads	→ 3

Help Cancel OK

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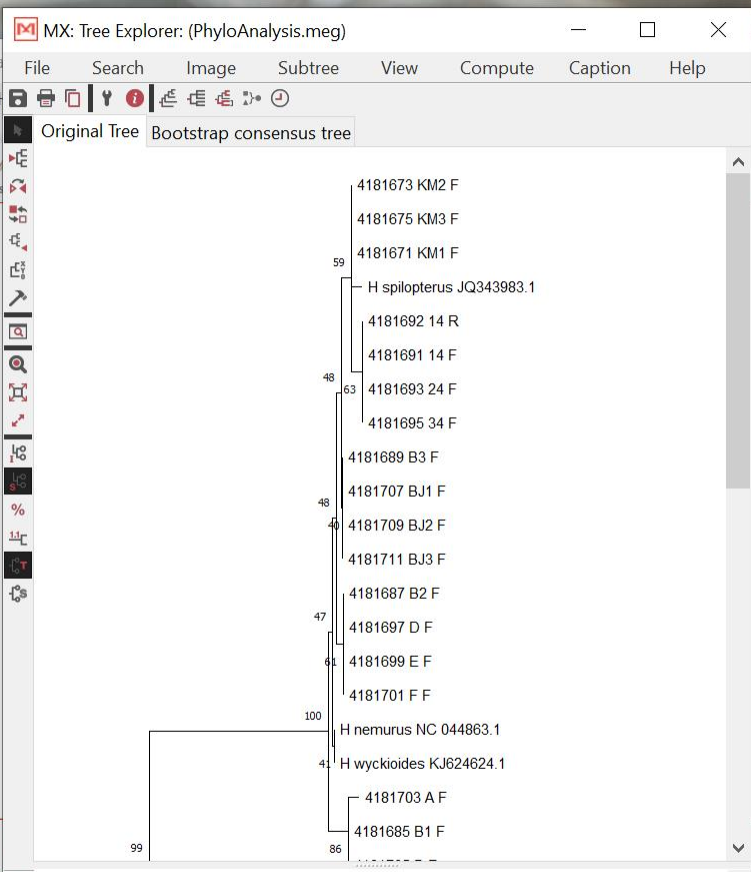
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Evolutionary relationships of taxa

The evolutionary history was inferred using the Neighbor-Joining method [1]. The optimal tree is shown. The percentage of replicate trees in which the associated

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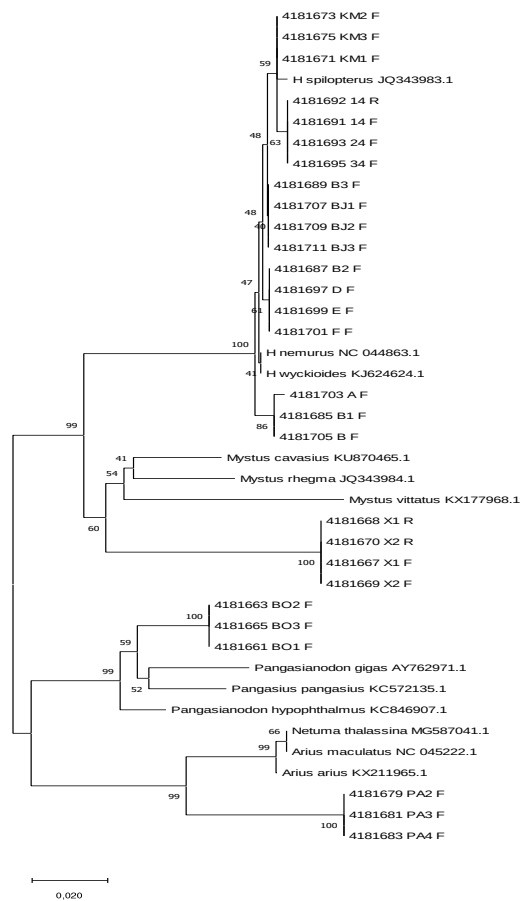
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MX: Analysis Preferences

Phylogeny Reconstruction

Option	Setting
ANALYSIS	
Scope	→ All Selected Taxa
Statistical Method	→ Neighbor-joining
PHYLOGENY TEST	
Test of Phylogeny	→ Bootstrap method
No. of Bootstrap Replications	→ 1000
SUBSTITUTION MODEL	
Substitutions Type	→ Amino acid
Genetic Code Table	→ Vertebrate Mitochondrial
Model/Method	→ Poisson model
Fixed Transition/Transversion Ratio	→ Not Applicable
Substitutions to Include	→ All
RATES AND PATTERNS	
Rates among Sites	→ Uniform Rates
Gamma Parameter	→ Not Applicable
Pattern among Lineages	→ Same (Homogeneous)
DATA SUBSET TO USE	
Gaps/Missing Data Treatment	→ Pairwise deletion
Site Coverage Cutoff (%)	→ Not Applicable
Select Codon Positions	→ Not Applicable
SYSTEM RESOURCE USAGE	
Number of Threads	→ 3

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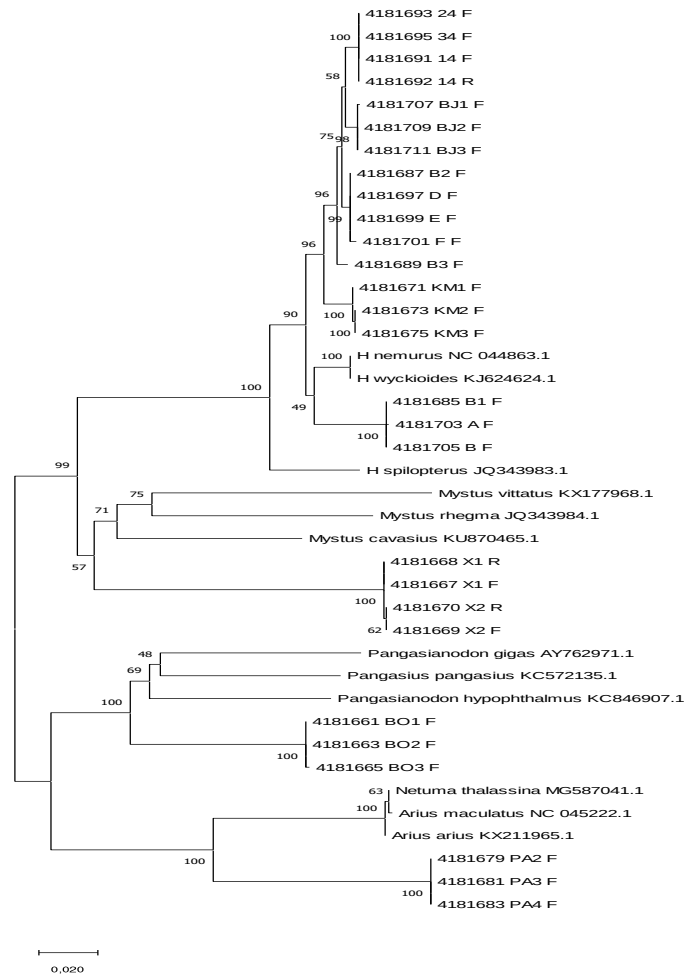
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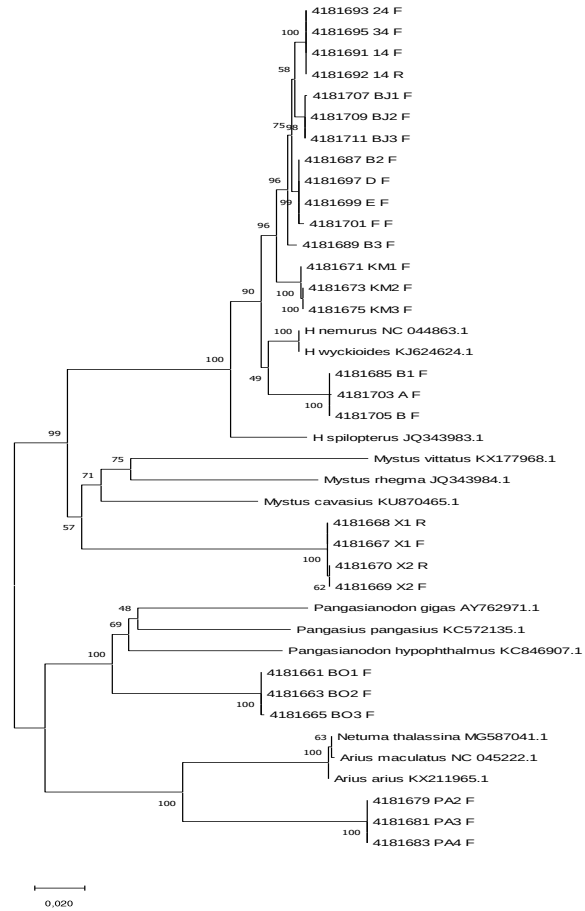
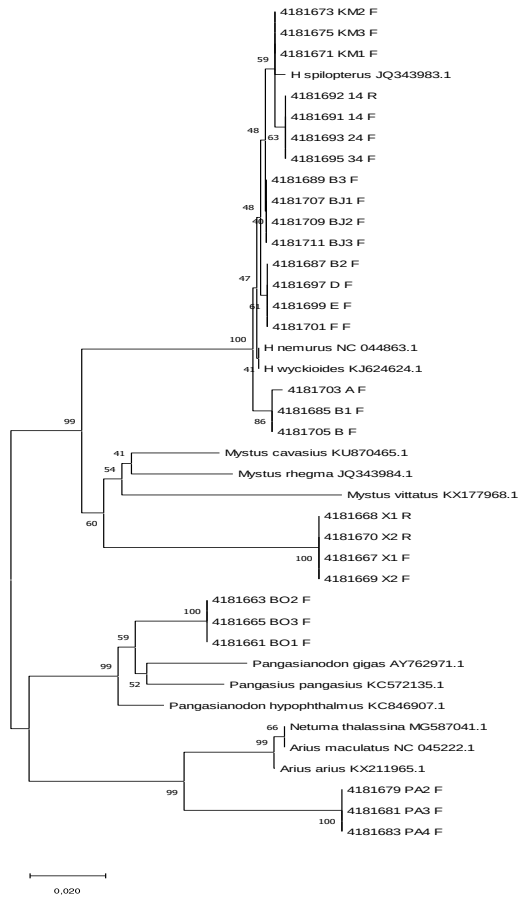
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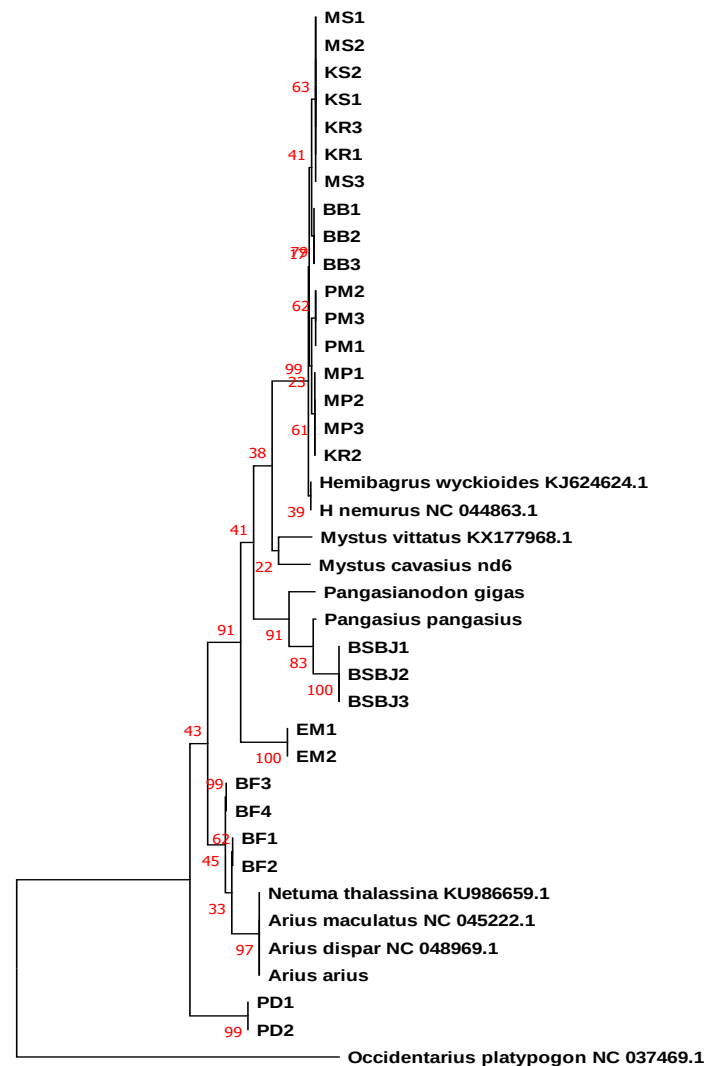
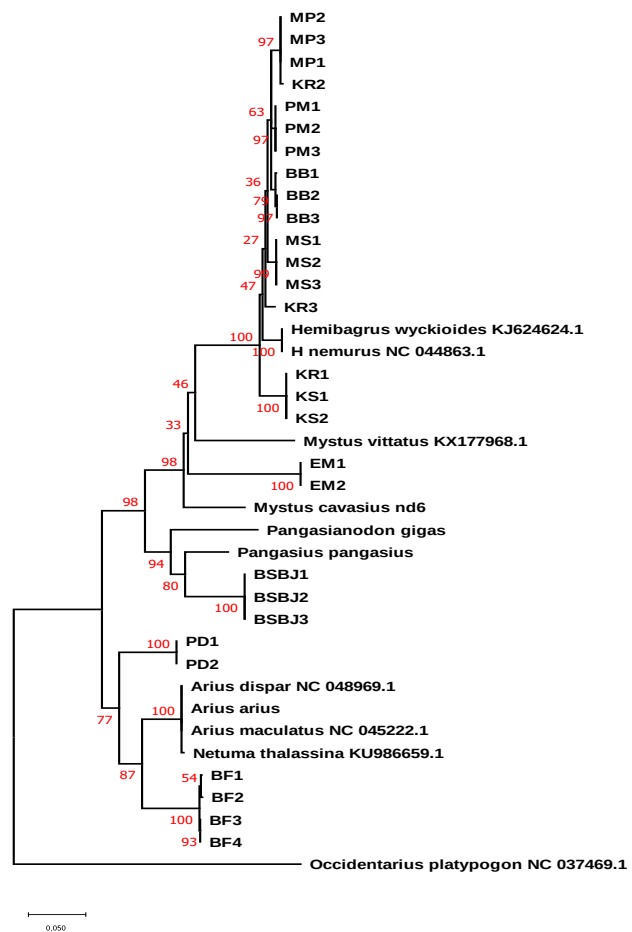
August

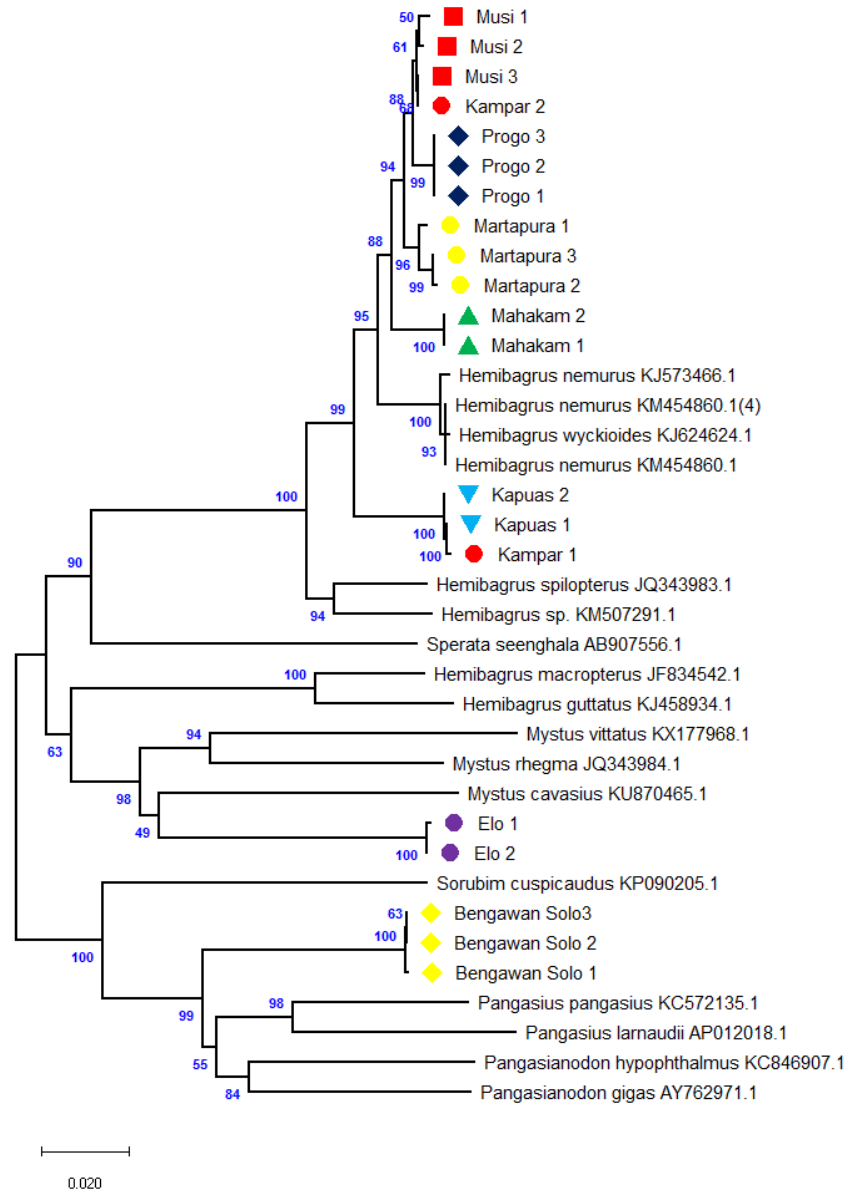
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ANALYZE
 PROTOTYPE











Terima kasih

Selamat mencoba.....