Name: Soham Landge Roll No:545
Sub Bioinformatics Sem : 1

Practical No: 1

Aim: Write a Python/Java code to perform pairwise alignment. Take 2

sequences from user and calculate the score.

Code:

```
se1=input("Enter the first sequence::")
se2=input("Enter the second
sequence::") seq1=list(se1)
seq2=list(se2) score=[]

def Pairwise_alignment(a,b):
    gap(a,b) print(a)
    print(b) value=0
    length=len(a) for i in
    range(0,length):
    if(a[i]==b[i]):
    score.append('1')
            value=value+1
        else:
        score.append('0')
    print(score)
    print(value)

def gap(a,b):
    if(len(a)==len(b)):
        print()
    else:
        k=int(input("enter the position to
        insert::")) if (len(a)<len(b)):
            a.insert(k,'-')
        else:
            b.insert(k,'-')
    return(a,b)

Pairwise_alignment(seq1,seq2)
```

Output:

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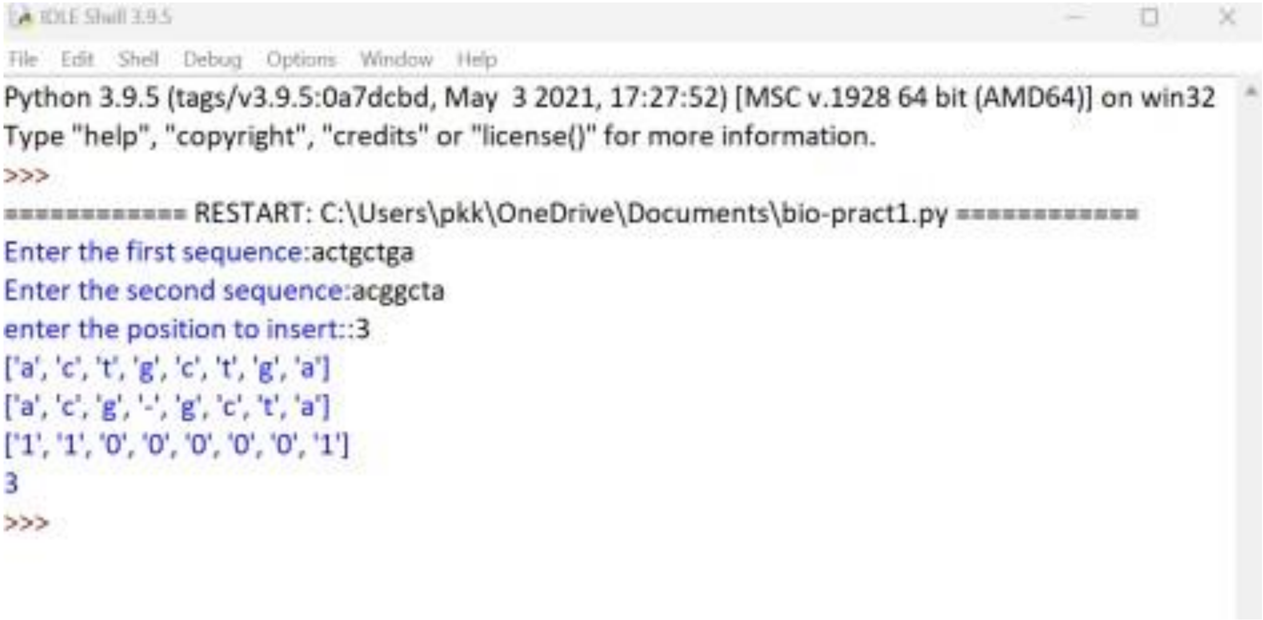


```
Python 3.9.5 (tags/v3.9.5:0a7dcbd, May  3 2021, 17:27:52) [MSC v.1928 64 bit (AMD64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
============ RESTART: C:\Users\pkk\OneDrive\Documents\bio-pract1.py ============
Enter the first sequence:actgctga
Enter the second sequence:acggcta
enter the position to insert::3
['a', 'c', 't', 'g', 'c', 't', 'g', 'a']
['a', 'c', 'g', '-', 'g', 'c', 't', 'a']
['1', '1', '0', '0', '0', '0', '0', '1']
3
>>>
```

Name: Manali Y. Bhaskar. RollNo:528

Practical No: 2

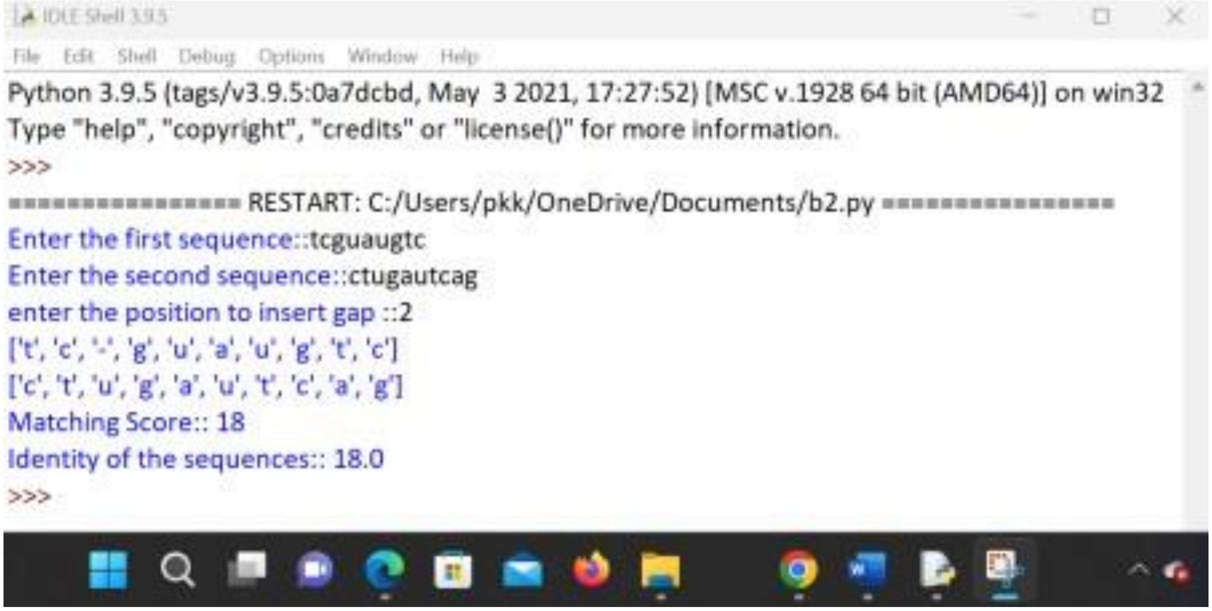
Aim: Write a Python/Java code to find the identity value of a given sequences. Take the sequence fromuser.

Code:

```
se1=input("Enter the first sequence::")
se2=input("Enter the second sequence::")

seq1=list(se1)
seq2=list(se2) def
find_identity(a,b):
    gap(a,b)
    print(a)
    print(b)
    score=0
    length=len(a)
    total_elements=len(a)*len(b)
    for i in range(0,length):
        for j in range(0,length):
            if(a[i]==b[j]):
                score=score+1
    identity=(score/total_elements)*100
    print("Matching Score::",score)
    print("Identity of the sequences::",identity)
def gap(a,b):
    if(len(a)==len(b)):
        print()
    else:
    k=int(input("
    enter the
    position to
    insert gap
    ::")) if
    (len(a)<len(b
    )):
            a.insert(k,'-')
        else:
            b.insert(k,'-')
    return(a,b)
find_identity(seq1,seq2)
```

Name: Manali Y. Bhaskar. RollNo:528 Output:



```
Python 3.9.5 (tags/v3.9.5:0a7dcbd, May  3 2021, 17:27:52) [MSC v.1928 64 bit (AMD64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
================ RESTART: C:/Users/pkk/OneDrive/Documents/b2.py ================
Enter the first sequence::tcguaugtc
Enter the second sequence::ctugautcag
enter the position to insert gap ::2
['t', 'c', '-', 'g', 'u', 'a', 'u', 'g', 't', 'c']
['c', 't', 'u', 'g', 'a', 'u', 't', 'c', 'a', 'g']
Matching Score:: 18
Identity of the sequences:: 18.0
>>>
```

Practical No: 3

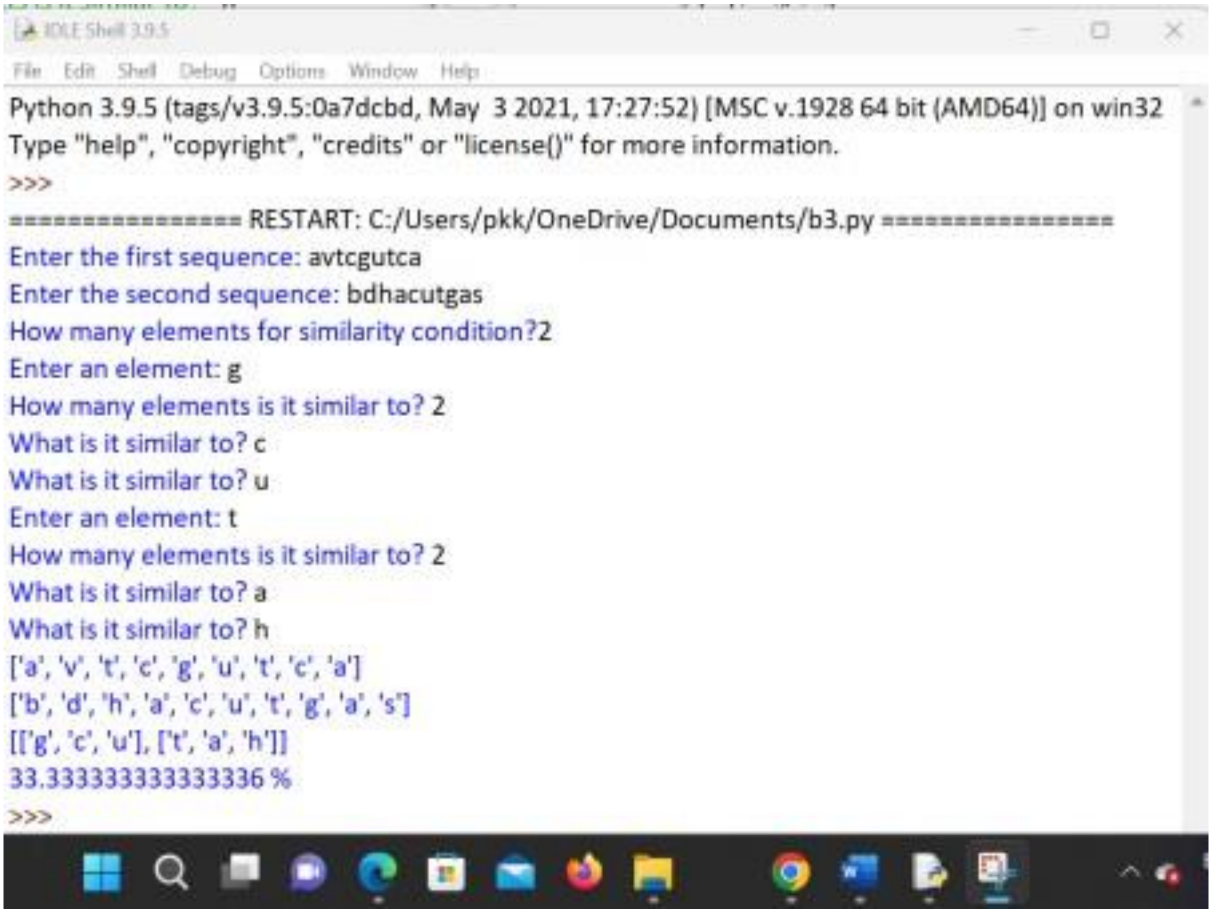
Aim: Write a Python/Java code to find the Similarity value of a given sequences. Take the sequence fromuser.

Code:

```
sequence_one=input("Enter the first sequence: ")
sequence_two=input("Enter the second sequence: ")
how_many=int(input("How many elements for similarity
condition?")) similarities=[] for i in range(0,how_many):
a=input("Enter an element: ")
    c=int(input("How many elements is it similar to? "))
    similarities.append([]) similarities[i].append(a)
    for j in range(0,c): b=input("What is
        it similar to? ")
        similarities[i].append(b)

def compare(o,t,s):
    print(o)
    print(t)
    print(s)
    #checking if similar
    score=0 for i in
    range(len(o)):
        for j in range(len(s)):
Name: Manali Y. Bhaskar.  RollNo:528 if o[i] in s[j] and t[i] in s[j] and o[i] !=
t[i]: score+=1 #calculating similarity similarity= (score*100)/len(o) return
similarity
print(compare(list(sequence_one),list(sequence_two),similarities),"%")
```

Output:



```
Python 3.9.5 (tags/v3.9.5:0a7dcbd, May  3 2021, 17:27:52) [MSC v.1928 64 bit (AMD64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
================= RESTART: C:/Users/pkk/OneDrive/Documents/b3.py =================
Enter the first sequence: avtcgutca
Enter the second sequence: bdhacutgas
How many elements for similarity condition?2
Enter an element: g
How many elements is it similar to? 2
What is it similar to? c
What is it similar to? u
Enter an element: t
How many elements is it similar to? 2
What is it similar to? a
What is it similar to? h
['a', 'v', 't', 'c', 'g', 'u', 't', 'c', 'a']
['b', 'd', 'h', 'a', 'c', 'u', 't', 'g', 'a', 's']
[['g', 'c', 'u'], ['t', 'a', 'h']]
33.333333333333336 %
>>>
```

Practical No: 4

Aim: Enter genome of five different organism and write a python/java program to find consensus sequence using Multiple Sequence Alignment (MSA) technique.

Code:

```
import java.io.*;

import java.util.*;

public class Consensus

 { public static void main(String str[]) throws

  IOException

   {

     int n, i,j,k,count;

     String seq[],cons[];

     ArrayList<Integer> a = new ArrayList<Integer>();

     ArrayList s = new ArrayList();

     BufferedReader br=new BufferedReader(new InputStreamReader(System.in));

     System.out.println("Enter the no of Sequences");

     n=Integer.parseInt(br.readLine()); seq=new String[n];

     System.out.println("Enter sequences");

     for(i=0;i<n;i++)
```

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```
seq[i]=br.readLine(); cons=new

     String[seq[0].length()];

     for(j=0;j<seq[0].length();j++)

     cons[j]=" ";

     for(j=0;j<seq[0].length();j++)

     {

       a.clear();

       s.clear();

       for(i=0;i<n;i++)

       { count=1;

         for(k=i+1;k<n;k++)

         {


           if(seq[i].charAt(j)==seq[k].charAt(j))

           count++;
```

```
          }
         System.out.println("count="+count);
         a.add(count);
         s.add(seq[i].charAt(j));
        }
       /**Updated Snippet 1**/
       Set<String> set = new HashSet<>(s);
       ArrayList setlist = new ArrayList(set);
Collections.sort(setlist); if (setlist.contains('-')
       &&setlist.size()==2){ cons[j]+="-
       "+setlist.get(1);
        }
       else if (setlist.size()==1){
       cons[j]+="-"+setlist.get(0);
       } else{ int m =
       Collections.max(a);
```

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```
       int index=a.indexOf(m);
       System.out.println("Max="+m);
       cons[j]+=s.get(index);
       System.out.println("index="+index);
       for(i=index+1;i<a.size();i++) {
       if(a.get(i)==m)
       cons[j]+="/"+s.get(i);
        }
        }
     }
     System.out.println("Consensus=");
     for(j=0;j<seq[0].length();j++){
        /**Updated Snippet 2**/
     if(cons[j].length()==2)
     System.out.print(cons[j].toLowerCase());
     else if(cons[j].length()==3)
     System.out.print(cons[j].replace("-",""));
     else
```

```
      System.out.print(cons[j]);
      }
    }
  }
```

Output:

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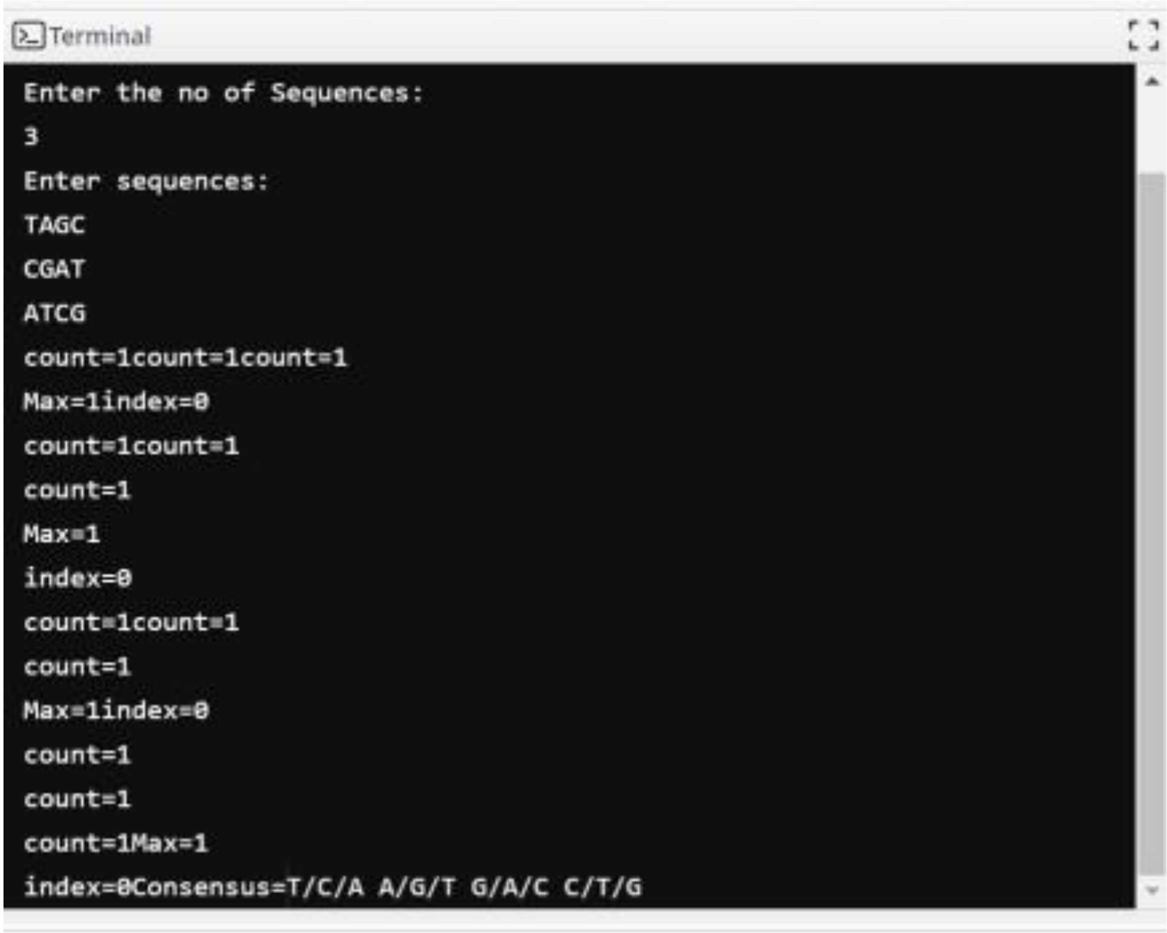

```
Enter the no of Sequences:
3
Enter sequences:
TAGC
CGAT
ATCG
count=1count=1count=1
Max=1index=0
count=1count=1
count=1
Max=1
index=0
count=1count=1
count=1
Max=1index=0
count=1
count=1
count=1Max=1
index=0Consensus=T/C/A A/G/T G/A/C C/T/G
```

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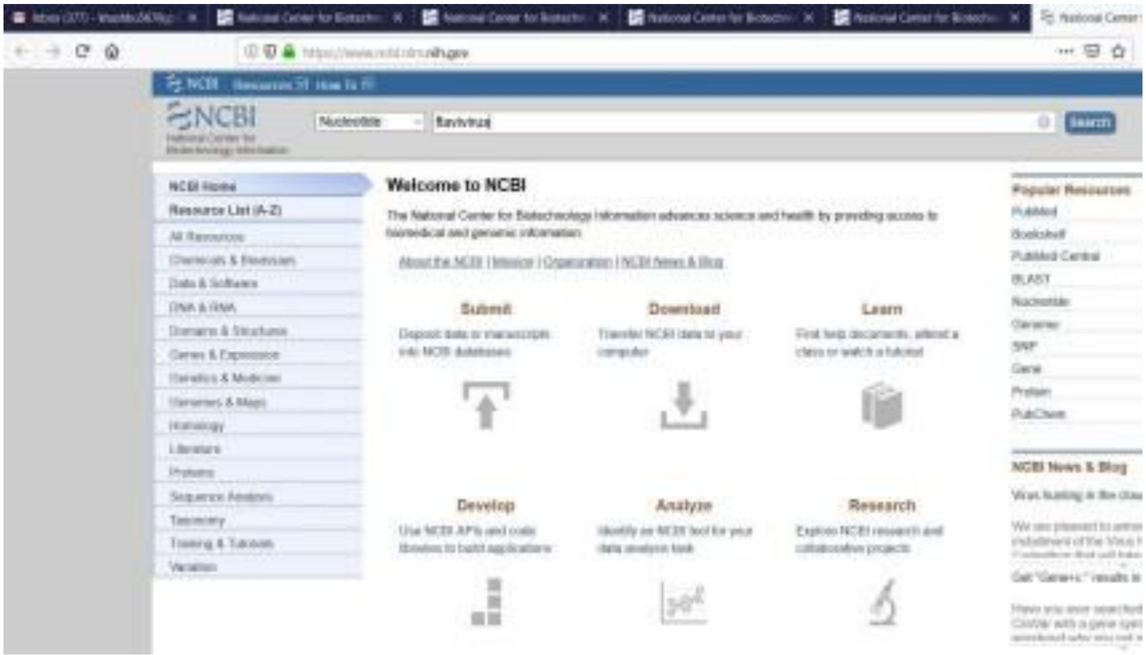
Practical No: 5

Aim: Perform a BLAST search on a specific gene sequence of a specify 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.



NCBI National Center for Biotechnology Information

Nucleotide flavivirus Search

NCBI Home
Resource List (A-Z)
All Resources
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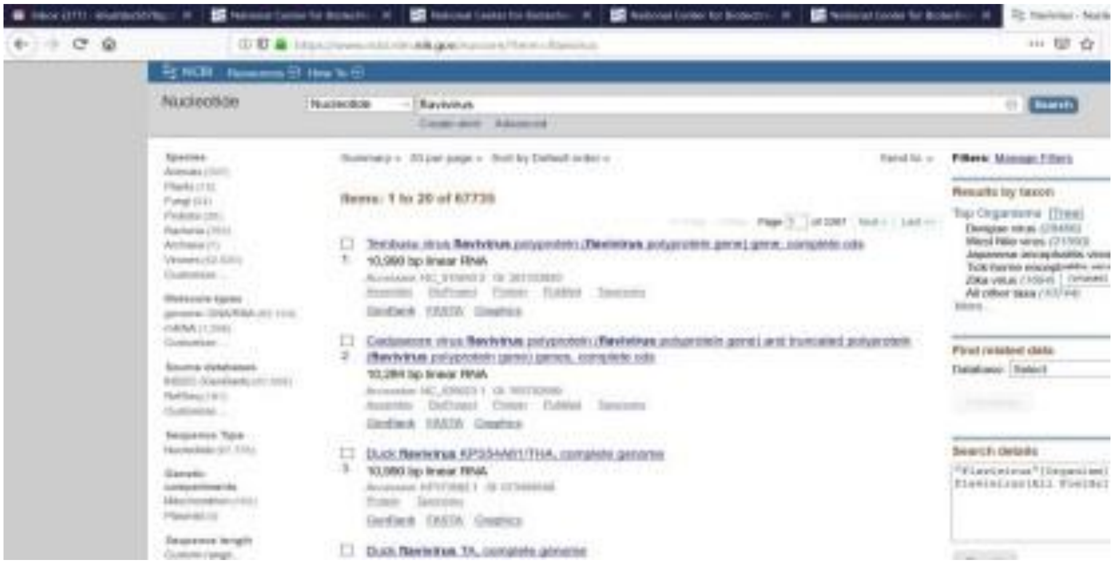


Nucleotide

Nucleotide flavivirus Search

Items: 1 to 20 of 67735

□ 1. Tembusu virus flavivirus polyprotein (flavivirus polyprotein gene) gene, complete cds
10,990 bp linear RNA
GenBank FASTA Graphics

□ 2. Cacipacore virus flavivirus polyprotein (flavivirus polyprotein gene) and truncated polyprotein (flavivirus polyprotein gene) genes, complete cds
10,284 bp linear RNA
GenBank FASTA Graphics

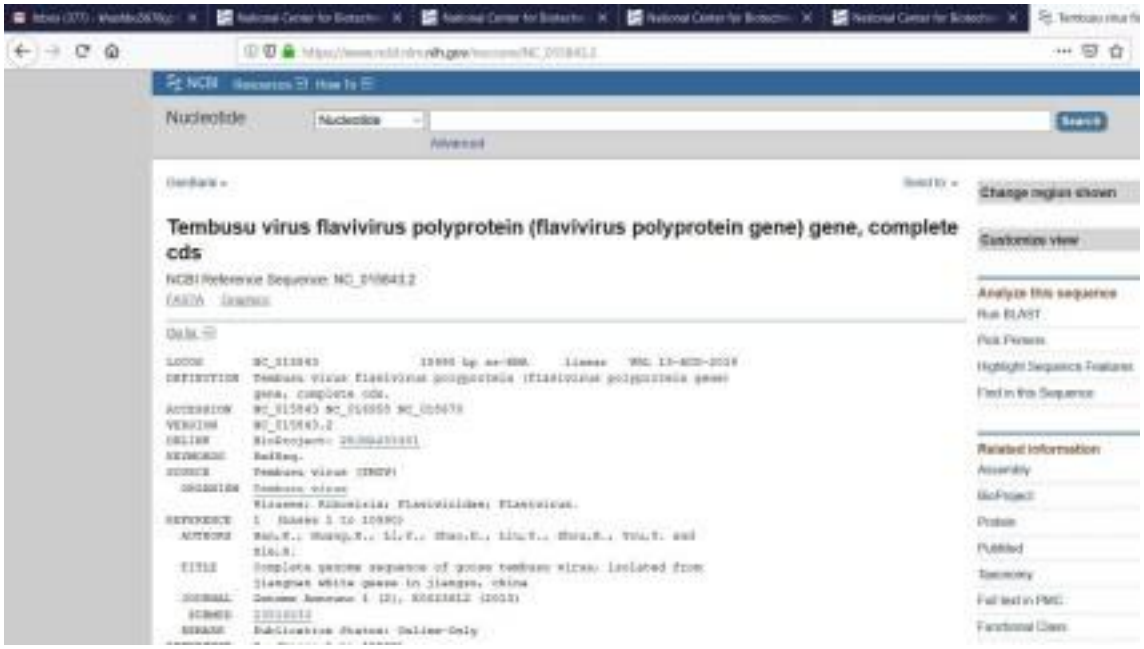
□ 3. Duck flavivirus KPS54A61/THA, complete genome
10,990 bp linear RNA
GenBank FASTA Graphics

□ Duck flavivirus TA, complete genome

Results by taxon
Top Organisms [Tree]
Dengue virus
West Nile virus
Japanese encephalitis virus
Tick-borne encephalitis virus
Zika virus
All other taxa

Find related data
Database: Select

Search details



NCBI Resources How To

Nucleotide | Nucleotide | Search

Advanced

GenBank | Send to

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 [illegible]
VERSION     NC_015843.2
DBLINK      BioProject: [illegible]
KEYWORDS    RefSeq.
SOURCE      Tembusu virus (TMUV)
  ORGANISM  Tembusu virus
            Viruses; Riboviria; Flaviviridae; Flavivirus.
REFERENCE   1  (bases 1 to 10990)
  AUTHORS   [illegible]
  TITLE     Complete genome sequence of goose tembusu virus, isolated from
            jiangnan white geese in jiangsu, china
  JOURNAL   Genome Announc 1 (2), [illegible] (2013)
   PUBMED   [illegible]
  REMARK    Publication Status: Online-Only
```

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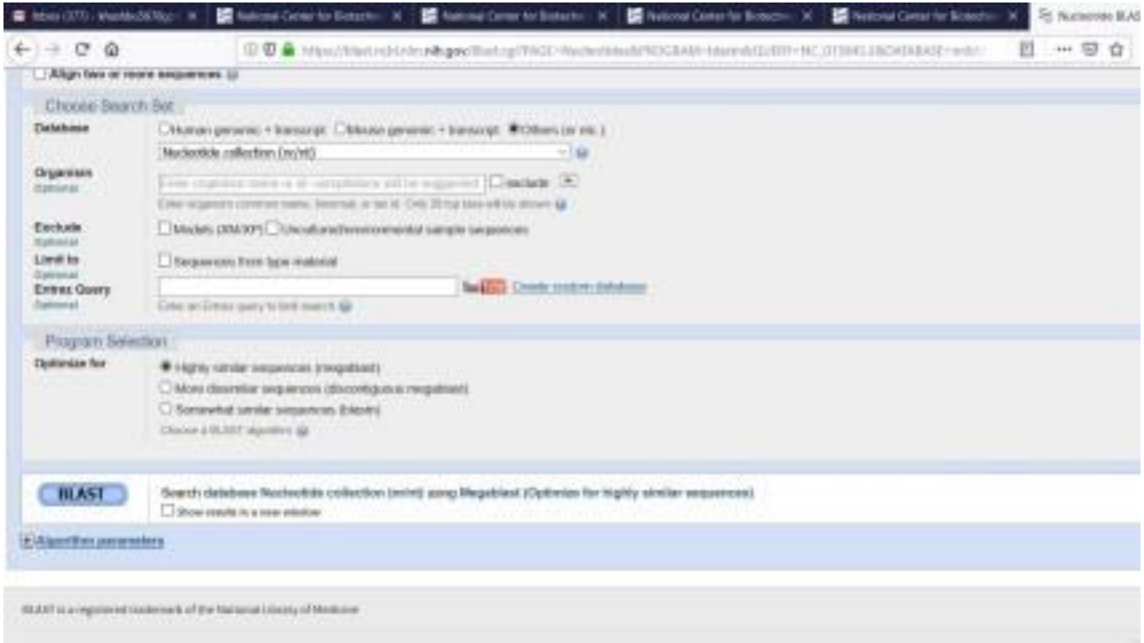
Run BLAST option we have to select



□ 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

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

Limit to (Optional): □ Sequences from type material

Entrez Query (Optional): 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

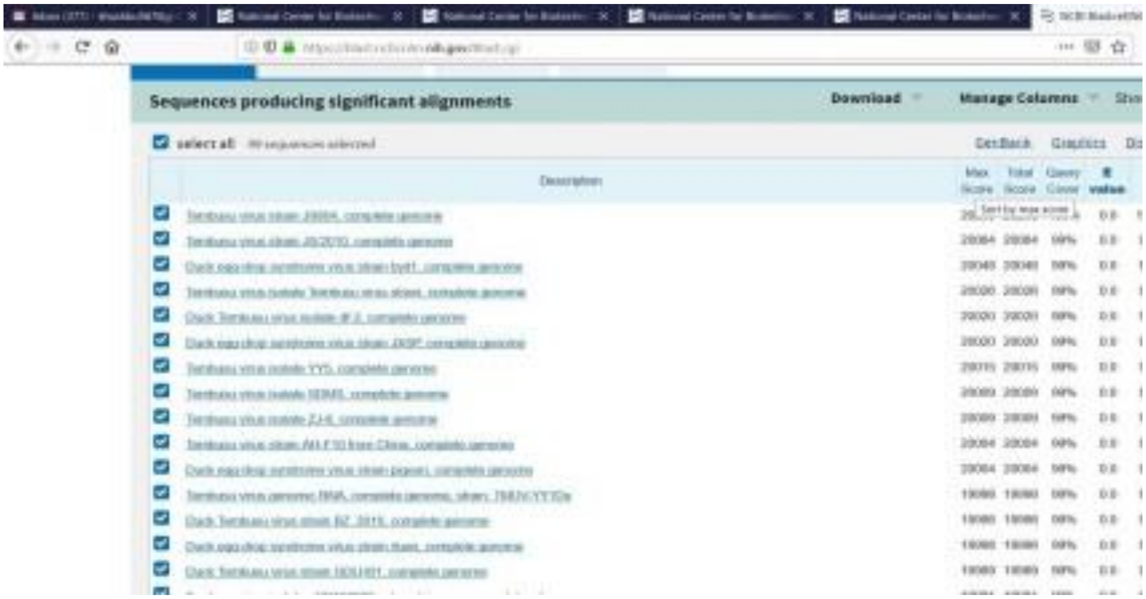
BLAST — Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)

□ Show results in a new window

Algorithm parameters

BLAST is a registered trademark of the National Library of Medicine

BLAST



Sequences producing significant alignments Download Manage Columns

☑ select all

	Description	Max Score	Total Score	Query Cover	E value
☑	Tembusu virus strain JS804, complete genome	[illegible]	[illegible]	[illegible]	0.0
☑	Tembusu virus strain JS/2010, complete genome	20084	20084	99%	0.0
☑	Duck egg drop syndrome virus strain byd1, complete genome	20048	20048	99%	0.0
☑	Tembusu virus isolate Tembusu virus strain [illegible], complete genome	20030	20030	99%	0.0
☑	Duck Tembusu virus isolate #2, complete genome	20020	20020	99%	0.0
☑	Duck egg drop syndrome virus strain JXSP, complete genome	20020	20020	99%	0.0
☑	Tembusu virus isolate YY5, complete genome	20015	20015	99%	0.0
☑	Tembusu virus isolate SDMS, complete genome	20009	20009	99%	0.0
☑	Tembusu virus isolate ZJ-6, complete genome	20009	20009	99%	0.0
☑	Tembusu virus strain AH-F10 from China, complete genome	20004	20004	99%	0.0
☑	Duck egg drop syndrome virus strain pigeon1, complete genome	20004	20004	99%	0.0
☑	Tembusu virus genomic RNA, complete genome, strain: TMUV-YY10a	19980	19980	99%	0.0
☑	Duck Tembusu virus strain BZ_2015, complete genome	19980	19980	99%	0.0
☑	Duck egg drop syndrome virus strain [illegible], complete genome	19980	19980	99%	0.0
☑	Duck Tembusu virus strain [illegible], complete genome	19980	19980	99%	0.0

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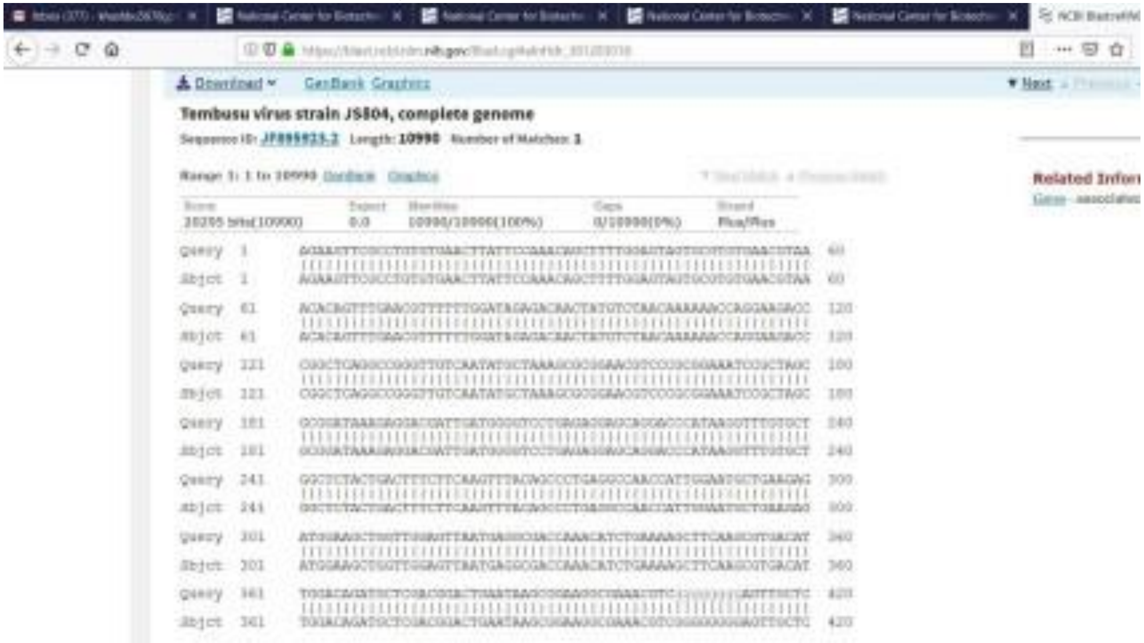
Here the result will be display



Download GenBank Graphics ▼ Next

Tembusu virus strain JS804, complete genome

Sequence ID: JF895923.2 Length: 10990 Number of Matches: 1

Range 1: 1 to 10990 GenBank Graphics

Related Information

```
Score              Expect  Identities            Gaps           Strand
20295 bits(10990)  0.0     10990/10990(100%)     0/10990(0%)    Plus/Plus

Query  1    [illegible]  60
Sbjct  1    [illegible]  60

Query  61   [illegible]  120
Sbjct  61   [illegible]  120

Query  121  [illegible]  180
Sbjct  121  [illegible]  180

Query  181  [illegible]  240
Sbjct  181  [illegible]  240

Query  241  [illegible]  300
Sbjct  241  [illegible]  300

Query  301  [illegible]  360
Sbjct  301  [illegible]  360

Query  361  [illegible]  420
Sbjct  361  [illegible]  420
```

Name: Manali Y. Bhaskar. RollNo:528 Practical No: 6

Aim: Write a Python/Java code to find motif in a given sequence.

Code:

```
import random l=int(input("Enter the

 length of motif"))

 file=open("mot.txt","r")
```

```
r=file.read() print("Sequence",r)
size=len(r) print("Size of the
sequence",size)
pos=random.randint(0,len(r)-5)
#pos=1
print("Position",pos)
motif=r[pos:pos+l]
print("Motif",motif)
i=pos+1 while(i<=size-
1):
    if(motif==r[i:i+1]): str1=r[i:i+1]
        print("Match motif",str1)
        file1=open("motoutput.txt","a")
        file1.write(str1+" ")
    i+=1
```

Output:

```
  Enter the length of motif4
Sequence AGAAGTTCGAGAAGCCGTAGT
Size of the sequence 21
Position 0
Motif AGAA
```

Name: Manali Y. Bhaskar. RollNo:528 import random

```
l=int(input("Enter the length of motif"))
file=open("mot.txt","r") r=file.read()
print("Sequence",r) size=len(r)
print("Size of the sequence",size)
pos=random.randint(0,len(r)-5)

#pos=1
print("Position",pos)
motif=r[pos:pos+l]
```

```
print("Motif",motif)

i=pos+1 while(i<=size-

1):

    if(motif==r[i:i+1]):

        str1=r[i:i+1] print("Match

        motif",str1)

        file1=open("motoutput.txt","a")

        file1.write(str1+" ")

    i+=1
```

Output:

```
   Enter the length of motif4

Sequence AGAAGTTCGAGAAGCCGTAGT

Size of the sequence 21

Position 0

Motif AGAA
```

Practical No: 7

Name: Manali Y. Bhaskar. RollNo:528 Aim: Perform a BLAST search on any genes sequence and writer a java/python code to count the no of repetition of each nucleotide in the sequence.

Code:

```
file=open("genes.txt","r"

) r=file.read() size=len(r)

score_A=0 score_C=0

score_T=0


score_G=0

for i in range(size):

    if(r[i]=='A'):

         score_A+=1

     elif (r[i]=='C'):

         score_C+=1
     elif (r[i]=='T'):
          score_T+=1
     elif (r[i]=='G'):
          score_G+=1
print("score of A is ",score_A)
print("score of C is ",score_C)
print("score of T is ",score_T)
print("score of G is ",score_G)
```

Output:

```
score of A is 6
score of C is 4
score of T is 7
score of G is 6
```

Practical No: 8

Aim: Generate a regular expression enter three protein sequence of three different organism. Write Python/Java code to find regular expression for this sequences.

Code:

```
def gen_reg_exp(seq_list, no_of_col):
     final_list=[]
     for colnum in range(no_of_col):
          collist=[] for colseq
          in seq_list:
               collist.append(colseq[colnum])
          if len(set(collist))==len(collist):
```

```
        #print(final_list)

        final_list.append('x') else:

            if len(set(collist))==1:

                final_list.append(collist[0])

            else:

                final_list.append(".join(set(collist)))

    display_output(final_list)
Name: Manali Y. Bhaskar.  RollNo:528 def display_output(final_list):

    print(*final_list, sep='-')


no_of_seq=int(input("Enter the number of sequence: "))

print("Enter all the sequences") seq_list=[] for _ in

range(no_of_seq):

    seq_list.append(list(map(str, input("").split())))

gen_reg_exp(seq_list, len(seq_list[0]))
```

Output:

```
Enter the number of sequence: 4

Enter all the sequences

A D L G A V F A L C D R Y F Q

S D V G P R S C F C E R F Y Q

A D L G R T Q L R C D R Y Y Q

A D I G Q P H S L C E R Y F Q SA-D-IVL-G-x-x-x-x-
FRL-C-ED-R-YF-YF-Q
```

Practical No: 9

Aim: Enter six protein sequence of different organism and write a program to find a fingerprint ofsequence.

Code:

```
def solve_fingerprint(seq_list, no_of_col):
    seq_dict=dict() for colnum in
    range(no_of_col):
       counta,countc,countt,countg=0,0,0,0
       for colseq in seq_list:
```

```
 if colseq[colnum]=='A':
            counta+=1 elif
        colseq[colnum]=='T':
        countt+=1 elif
        colseq[colnum]=='C':
        countc+=1 elif
        colseq[colnum]=='G':
            countg+=1
    seq_dict[colnum]=[counta,countc,countt,countg]
    display_results(seq_dict)


def display_results(seq_dict):
    print("\tA \tC \tT \tG") for key in
    seq_dict:
    print("\n",*seq_dict[key],sep="\t")


no_of_seq=int(input("Enter the number of sequence: "))
print("Enter all the sequences") seq_list=[]

for _ in range(no_of_seq):
    seq_list.append(list(map(str, input("").split())))
solve_fingerprint(seq_list,len(seq_list[0]))
```

Output:

```
Enter the number of sequence: 4
```

Name: Manali Y. Bhaskar. RollNo:528 Enter all the sequences

```
 A C T G A T G

 A T C A G A A

 A T A A G C A

 A G T T A G C
         A C T G


         4 0 0 0


         0 1 2 1


         1 1 2 0


         2 0 1 1


         2 0 0 2


         1 1 1 1


         2 1 0 1
```