

Practical No: 5

Aim:

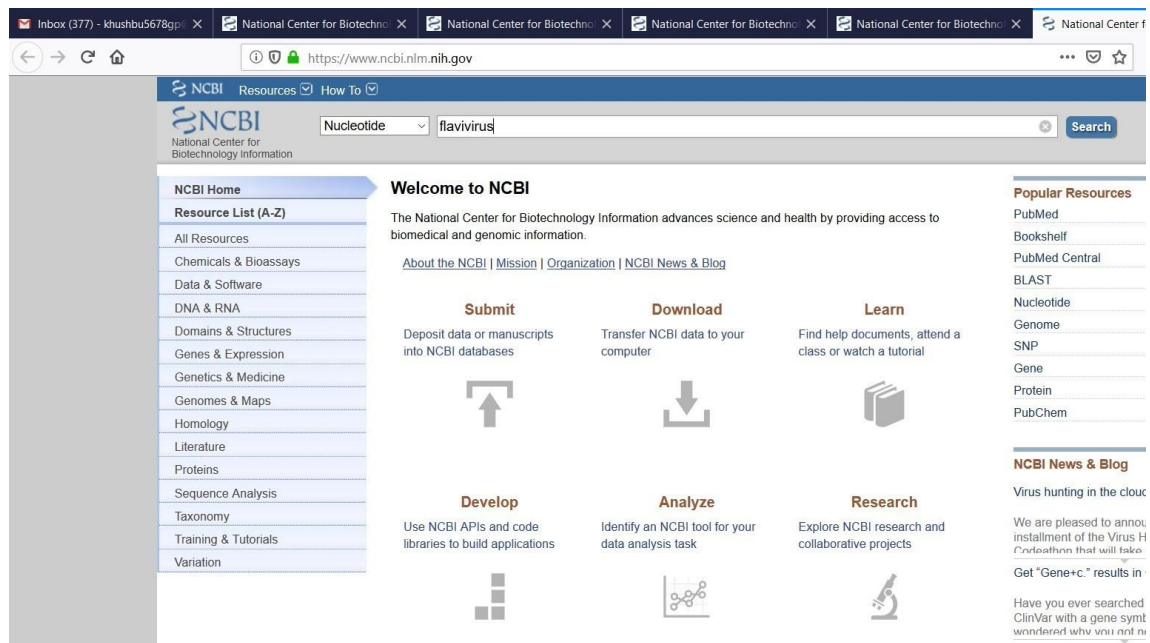
Perform a BLAST search on a specific gene sequence of a specific organism.

Steps:

Go to the National Center for Biotechnology Information Site

<https://www.ncbi.nlm.nih.gov/>

Select Nucleotide from All Databases and find any organism in a search bar.



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flavivirus - Nucleo

https://www.ncbi.nlm.nih.gov/nuccore/?term=flavivirus

NCBIResourcesHow To

Nucleotide

Nucleotide

flavivirus

Create alertAdvanced

Species

Animals (307)

Plants (12)

Fungi (24)

Protists (20)

Bacteria (783)

Archaea (7)

Viruses (62,020)

Customize ...

Molecule types

genomic DNA/RNA (65,124)

mRNA (1,298)

Customize ...

Source databases

INSDC (GenBank) (67,508)

RefSeq (191)

Customize ...

Sequence Type

Nucleotide (67,735)

Genetic compartments

Mitochondrion (163)

Plasmid (4)

Sequence length

Custom range...

Summary20 per pageSort by Default order

Send toFilters: Manage Filters

Items: 1 to 20 of 67735

<< First< PrevPage 1 of 3387Next>Last >>

☐ [Tembusu virus flavivirus polyprotein \(flavivirus polyprotein gene\) gene, complete cds](#)

1. [10,990 bp linear RNA](#)

Accession: NC_015843.2 GI: 381333920

[Assembly](#) [BioProject](#) [Protein](#) [PubMed](#) [Taxonomy](#)

[GenBank](#) [FASTA](#) [Graphics](#)

☐ [Cacipacore virus flavivirus polyprotein \(flavivirus polyprotein gene\) and truncated polyprotein \(flavivirus polyprotein gene\) genes, complete cds](#)

2. [10,284 bp linear RNA](#)

Accession: NC_026623.1 GI: 765702599

[Assembly](#) [BioProject](#) [Protein](#) [PubMed](#) [Taxonomy](#)

[GenBank](#) [FASTA](#) [Graphics](#)

☐ [Duck flavivirus KPS54A61/THA, complete genome](#)

3. [10,990 bp linear RNA](#)

Accession: KF573582.1 GI: 673459548

[Protein](#) [Taxonomy](#)

[GenBank](#) [FASTA](#) [Graphics](#)

☐ [Duck flavivirus TA, complete genome](#)

Results by taxon

Top Organisms [Tree]

[Dengue virus \(28466\)](#)

[West Nile virus \(21550\)](#)

[Japanese encephalitis virus](#)

[Tick-borne encephalitis virus](#)

[Zika virus \(1694\) \(viruses\)](#)

[All other taxa \(10744\)](#)

More...

Find related data

Database: Select

Find items

Search details

"Flavivirus" [Organism]

flavivirus [All Fields]

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https://www.ncbi.nlm.nih.gov/nuccore/NC_015843.2

NCBI Resources How To

Nucleotide Nucleotide Search

Advanced

GenBank Send to Change region shown

Tembusu virus flavivirus polyprotein (flavivirus polyprotein gene) gene, complete cds

NCBI Reference Sequence: NC_015843.2

FASTA Graphics

Go to:

LOCUS NC_015843 10990 bp ss-RNA linear VRL 13-AUG-2018

DEFINITION Tembusu virus flavivirus polyprotein (flavivirus polyprotein gene) gene, complete cds.

ACCESSION NC_015843 NC_016958 NC_018670

VERSION NC_015843.2

DBLINK BioProject: PRJNA485481

KEYWORDS RefSeq.

SOURCE Tembusu virus (TMUV)

ORGANISM Tembusu virus

Viruses; Riboviria; Flaviviridae; Flavivirus.

REFERENCE 1 (bases 1 to 10990)

AUTHORS Han,K., Huang,X., Li,Y., Zhao,D., Liu,Y., Zhou,X., You,Y. and Xie,X.

TITLE Complete genome sequence of goose tembusu virus, isolated from jiangnan white geese in jiangsu, china

JOURNAL Genome Announc 1 (2), E0023612 (2013)

PUBMED 23516233

REMARK Publication Status: Online-Only

REFERENCE 2 (bases 1 to 10990)

Analyze this sequence

Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

Related information

Assembly

BioProject

Protein

PubMed

Taxonomy

Full text in PMC

Functional Class

Run BLAST option we have to select

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https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Nucleotides&PROGRAM=blastn&QUERY=NC_015843.2&DATABASE=nr&M

Align two or more sequences

Choose Search Set

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

Nucleotide collection (nr/nt)

Organism Optional

Enter organism name or id--completions will be suggested ☐ 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

Limit to Optional

☐ Sequences from type material

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

BLAST

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

☐ Show results in a new window

Algorithm parameters

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BLAST

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NCBI Blastref/NC

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

...

Sequences producing significant alignments		Download	Manage Columns	Show	
<input checked="" type="checkbox"/> select all 99 sequences selected		GenBank	Graphics	Dis	
	Description	Max Score	Total Score	Query Cover	E value
<input checked="" type="checkbox"/>	Tembusu virus strain JS804, complete genome	20064	20064	99%	0.0
<input checked="" type="checkbox"/>	Tembusu virus strain JS/2010, complete genome	20064	20064	99%	0.0
<input checked="" type="checkbox"/>	Duck egg-drop syndrome virus strain byd1, complete genome	20048	20048	99%	0.0
<input checked="" type="checkbox"/>	Tembusu virus isolate Tembusu virus strain, complete genome	20026	20026	99%	0.0
<input checked="" type="checkbox"/>	Duck Tembusu virus isolate df-2, complete genome	20020	20020	99%	0.0
<input checked="" type="checkbox"/>	Duck egg-drop syndrome virus strain JXSP, complete genome	20020	20020	99%	0.0
<input checked="" type="checkbox"/>	Tembusu virus isolate YY5, complete genome	20015	20015	99%	0.0
<input checked="" type="checkbox"/>	Tembusu virus isolate SDMS, complete genome	20009	20009	99%	0.0
<input checked="" type="checkbox"/>	Tembusu virus isolate ZJ-6, complete genome	20009	20009	99%	0.0
<input checked="" type="checkbox"/>	Tembusu virus strain AH-F10 from China, complete genome	20004	20004	99%	0.0
<input checked="" type="checkbox"/>	Duck egg-drop syndrome virus strain pigeon, complete genome	20004	20004	99%	0.0
<input checked="" type="checkbox"/>	Tembusu virus genomic RNA, complete genome, strain: TMUV-YY1Du	19998	19998	99%	0.0
<input checked="" type="checkbox"/>	Duck Tembusu virus strain BZ_2010, complete genome	19998	19998	99%	0.0
<input checked="" type="checkbox"/>	Duck egg-drop syndrome virus strain duan, complete genome	19998	19998	99%	0.0
<input checked="" type="checkbox"/>	Duck Tembusu virus strain GDLH01, complete genome	19989	19989	99%	0.0

Here the result will be display

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NCBI BlastreflNC

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https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_381283018

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Download

GenBank

Graphics

▼ Next ▲ Previous

Tembusu virus strain JS804, complete genome

Sequence ID: [JF895923.2](#) Length: 10990 Number of Matches: 1

Range 1: 1 to 10990

[GenBank](#)

[Graphics](#)

▼ Next Match ▲ Previous Match

Score

20295 bits(10990)

Expect

0.0

Identities

10990/10990(100%)

Gaps

0/10990(0%)

Strand

Plus/Plus

Query 1

AGAAGTTCGCCTGTGTGAACCTATTCCAAACAGCTTTTGGAGTAGTGCCTGTGAACGTAA

60

Sbjct 1

AGAAGTTCGCCTGTGTGAACCTATTCCAAACAGCTTTTGGAGTAGTGCCTGTGAACGTAA

60

Query 61

ACACAGTTTGAACGTTTTTTGGATAGAGACAACTATGTCTAACAAAAAACAGGAAGACC

120

Sbjct 61

ACACAGTTTGAACGTTTTTTGGATAGAGACAACTATGTCTAACAAAAAACAGGAAGACC

120

Query 121

CGGCTCAGGCCGGGTTGTCAATATGCTAAAGCGCGGAACGTCCCGCGGAAATCCGCTAGC

180

Sbjct 121

CGGCTCAGGCCGGGTTGTCAATATGCTAAAGCGCGGAACGTCCCGCGGAAATCCGCTAGC

180

Query 181

GCGGATAAAGAGGACGATTGATGGGTCCTGAGAGGAGCAGGACCCATAAGGTTTGTGCT

240

Sbjct 181

GCGGATAAAGAGGACGATTGATGGGTCCTGAGAGGAGCAGGACCCATAAGGTTTGTGCT

240

Query 241

GGCTCTACTGACTTTCTTCAAGTTTACAGCCCTGAGGCCAACCATTTGGAATGCTGAAGAG

300

Sbjct 241

GGCTCTACTGACTTTCTTCAAGTTTACAGCCCTGAGGCCAACCATTTGGAATGCTGAAGAG

300

Query 301

ATGGAAGCTGGTTGGAGTTAATGAGCGGACCAAAACATCTGAAAAGCTTCAAGCGTGACAT

360

Sbjct 301

ATGGAAGCTGGTTGGAGTTAATGAGCGGACCAAAACATCTGAAAAGCTTCAAGCGTGACAT

360

Query 361

TGGACAGATGCTCGACGGACTGAATAAGCGGAAGGCGAAACGTCggggggggAGTTGCTC

420

Sbjct 361

TGGACAGATGCTCGACGGACTGAATAAGCGGAAGGCGAAACGTCGGGGGGGAGTTGCTC

420

Related Inform

[Gene](#) - associated