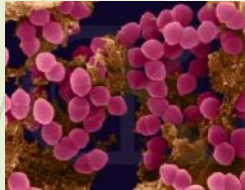


# Pembuatan Pohon Filogenetik

**RINI WIDAYANTI**

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



PCR

Sequence the  
PCR product



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GT
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# ANALISIS DATA SEKUEN DNA



On line: NCBI (BLAST)



Off line: MEGA

Molecular Evolutionary Genetics Analysis

File Analysis Help

EDIT BUILD ALIGNMENT PHYLOGENY USER TREE ANCESTORS SELECTION RATES CLOCKS DIAGNOSE

- Edit/Build Alignment
- Edit/View Sequencer Files (Trace)...
- Open Saved Alignment Session...
- Show Web Browser
- Query Databanks
- Do BLAST Search

RECENT PUBLICATIONS

HELP DOCS EXAMPLES CITATION REPORT BUG UPDATES MEGA LINKS TOOLBAR PREFERENCES

ANALYZE PROTOTYPE

20:56 26/07/2021

Open existing file

« Seku... > SeqResul... Search SeqResult-173953-19...

Organize New folder

Home OneDrive - Persc

Name	Date modified
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1st_BASE_4135659_1_BR.seq	11/03/2021 13:02
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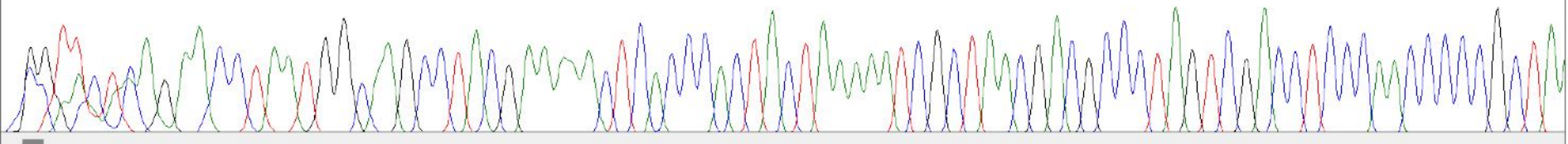
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NEXIS

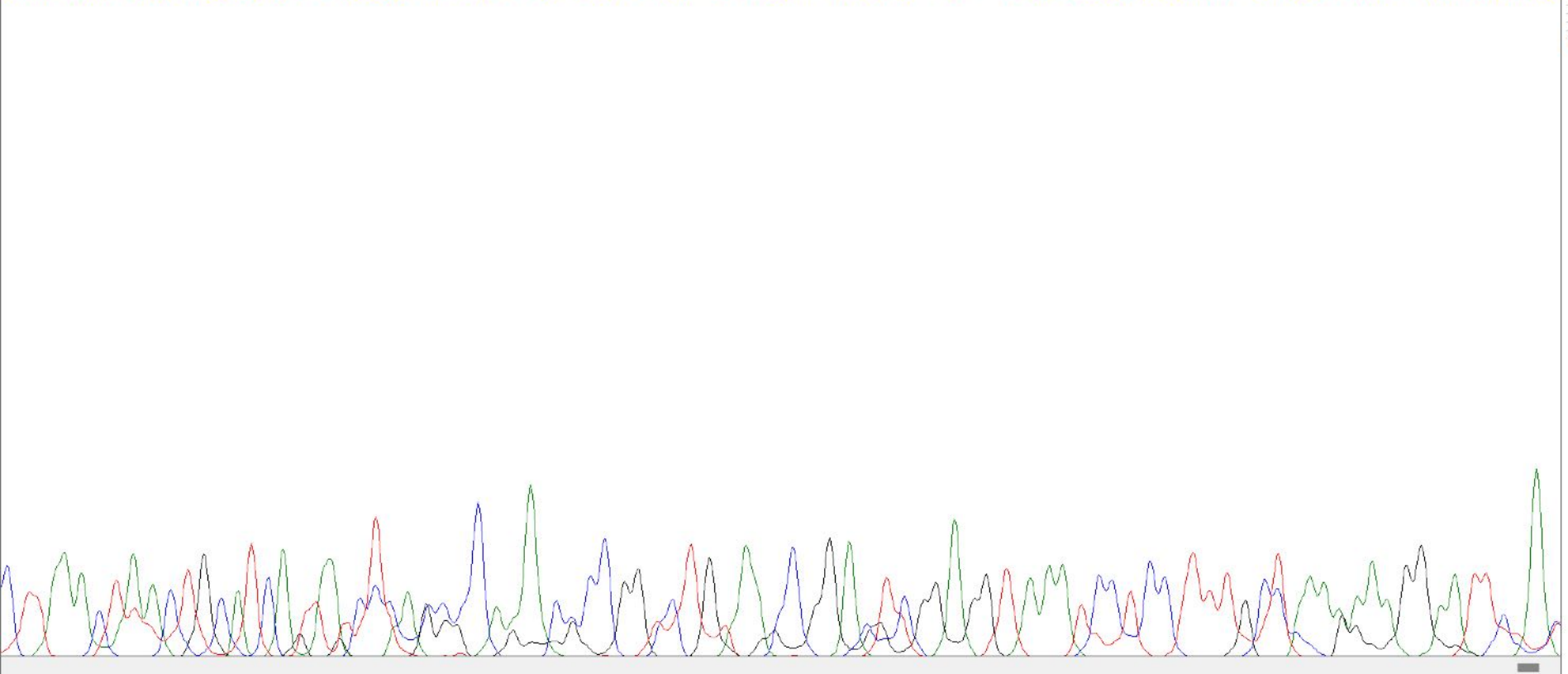
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DATAMONKEY

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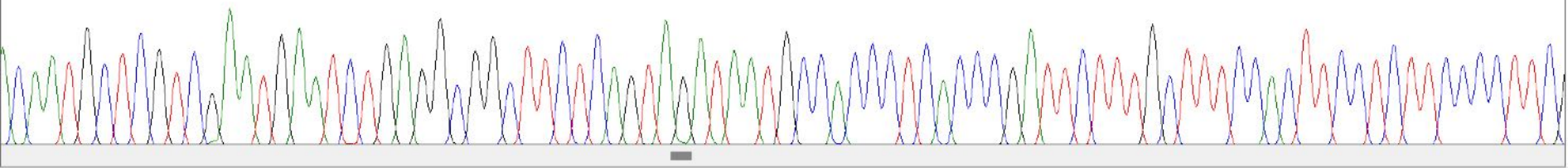


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- Open File in New Window
- Open File
- Save File
- Print
- Add to Alignment Explorer
- Export FASTA File
- Exit

0 510 520 530 540 550 560 570  
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Molecular Evolutionary Genetics Analysis

File Analysis Help

MX: Alignment Explorer

Data Edit Search Alignment Web Sequencer Display Help

DNA Sequences Translated Protein Sequences

Species/Abbrv	
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Molecular Evolutionary Genetics Analysis

File Analysis Help

MX: Alignment Explorer

Data Edit Search Alignment Web Sequencer Display Help

Undo

DNA Seq

Species

1. 4135

Copy

Cut

Paste

Delete

Delete Gaps

Insert Blank Sequence

Insert Sequence From File

Select Site(s)

Select Sequence(s)

Select All

Allow Base Editing

Modify All Bases To Upper Case

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12:05 21/11/2022

Open existing file

« Seku... » SeqRe... »

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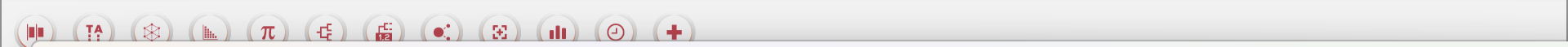
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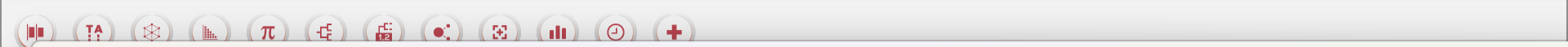
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- Create New
- Open
- Open a Recently Used File
- Close
- Phylogenetic Analysis
- Save Session
- Export Alignment
- DNA Sequences
- Protein Sequences
- Translate/Untranslate Genetic Code
- Reverse Complement
- Reverse Complement
- Quit

Sequence ID	Sequence
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20. 1st_BASE_4135666_B_BF	TTTGGGGATGACTCTCTCTTTGAGCAAAGGGAGGATTTTAACTCCGACGTCGGGCTTACAAGACCGGGCGCTCTGGCGCTGAGCTACTGATGCAGTATAGTTAAGGAGTTTGTCTGTTACGCTGCAAG
21. 1st_BASE_4135668_C_BF	TTAGGGGATGATCCCTCTCTTTGAGCAAAGGGAGGATTTTAACTCCGACGTCGGGCTTACAAGACCGGGCGCTCTGGCGCTGAGCTACTGATGCAGTATAGTTAAGGAGTTTGTCTGTTACGCTGCAAG
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26. 1st_BASE_4135678_H_BF	NCTCCTCTCTTTGAGCAAAGGGGGGATTTTAACTCCGACGTCGGGCTTACAAGACCGGGCGCTCTGGGAACTGAGCTACTGTTGCAGGGTAGGTCAAGGAGCTTGTCTGTTACGCTGTGAGG
27. 1st_BASE_4135680_I_BF	TCGGGGATGAAGCTCCTCTCTTTGAGCAAAGGGGGGATTTTAACTCCGACGTCGGGCTTACAAGACCGGGCGCTCTGGGAACTGAGCTACTGTTGCAGGGTAGGTCAAGGAGCTTGTCTGTTACGCTGTGAGG
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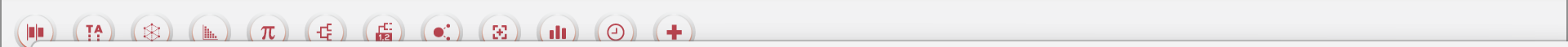


MX: Alignment Explorer

Data Edit Search Alignment Web Sequencer Display Help

DNA Sequences Translated Protein

Species/Abbrv	Sequence
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3. 1st_BASE_4135663_3_BR	ACCTGCCGAATGATGAATAAAGGGTGTGTTTGGCTGGCATTCCGCCTGATTCAGGATTTGAATTTCTACGTTTGTGATTTCGGGATTCAGAATGGAAAATGGGGAGCCTGTTCT
4. 1st_BASE_4135665_A_BR	TGGCATTCCCTCTGATTCAGGATTTAAACTTCCGACGTACTTAATTTGGGGTCCAGAAATGAGAAATGGGGGATCCTTGTTTGTAAAGTTGGCATCTAACTTGCTCATAGGTA
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6. 1st_BASE_4135669_C_BR	ATGAAAGGGCTGTTCTGGTTGGCATGGCCCCAGATTTCAAGGGGAGGATGGCTTACGCTCGNAATTTAGGGCCTCAGNNACAGGAAATGAGAAAATCGTTCGTAATGTA
7. 1st_BASE_4135673_E_BR	TGAATANNAGCTTGCTCGAAGTAGAATTTAGGGTGTGTTTCAAGGTGNCATTCCTCCGTTCCGAGGATTAGAACTTCTGAATTAGGAAATGGGGGTTTAGTAAGAAAATGGG
8. 1st_BASE_4135671_D_BR	TCCTGGCTGNATNCGTNNGTTTNNAGATTATGAACTTTCNNCTACGTAATTCNNNGGTTCTGCACGAGAAATGGGGAATCCTTTTTTACGTTAGCATTTACTGGTACAA
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23. 1st_BASE_4135672_E_BF	CTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCTACTACTAAAATCGCTAACGACGCCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCATGATGAAACTTCGGCTCACTACTTGGCCTTT
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Species/Abbrv	
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4. 1st_BASE_4135665_A_BR	GAATTTAAGGGTTGTTCCGGGTGGCATTCCCT
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6. 1st_BASE_4135669_C_BR	CGCCTAGTTGATCCAATAATAATGAAAGGGCT
7. 1st_BASE_4135673_E_BR	AAAAGGTACTTGTCCGAGGCATGAATANNAGC
8. 1st_BASE_4135671_D_BR	GAAGAATGAATTAGGGTTGTTCTCCGCTGNN
9. 1st_BASE_4135675_F_BR	AGGGACGTTTCCCTGGGAATGAAGNAACTCGC
10. 1st_BASE_4135677_C1_BR	ATGAAAAGGCTTTTTCNGTGGGGCATGGCC
11. 1st_BASE_4135679_C2_BR	TGAGGATGGCCAAAATGNNNGAGGAGGAT
12. 1st_BASE_4135681_C3_BR	TTACCCCTAATAATGAAAGGGCNTTTGGCT
13. 1st_BASE_4135683_M1_BR	TTTTAGCAAAAAGGGGGGTTTAAATCCGGGC
14. 1st_BASE_4135685_M2_BR	GGGAAAGAAGATGACGAACAGGGGACGATCCA
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16. 1st_BASE_4135658_1_BF	CGGTTCTCAGAACCTAATGGCAAGCCTACGAA
17. 1st_BASE_4135660_2_BF	GGTTCTCAGAACCTAATGGCAAGCCTACGAA
18. 1st_BASE_4135662_3_BF	CGGTACTCAGAACCTAATGGCAAGCCTACGAA
19. 1st_BASE_4135664_A_BF	CGGTTCTCAGAACCTAATGGCAAGCCTACGAA
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21. 1st_BASE_4135668_C_BF	CGGTTCTCAGAACCTAATGGCAAGCCTACGAA
22. 1st_BASE_4135670_D_BF	GTNCTCAGAACCTAATGGCAAGCCTACGAA
23. 1st_BASE_4135672_E_BF	CTTCTCAGAACCTAATGGCAAGCCTACGAA
24. 1st_BASE_4135674_F_BF	CGGTTCTCAGAACCTAATGGCAAGCCTACGAA
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27. 1st_BASE_4135680_C3_BF	GGTTCTCAGAACCTAATGGCAAGCCTACGAA
28. 1st_BASE_4135682_M1_BF	GTTCTCAGAACCTAATGGCAAGCCTACGAA
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ClustalW Options

Alignment

Pairwise Alignment

Gap Opening Penalty: 15,00

Gap Extension Penalty: 6,66

Multiple Alignment

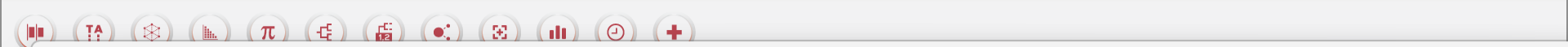
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Gap Extension Penalty: 6,66

Matrix

Help Cancel OK

Done Loading



Species/Abbrv		
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8. 1st_BASE_4135671_D_BR	GAAGAATGAATAGGGTTGTTCCCTGCGTGNN	NGGTTCTGCACGAGAAATGGGAACTCCTTTTTTACGTTAGCATTTACTGGTACA
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16. 1st_BASE_4135658_1_BF	CGGTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
17. 1st_BASE_4135660_2_BF	GGTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
18. 1st_BASE_4135662_3_BF	CGGTACTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
19. 1st_BASE_4135664_A_BF	CGGTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
20. 1st_BASE_4135666_B_BF	CGGTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
21. 1st_BASE_4135668_C_BF	CGGTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
22. 1st_BASE_4135670_D_BF	GTNCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
23. 1st_BASE_4135672_E_BF	CTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
24. 1st_BASE_4135674_F_BF	CGGTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
25. 1st_BASE_4135676_C1_BF	CGGGTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
26. 1st_BASE_4135678_C2_BF	CGGGTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
27. 1st_BASE_4135680_C3_BF	GGTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
28. 1st_BASE_4135682_M1_BF	GTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
29. 1st_BASE_4135684_M2_BF	TTNCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
30. 1st_BASE_4135686_M3_BF	GTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT
31. 4135658_1_BF	CGGTTCTCAGAACCTAATGGCAAGCCTACGAAAAACTCACCCACTACTAA	AAATCGCTAACGACGCCCTAGTCGACCTCCCAACCCCGCTAACATCTCTGCAT

ClustalW Progress

ALIGNMENT BY CLUSTALW (00:02:56)

PAIRWISE ALIGNMENT

MULTIPLE ALIGNMENT

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

## 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

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.):

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)

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

#Scomberomorus Banjarmasin1

Query subrange [?](#)

From

To

Or, upload file

Choose File No file chosen [?](#)

Job Title

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

Align two or more sequences [?](#)

Choose Search Set

Nucleotide BLAST: S... x

blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&BLAST\_PROGRAMS=megaBlast&PAGE\_TYPE=BlastSearch&SHOW\_DEFAULTS=on&LINK\_LOC=t

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

```
ATGCCCAACTAAATACATCAACATGATTTATTACCCCTCTATCTATAACACTAACAC
TTATCCTATTTCAACTGAACATTTCAAACCTGACTTATCCTCTCAATCTAACCTAAAAA
TATTAATACAGAATCATTAAACTCCCTGAGAACTAAATGAACGAAAACCTATTGCGCT
CTTTCATTACCCCAAA
```

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

18:55 09/05/2012

Align two or more sequences ?

### Choose Search Set

**Database**  Standard databases (nr etc.):  rRNA/ITS databases  Genomic + transcript databases  Betacoronavirus

Nucleotide collection (nr/nt) ?

**Organism** Optional   exclude [Add organism](#)

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

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

**Limit to** Optional  Sequences from type material

**Entrez Query** Optional  [YouTube](#) Create custom database

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 ?

**BLAST**

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

Show results in a new window

+ Algorithm parameters



NCBI Blast:Nucleotide Sequenc X +

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

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**BLAST** » **blastn suite** » results for RID-VGF6YRSX014 Home Recent Results Saved Strategies Help

[← Edit Search](#) [Save Search](#) [Search Summary](#) ▼

**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  [?](#)

select all *0 sequences selected*

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8:22 PM  
10/29/2019

Query Length 1141

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

**Descriptions** Graphic Summary Alignments Taxonomy

Sequences producing significant alignments Download Select columns Show 100 ?

select all 100 sequences selected [GenBank](#) [Graphics](#) [Distance tree of results](#) [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate Banjarmasin1 cytochrome B (cytb) gene, complete cds; mitochondrial</a>	Scomberomoru...	2108	2108	100%	0.0	100.00%	1141	<a href="#">OM799597.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate Palembang2 cytochrome B (cytb) gene, complete cds; mitochondrial</a>	Scomberomoru...	2097	2097	100%	0.0	99.82%	1141	<a href="#">OM799601.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate Palembang1 cytochrome B (cytb) gene, complete cds; mitochondrial</a>	Scomberomoru...	2097	2097	100%	0.0	99.82%	1141	<a href="#">OM799600.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate Rembang1 cytochrome B (cytb) gene, complete cds; mitochondrial</a>	Scomberomoru...	2097	2097	100%	0.0	99.82%	1141	<a href="#">OM799594.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate SC2 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	Scomberomoru...	2095	2095	99%	0.0	99.82%	1140	<a href="#">DQ497866.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate Palembang3 cytochrome B (cytb) gene, complete cds; mitochondrial</a>	Scomberomoru...	2091	2091	100%	0.0	99.74%	1141	<a href="#">OM799602.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate SC3 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	Scomberomoru...	2089	2089	99%	0.0	99.74%	1140	<a href="#">DQ497867.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate Rembang2 cytochrome B (cytb) gene, complete cds; mitochondrial</a>	Scomberomoru...	2085	2085	100%	0.0	99.65%	1141	<a href="#">OM799595.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate SC1 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	Scomberomoru...	2084	2084	99%	0.0	99.65%	1140	<a href="#">DQ497865.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate Ambon3 cytochrome B (cytb) gene, complete cds; mitochondrial</a>	Scomberomoru...	2008	2008	100%	0.0	98.42%	1141	<a href="#">OM799608.1</a>

<input checked="" type="checkbox"/>	<a href="#">Scomberomorus monitor</a> <a href="#">Scomberomorus semimasolatus strain SKL-FSSCKC0730 mitochondrion, comp...</a> <a href="#">Scomberomoru...</a>	1376	1376	100%	0.0	80.45%	16538	<a href="#">JX359749.1</a>	
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate DYM SC6 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1363	1363	64%	0.0	99.87%	743	<a href="#">KX002083.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus cavalla mitochondrion, complete genome</a>	<a href="#">Scomberomoru...</a>	1362	1362	99%	0.0	88.35%	16548	<a href="#">DQ536428.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate DYM SC4 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1328	1328	64%	0.0	99.32%	734	<a href="#">KX002081.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate DYM SC5 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1327	1327	63%	0.0	99.72%	724	<a href="#">KX002082.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate DYM SC2 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1315	1315	64%	0.0	99.05%	733	<a href="#">KX002076.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate DYM SC10 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1310	1310	62%	0.0	99.72%	715	<a href="#">KX002087.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate DYM SC7 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1288	1288	62%	0.0	99.30%	712	<a href="#">KX002084.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate DYM SC14 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1282	1282	62%	0.0	99.02%	715	<a href="#">KX002091.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate DYM SC1 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1282	1282	64%	0.0	98.10%	736	<a href="#">KX002075.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus nipponius mitochondrion, complete genome</a>	<a href="#">Scomberomoru...</a>	1273	1273	99%	0.0	86.99%	16646	<a href="#">KY228987.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus sierra mitochondrion, complete genome</a>	<a href="#">Scomberomoru...</a>	1273	1273	99%	0.0	86.94%	16699	<a href="#">KX925517.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus nipponius isolate SN1 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1273	1273	99%	0.0	86.99%	1140	<a href="#">DQ497885.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate DYM SC8 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1267	1267	60%	0.0	99.71%	692	<a href="#">KX002085.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate DYM SC3 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1267	1267	63%	0.0	98.08%	729	<a href="#">KX002077.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus nipponius voucher Zhang Q. SNDG1 cytochrome b (cytb) gene, complete cds; mitochon...</a>	<a href="#">Scomberomoru...</a>	1267	1267	99%	0.0	86.90%	1141	<a href="#">AY986969.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus nipponius isolate SN2 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1262	1262	99%	0.0	86.81%	1140	<a href="#">DQ497886.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus commerson isolate DYM SC16 cytochrome b (cytb) gene, partial cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1260	1260	60%	0.0	99.57%	691	<a href="#">KX002093.1</a>
<input checked="" type="checkbox"/>	<a href="#">Scomberomorus koreanus isolate Cilacap1 cytochrome B (cytb) gene, complete cds; mitochondrial</a>	<a href="#">Scomberomoru...</a>	1258	1258	99%	0.0	86.75%	1141	<a href="#">OM799603.1</a>
<input checked="" type="checkbox"/>	<a href="#">Sarda sarda isolate SarSar2 cytochrome b (Cytb) gene, partial cds; mitochondrial</a>	<a href="#">Sarda sarda</a>	1258	1258	99%	0.0	86.74%	1141	<a href="#">DQ080305.1</a>

Feedback

Query Length 1141

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

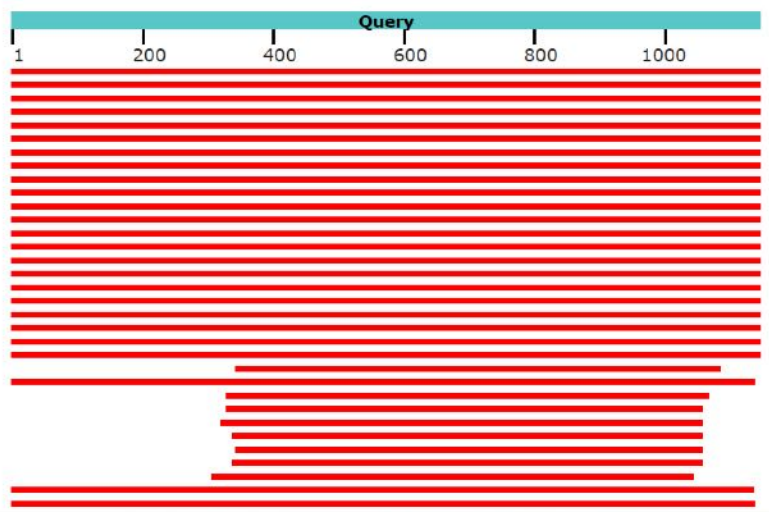
Descriptions **Graphic Summary** Alignments Taxonomy

hover to see the title click to show alignments

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

100 sequences selected ?

### Distribution of the top 100 Blast Hits on 100 subject sequences



Feedback

Query Length 1141

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

Descriptions Graphic Summary **Alignments** Taxonomy

Alignment view Pairwise  CDS feature ? [Restore defaults](#) Download ▾

100 sequences selected ?

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### **Scomberomorus commerson isolate Banjarmasin1 cytochrome B (cytb) gene, complete cds; mitochondrial**

Sequence ID: [OM799597.1](#) Length: 1141 Number of Matches: 1

Range 1: 1 to 1141 [GenBank](#) [Graphics](#) [Next Match](#) ▲ [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
2108 bits(1141)	0.0	1141/1141(100%)	0/1141(0%)	Plus/Plus
Query 1		ATGGCAAGCCTACGAAAACTCACCCACTACTAAAAATCGCTAACGACGCCCTAGTCGAC		60
Sbjct 1		ATGGCAAGCCTACGAAAACTCACCCACTACTAAAAATCGCTAACGACGCCCTAGTCGAC		60
Query 61		CTCCCAACCCCGCTAACATCTCTGCATGATGAAACTTCGGCTCACTACTTGGCCTTTGC		120
Sbjct 61		CTCCCAACCCCGCTAACATCTCTGCATGATGAAACTTCGGCTCACTACTTGGCCTTTGC		120
Query 121		CTAATCTCCCAAATCCTCACAGGACTGTTCTTGCAATACATTACACCCAGACATCGAA		180

Feedback

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Scomberomorus commerson isolate SC2 cytochrome b (cytb) gene, partial cds; mitochondrial

Sequence ID: DQ497866.1 Length: 1140 Number of Matches: 1

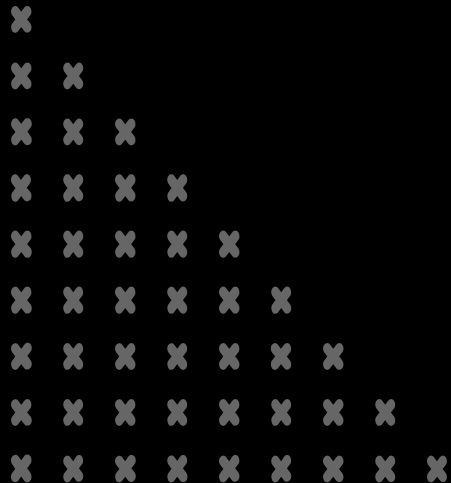
Range 1: 1 to 1140 GenBank Graphics Next Match Previous Match

Table with 5 columns: Score, Expect, Identities, Gaps, Strand. It shows sequence alignment between Query and Sbjct with vertical bars indicating matches. The alignment is 100% identical across the entire length.

Feedback

# MEGA (Molecular Evolutionary Genetics Analysis)

- 
- 01** Alignment/ multiple alignment
  - 02** Komposisi nukleotida, asam amino
  - 03** Perbedaan nukleotida
  - 04** Perbedaan asam amino
  - 05** Jarak genetik/ distance
  - 06** Phylogenetic tree







- Create New
- Open
- Open a Recently Used File
- Close
- Phylogenetic Analysis
- Save Session
- Export Alignment
- DNA Sequences
- Protein Sequences
- Translate/Untranslate
- Genetic Code
- Reverse Complement
- Reverse
- Complement
- Quit

Sequence Name	Sequence
19. <i>S. munroi</i> x <i>S. semifasciatus</i> st Grey JX559746.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT
20. <i>S. semifasciatus</i> st GREY JX559745.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT
21. <i>Scomberomorus commerson</i> EF141176.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT
22. <i>Scomberomorus concolor</i> KY091265.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT
23. <i>Scomberomorus sinensis</i> DQ497892.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT
24. <i>Scomberomorus sierra</i> KX925517.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT
25. <i>Scomberomorus semifasciatus</i> st GREY JX559745.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT
26. <i>Scomberomorus koreanus</i> DQ497884.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT
27. <i>Scomberomorus guttatus</i> DQ497878.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT
28. <i>Scomberomorus brasiliensis</i> DQ080322.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT
29. <i>Scomberomorus nipponius</i> KY228987.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT
30. <i>Auxis rochei</i> DQ080312.1	ATGGCAAGCCTACGAAAAA...TCA...CTACTAAAAATCGCAAACGACGCACTAGTTGACCTCCCA...CCCCCGCTAGCATCTCCGCATGATGAAACTTCGGCTCACTACTTGGTCTT





### Molecular Evolutionary Genetics Analysis

File Analysis Help

ALIGN DATA MODELS DISTANCE DIVERSITY TAXA DIAGNOSE

- Construct/Test Maximum Likelihood Tree...
- 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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Molecular Evolutionary Genetics Analysis

File Analysis Help

ALIGN DATA MODELS DISTANCE DIVERSITY PHYLOGENY USER TREE ANCESTOR

Close Data

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MX: Analysis Preferences

Phylogeny Reconstruction

Option	Setting
<b>ANALYSIS</b>	
Scope	→ All Selected Taxa
Statistical Method	→ Neighbor-joining
<b>PHYLOGENY TEST</b>	
Test of Phylogeny	→ Bootstrap method
No. of Bootstrap Replications	→ 1000
<b>SUBSTITUTION MODEL</b>	
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
<b>RATES AND PATTERNS</b>	
Rates among Sites	→ Uniform Rates
Gamma Parameter	→ Not Applicable
Pattern among Lineages	→ Same (Homogeneous)
<b>DATA SUBSET TO USE</b>	
Gaps/Missing Data Treatment	→ Pairwise deletion
Site Coverage Cutoff (%)	→ Not Applicable
Select Codon Positions	→ <input checked="" type="checkbox"/> 1st <input checked="" type="checkbox"/> 2nd <input checked="" type="checkbox"/> 3rd <input checked="" type="checkbox"/> Noncoding Sites
<b>SYSTEM RESOURCE USAGE</b>	
Number of Threads	→ 3

Help Cancel OK

Rini Widayanti RW

NEXUS

TIMETREE

DATAMONKEY

ANALYZE

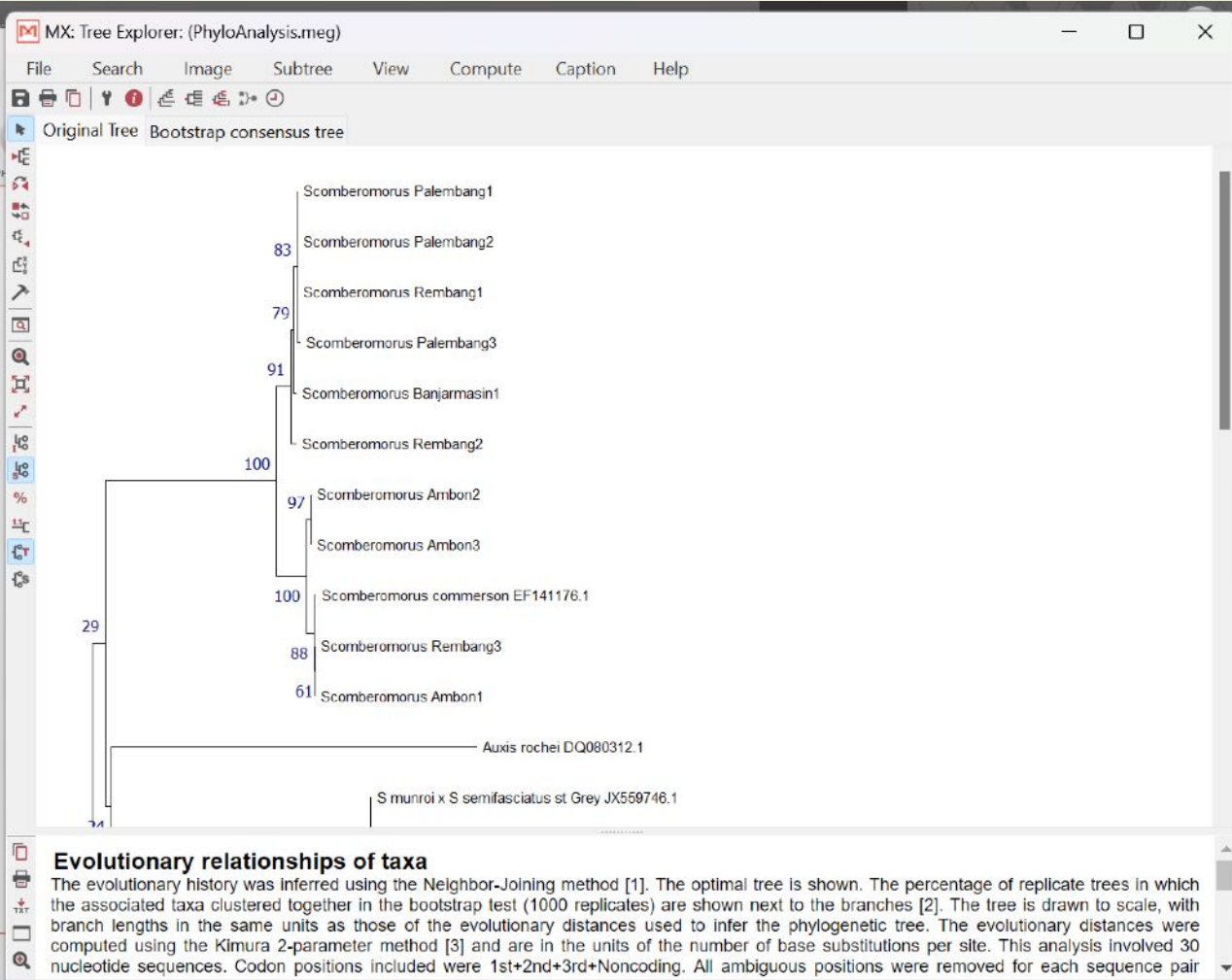
Molecular Evolutionary Genetics Analysis

File Analysis Help

ALIGN DATA MODELS DISTANCE DIVERSITY

Close Data

RECENT PUBLICATIONS



NEXUS

TIMETREE

DATAMONKEY

ANALYZE

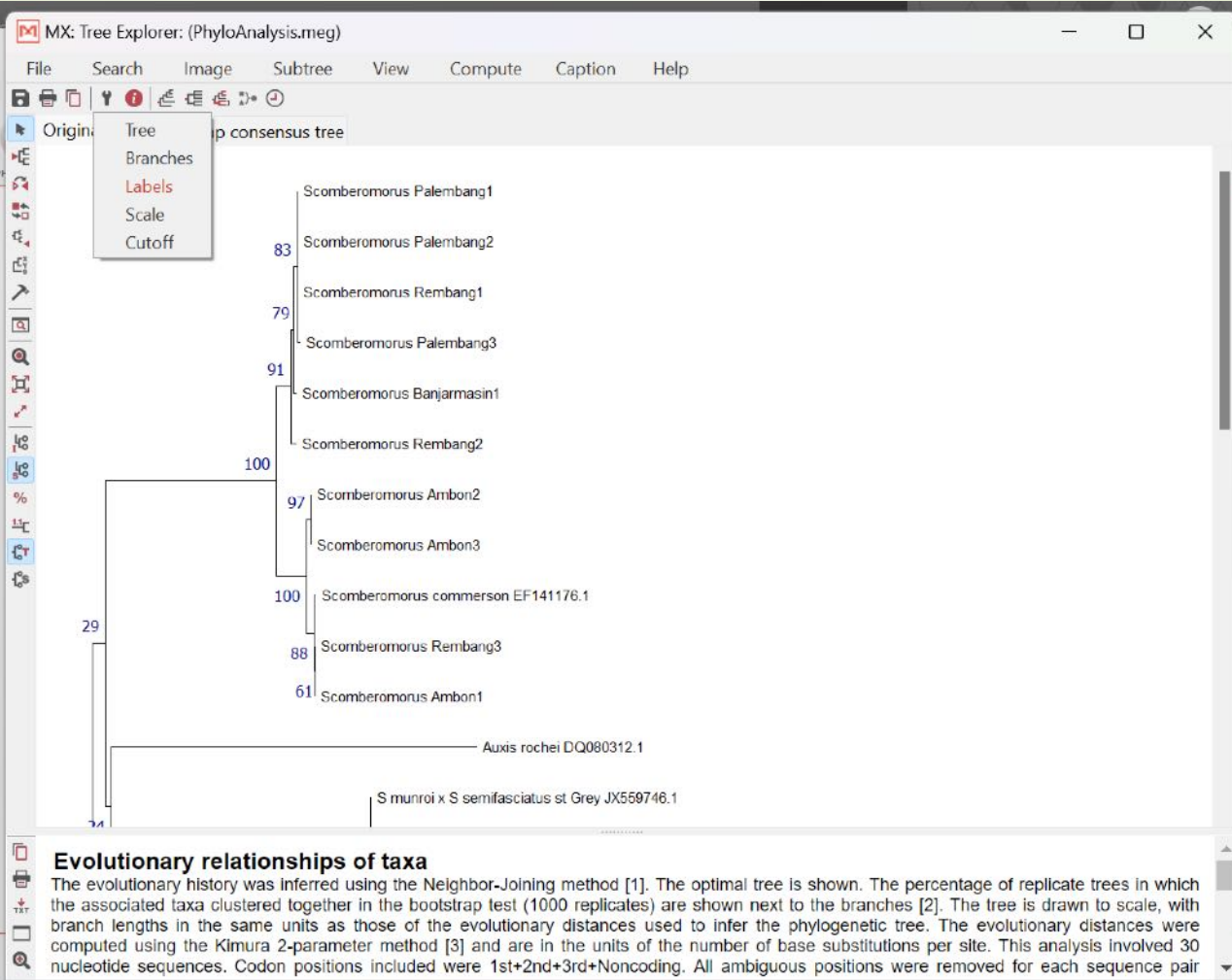
Molecular Evolutionary Genetics Analysis

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ALIGN DATA MODELS DISTANCE DIVERSITY

Close Data

RECENT PUBLICATIONS

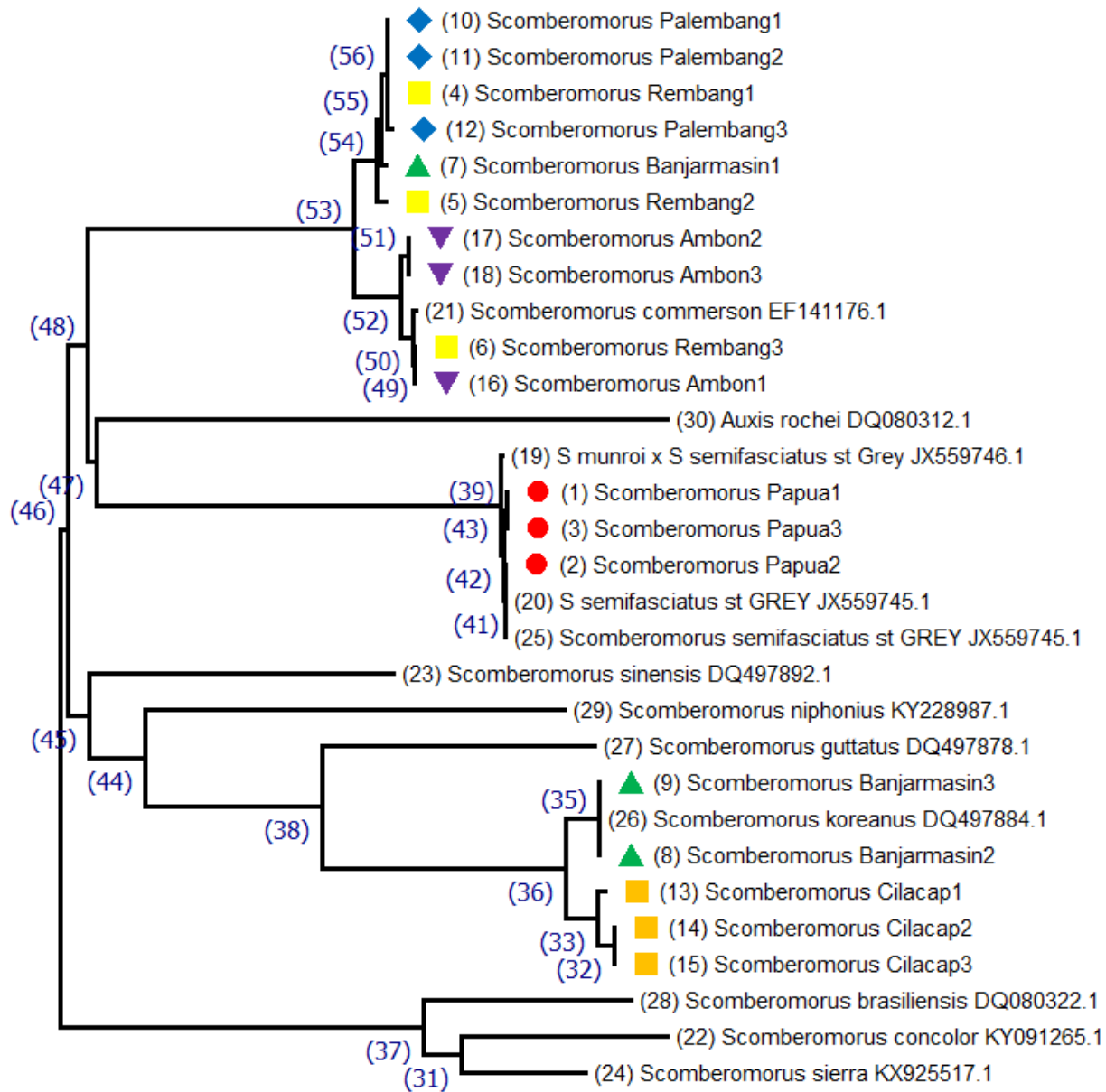


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TIMETREE

DATAMONKEY

ANALYZE



0.020





# Terima kasih

Selamat mencoba.....