

Importing Essential libraries

In []:

```
import numpy as np
import operator
import multiprocessing
import time
import math
```

Main Blast Methods

Blast_multiprocessing() - This is the main BLAST function with is called first, this function divides the BLAST computation into different processes. Each individual BLAST on a database sequence is done on a different process.

blast_per_seq() - This function applies the BLAST algorithm on the between the query sequence and the specified Database Genome sequence.

Optimization - Multiprocess is allowing us to have almost 5 times the computation speed.

```
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+ Code + Text + Code + Text + Code + Text
Bitscore = 6.927689735164614
p-value = 0.000980262921375244
e-value = 6.046261699042505

Alignment - 226 -----
Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2
Sequence 2 = Query sequence
sequence1: CGAACTTTAAAA-T
||||||| : 
sequence2: CGAACTTTAAAATC

Sequence Identity = 0.8571428571428571
Score = 62
Database sequence range: 39 - 50
Query sequence range: 1 - 13
Length :14
Bitscore = 6.927689735164614
p-value = 0.000980262921375244
e-value = 6.046261699042505

Total number of alignments in complete database = 226
Execution time : 1.0462868213653564 Seconds.

Sequence Identity = 0.8571428571428571
Bit score = 62
Database sequence range: 39 - 51
Query sequence range: 1 - 12
Length :14

Alignment - 226 -----
Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2
Sequence 2 = Query sequence
sequence1: CGAACTTTAAAA-T
||||||| : 
sequence2: CGAACTTTAAAATC

Sequence Identity = 0.8571428571428571
Score = 62
Database sequence range: 39 - 50
Query sequence range: 1 - 13
Length :14
Bitscore = 6.927689735164614
p-value = 0.000980262921375244
e-value = 6.046261699042505

Total number of alignments in complete database = 226
Execution time : 5.248266220092773 Seconds.
```

In []:

```
# This is the main BLAST function with is called first, this function divides the BLAST computation into different processes.
# Each individual BLAST on a database sequence is done on a different process.
def Blast_multiprocessing(query_seq, database_seqs, w, match, mismatch, gap, extension_threshold, hssp_threshold, names):
    processes = []
    manager = multiprocessing.Manager()
    return_dict = manager.dict()
    for i in names:
        p = multiprocessing.Process(target=blast_per_seq, args=(query_seq, database_seqs, w, match, mismatch, gap, extension_threshold, hssp_threshold, names, i, return_dict))

        processes.append(p)

    for i in processes:
        i.start()

    for p in processes:
        p.join()

    total_alignments = 0
    complete_output = ""

    for name in names:

        output = return_dict.get(name)
        total_alignments += output.count("Alignment")
        complete_output += output

    i = 0
    count = 1
    ind = complete_output.find("Alignment",i)
    while(ind != -1):
        ind2 = complete_output.find("--",ind)
        complete_output = complete_output[:ind] + "Alignment - " + str(count) +
" " + complete_output[ind2:]
        i = ind+1
        ind = complete_output.find("Alignment",i)
        count+=1

    print(complete_output)
    print("Total number of alignments in complete database = " + str(total_alignments))

# This function applies the BLAST algorithm on the between the query sequence and the specified Database Genome sequence.
def blast_per_seq(query_seq, database_seqs, w, match, mismatch, gap, extension_threshold, hssp_threshold, names, i, return_dict):
    db_seq_name = i
    database_seq = database_seqs[i]
    words_seq = []

    db_seq_len = len(database_seq)
    qry_len = len(query_seq)

    frag_start_db_arr = fragment_db_sequence(database_seq, db_seq_len, w)
```

```

frag_start_query_arr = fragment_query_sequence(query_seq, qry_len, w, hssp_threshold)

hssp_pairs = find_hssp_pairs( frag_start_query_arr, frag_start_db_arr)

seed_output = find_seed(query_seq, database_seq, hssp_pairs, w)
max_length = [0]
ali_count = [1]
output = []
total_alignments = [0]
score_freq = {}
for seed in seed_output:
    SMAlignment(seed[3], seed[2], match, mismatch, gap, extension_threshold
, db_seq_name, seed[0], seed[1], ali_count, max_length, output, total_alignments, score
_freq)

total_alignments2 = [qry_len*db_seq_len - (qry_len*(qry_len+1))//2]

temp_score_arr = []
for j in score_freq:
    temp_score_arr.append([j, score_freq[j]])
temp_score_arr = sorted(temp_score_arr, key = lambda x:x[0])
l = len(temp_score_arr)
s = 0
for index in range(l-1,-1,-1):
    s+=temp_score_arr[index][1]
    score_freq[temp_score_arr[index][0]] = s
l = len(output)

for k in range(l):
    out = output[k]

    s = int(out[5][out[5].find("= ")+2:-1])
    # print(score_freq[s], s)
    nume = score_freq[s]
    pvalue = nume/total_alignments2[0]
    evalue = total_alignments[0]*pvalue
    bitscore = math.log((total_alignments[0])/evalue)
    out.append("Bitscore = " + str(bitscore) + "\n")
    out.append("p-value = " + str(pvalue) + "\n")
    out.append("e-value = " + str(evalue) + "\n")

output_string = ""

for arr in range(l):

    for ind in range(len(output[arr])):
        output_string+=output[arr][ind]

print(i)
return_dict[i] = output_string

return return_dict

```

Fragmentation and Pre Processing

fragment_db_sequence() - This is a pre-processing function which breaks the database Genome sequence provided to the function to it's 'W' lengthed words mapping them to their starting positions in the database genome sequence. It returns a sorted array, sorted on the basis of the number representations of the words so that Binary Search can be applied.

fragment_query_sequence() - This function query sequence breaks the query sequence into 'W' lengthed words

get_neighbours - This function finds all the neighbours of the query word with matching score > hssp_threshold

In [14]:

```
# This function is used to get the number representation of the nucleotide sequence
def WordToNum(word):
    tmp = []
    trans = {'A':1,'C':2,'G':3,'T':4}
    for w in word:
        tmp.append(trans[w])
    return tmp

# This function transforms evaluates the index of the number representation of the nucleotide sequence
def WordToIndex(word,word_len):
    tmp = 0
    word_num = WordToNum(word)
    for i,v in enumerate(word_num):
        tmp += (v-1)*(4***(word_len-i-1))
    return tmp

# This is a pre-processing function which breaks the database Genome sequence provided to the function to it's 'W' Lengthed words mapping them to their starting positions in the database genome sequence. It returns a sorted array, sorted on the basis of the number representations of the words so that Binary Search can be applied.
def fragment_db_sequence(database_seq, db_seq_len, w):
    frag_start_dict = {}

    i = 0
    while(i+w-1<db_seq_len):
        word = database_seq[i:i+w]
        word_index = WordToIndex(word, w)
        if(frag_start_dict.get(word_index) != None):
            frag_start_dict[word_index].append(i)
        else:
            frag_start_dict[word_index] = [i]
        i+=1

    frag_start_arr = []
    for j in frag_start_dict:
        frag_start_arr.append([j, frag_start_dict[j]])
    frag_start_arr = sorted(frag_start_arr, key = lambda x:x[0])

    return frag_start_arr

# This function query sequence breaks the query sequence into 'W' Lengthed words
def fragment_query_sequence(query_seq, qry_len, w, hssp_threshold):
    match = 5
    mismatch = -4
    index_arr = []
    i = 0

    query frags = []
    while(i+w-1<qry_len):
        word = query_seq[i:i+w]
        neighbours = set({})
        get_neighbours(word, w, match, mismatch, 0, match*w, neighbours, hssp_threshold)
        neighbours = list(neighbours)
```

```

        for j in neighbours:
            query_frags.append([WordToIndex(j,w),i])
    i+=1
    return query_frags

# This function finds all the neighbours of the query word with matching score > hssp_threshold
def get_neighbours(word, w, match, mismatch, i, score, neighbours, hssp_threshold):
    if(score<hssp_threshold or i==w):
        return

    neighbours.add(word)

    residues = ["A","T","G","C"]

    for r in residues:
        if(r!=word[i]):
            neighbour_word = word[:i] + r + word[i+1:]
            get_neighbours(neighbour_word, w, match, mismatch, i+1, score-m
atch+mismatch, neighbours, hssp_threshold)

    get_neighbours(word, w, match, mismatch, i+1, score, neighbours, hssp_threshold
)

```

Aligning words and finding combining adjacent matched HSSPs

binary_search_in_seq() - Binary search on the given database genome sequence for matching query word.

find_hssp_pairs() - Main method which calls binary search for all query words. Finding HSSP pairs between the query and the db_sequence words

find_seed() - Creating the union of all the adjacent matched words.

In []:

```
# Binary search on the given database genome sequence for matching query word.
def binary_search_in_seq(word, frag_start_db_arr, l, r):
    # Check base case
    if r >= l:

        mid = l + (r - 1) // 2

        if frag_start_db_arr[mid][0] == word[0]:
            return frag_start_db_arr[mid][1]

        elif frag_start_db_arr[mid][0] > word[0]:
            return binary_search_in_seq(word, frag_start_db_arr, l, mid-1)
        else:
            return binary_search_in_seq(word, frag_start_db_arr, mid+1, r)
    else:
        return []

# Finding HSSP pairs between the query and the db_sequence words
def find_hssp_pairs( frag_start_query_arr, frag_start_db_arr):

    hssp_pairs = []
    for word in frag_start_query_arr:
        matching_starting_positions = binary_search_in_seq(word, frag_start_db_arr, 0, len(frag_start_db_arr)-1)

        if(matching_starting_positions != []):
            for i in matching_starting_positions:
                hssp_pairs.append([word[1], i])
    return hssp_pairs

# This is function to find all the seeds from the exact gapped matches length equal to
# the world length
# The output is the span of the possible union of seeds in a form of a 2D List
def find_seed(query_seq, database_seq, start_list, w):
    new_list = []
    for i in start_list:
        for j in range(1, w):
            n = [i[0]+j, i[1]+j]
            if(n not in new_list and n not in start_list):
                new_list.append(n)

    coord_list = start_list + new_list

    MatrixPos = np.full([len(query_seq), len(database_seq)], 0, dtype=int)
    for curr_coord in coord_list:
        MatrixPos[curr_coord[0]][curr_coord[1]] = 1

    visited = np.full([len(query_seq), len(database_seq)], 0, dtype=int)

    seed_collection = []
    seed_range = []
    total_seeds = 0

    for curr_coord in start_list:
        i, j = curr_coord
        curr_seed = []
        if(MatrixPos[i][j] == 1 and visited[i][j] == 0):
```

```

        dfs(MatrixPos, i, j, visited, curr_seed, database_seq)
        total_seeds += 1
    # print(curr_seed)
    if(len(curr_seed) > 0):
        x_min = curr_seed[0][0]
        x_max = curr_seed[len(curr_seed)-1][0]
        y_min = curr_seed[0][1]
        y_max = curr_seed[len(curr_seed)-1][1]

        sub_query_seq = query_seq[x_min:x_max+1]
        sub_database_seq = database_seq[y_min:y_max+1]
        seed_collection.append(curr_seed)
        seed_range.append([[x_min, x_max], [y_min, y_max],
                           sub_query_seq, sub_database_seq])

    # print((seed_collection))
    # print(seed_range)
    return seed_range

# function to check if the neighbours are correct consideration for DFS
def check(MatrixPos, i, j, visited, database_seq):
    return (i >= 0 and i < len(query_seq) and j >= 0 and j < len(database_seq) and (not
visited[i][j] and MatrixPos[i][j] == 1))

# dfs for finding the seeds
def dfs(MatrixPos, i, j, visited, curr_seed, database_seq):
    # checking the right, down and diagonally right blocks
    row_next = [1, 0, 1]
    col_next = [0, 1, 1]
    visited[i][j] = 1
    curr_seed.append([i, j])

    for k in range(3):
        if(check(MatrixPos, i + row_next[k], j + col_next[k], visited, database_seq)):
            dfs(MatrixPos, i + row_next[k], j + col_next[k], visited, curr_seed, database_seq)

```

Applying the Smith- Waterman algoithm on the small region of extended/union of adjacent words

SMalignment() - Smith-Waterman Alignment on the unions of the neighbouring matching words.

backtracking() - This function applies backtracking from the cells which have a score greater than the Extension threshold valus.

In []:

```
# Smith-Waterman Alignment on the unions of the neighbouring matching words
def SMalignment(seq1, seq2, match, mismatch, g, extension_threshold, db_seq_name, query
_range, database_range, ali_count, max_length, output, total_alignments, score_freq):
    m = len(seq1)
    n = len(seq2)
    # print(seq1)
    # print(seq2)
    matrix = []

    for i in range(0, m):
        tmp = []
        for j in range(0, n):
            tmp.append(0)
        matrix.append(tmp)
    for sii in range(0, m):
        matrix[sii][0] = sii*g
    for sjj in range(0, n):
        matrix[0][sjj] = sjj*g

    maxx_score = 0
    starting_point = []
    starting_point_visited = {}

    for siii in range(1, m):
        for sjjj in range(1, n):
            matrix[siii][sjjj] = max(matrix[siii-1][sjjj] + g, matrix[siii - 1][sjjj -
1] + SingleBaseCompare(seq1,seq2,siii, sjjj, match, mismatch), matrix[siii][sjjj-1] + g
)
            if(score_freq.get(matrix[siii][sjjj]) == None):
                score_freq[matrix[siii][sjjj]] = 1
            else:
                score_freq[matrix[siii][sjjj]] += 1
            total_alignments[0] += 1
            if(matrix[siii][sjjj] >= extension_threshold):
                tup = (siii, sjjj, matrix[siii][sjjj])
                starting_point.append(tup)
                starting_point_visited[(tup[0], tup[1])] = False

    starting_point = sorted(starting_point, key = lambda x:(x[0], x[1]))
    l = len(starting_point)

    for j in range(l-1,-1,-1):
        i = starting_point[j]
        if(not(starting_point_visited[(i[0],i[1])])):
            temp = []
            a = backtracking(i[0], i[1], seq1, seq2, matrix, starting_point_visited
)
            temp.append("\n")
            temp.append("\n")
            temp.append("Alignment - " + str(ali_count[0]) + " -----")
            temp.append("\n")
            ali_count[0]+=1
            disp = Display(a[0], a[1], db_seq_name)
            temp.append(disp + "\n")
            temp.append("Sequence Identity = " + str(a[2]) + "\n")
            temp.append("Score = " + str(i[2]) + "\n")
            temp.append("Database sequence range: " + str(database_range[0] + a[3]))
```

```

+ " - " + str(database_range[0] + a[5]) + "\n")
        temp.append("Query sequence range: " + str(query_range[0] + a[4]) + " - "
" + str(query_range[0] + a[6]) + "\n")
        temp.append("Length :" + str(len(a[0])) + "\n")
        max_length[0] = max(max_length[0], len(a[0]))
        output.append(temp)

# compare single base
def SingleBaseCompare(seq1,seq2,i,j, match, mismatch):
    if seq1[i] == seq2[j]:
        return match
    else:
        return mismatch

# Backtracking on the Smith Waterman matrix from the points having score greater than t
he extension threshold
def backtracking(m, n, seq1, seq2, matrix, starting_point_visited):
    sequ1 = [seq1[m-1]]
    sequ2 = [seq2[n-1]]

    ending_seq1 = m-1
    ending_seq2 = n-1
    starting_seq1 = m-1
    starting_seq2 = n-1
    while m > 1 and n > 1:
        if max(matrix[m-1][n-2], matrix[m-2][n-2], matrix[m-2][n-1]) == matrix[
m-2][n-2]:
            m -= 1
            n -= 1
            if(starting_point_visited.get((m,n)) != None):
                starting_point_visited[(m,n)] = True

            starting_seq1 = m
            starting_seq2 = n

            sequ1.append(seq1[m-1])
            sequ2.append(seq2[n-1])
        elif max(matrix[m-1][n-2], matrix[m-2][n-2], matrix[m-2][n-1]) == matrix[
x[m-1][n-2]]:
            n -= 1
            if(starting_point_visited.get((m,n)) != None):
                starting_point_visited[(m,n)] = True
            starting_seq2 = n
            sequ1.append('-')
            sequ2.append(seq2[n-1])

        else:
            m -= 1
            if(starting_point_visited.get((m,n)) != None):
                starting_point_visited[(m,n)] = True
            starting_seq1 = m
            sequ1.append(seq1[m-1])
            sequ2.append('-')

    sequ1.reverse()
    sequ2.reverse()
    align_seq1 = ''.join(sequ1)
    align_seq2 = ''.join(sequ2)

    align_score = 0
    for k in range(0, len(align_seq1)):
        if align_seq1[k] == align_seq2[k]:

```

```

        align_score += 1
align_score = float(align_score)/len(align_seq1)

return [align_seq1, align_seq2, align_score, starting_seq1, starting_seq2, ending_seq1, ending_seq2]

```

Displaying BLAST alignment

In []:

```

# Display BLAST result
def Display(seque1, seque2, db_seq_name):
    le = 0
    l = len(seque1)
    output = ""
    output+="\n"
    output += "Sequence 1 = " + db_seq_name + "\n"
    output += "Sequence 2 = Query sequence" + "\n"
    output+="\n"
    output += 'sequence1: '
    for a in list(seque1):
        output += a
    output += "\n"
    output += "\n"
    output += '      '
    for k in range(l):
        if seque1[k] == seque2[k]:
            output += '|'
        elif(seque1[k] != "-" and seque2[k]!="-"):
            output += ':'
        else:
            output += ' '
    output += "\n"
    output += "\n"
    output += 'sequence2: '
    for b in list(seque2):
        output += b
    output += "\n"

return output

```

Driver Code

In []:

```
# Driver Code

# File Input
database_file = open("abin_database.txt", "r")
database_seqs = {}
sequence = ""
name = ""
names = []
for line in database_file:
    if(line[0] == ">"):
        if(name!=""):
            database_seqs[name] = sequence
        sequence = ""
        name = line[:-1]
        names.append(name)
    else:
        sequence += line[:-1]
database_seqs[name] = sequence

# complete query sequence
# query_seq = "CGTGAGTCAGCTATTGAACCTGGCCGCGCAATGGAAGAGTTGTTAATCCGAAAATCTGGCAAC"
# query_seq = "ATTAAGGTTTATACCTTCCCAGGTAACAAACCAACCAACTTCGATCTTTGAGATCTGTTCTCTAAA"
query_seq = input("Query sequence (for example - CGAACTTAAAATCTGTGGCTGTCACTGGCTGCATGCTTAGTGCACTCACGCAGTATAATTAAC )")

# word size
w = int(input("Word length input (For example - 11): "))
hssp_threshold = int(input("HSSP Threshold (For example 45): ")) ## 50 allows only exact matches, 45 allows 1 mismatch
extension_threshold = int(input("Extension Threshold (For example 60): "))
match = 5
mismatch = -4
gap = -3

start_time = time.time()
Blast_multiprocessing(query_seq, database_seqs, w, match, mismatch, gap, extension_threshold, hssp_threshold, names)
end_time = time.time()

print("Execution time : " + str(end_time - start_time) + " Seconds")
```

```
Query sequence (for example - CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCGAGTATAATTAAATAAC )CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCGAGTATAATTAAATAAC
Word length input (For example - 11): 11
HSSP Threshold (For example 45): 45
Extension Threshold (For example 60): 60
>JQ765564.1 Human coronavirus NL63 strain NL63/DEN/2009/14, complete genome
>JQ765563.1 Human coronavirus NL63 strain NL63/DEN/2009/9, complete genome
>MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
>MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
```

Alignment - 1 -----

1

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCCAGTATAATTAAATAA

1

A standard linear barcode consisting of vertical black bars of varying widths on a white background.

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAATTAA

Sequence Identity = 1.0

Score = 345

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 68

Length :69

Bitscore = 14.553021453740739

p-value = 4.783029810233292e-07

e-value = 0.0029501727869518947

Alignment - 2 -----

1

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCCAGTATAATTAA

1

Barcode

sequence2: CGAACTTAAATCTGTGTGGCTGTCACTCGGCTGCATGCTAGTGCACTCACGCAGTATAAT
TAAT-A

Sequence Identity = 0.9855072463768116

Score = 337

Database sequence range: 71 - 138

Query sequence range: 1 - 67

Length :69
Bitscore = 13.166727092620848
p-value = 1.913211924093317e-06
e-value = 0.011800691147807579

Alignment - 3 -----
-

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

||||| : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAA--T

Sequence Identity = 0.9565217391304348

Score = 329

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 66

Length :69

Bitscore = 12.250436360746692

p-value = 4.7830298102332925e-06

e-value = 0.02950172786951895

Alignment - 4 -----
-

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|| | : |||||||||||||||||||||||||||||||||||||||||||||||||||||

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TA---A

Sequence Identity = 0.9565217391304348

Score = 321

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 65

Length :69

Bitscore = 11.608582474574298

p-value = 9.087756639443255e-06

e-value = 0.056053282952085996

Alignment - 5 -----
-

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAA-
-----T

Sequence Identity = 0.8985507246376812

Score = 297

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 62

Length :69

Bitscore = 10.363366711714312

p-value = 3.156799674753973e-05

e-value = 0.19471140393882505

Alignment - 8 -----

-

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

|

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAA-
-----A

Sequence Identity = 0.8985507246376812

Score = 289

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 61

Length :69

Bitscore = 10.075684639262532

p-value = 4.209066233005297e-05

e-value = 0.25961520525176673

Alignment - 9 -----

-

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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|

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAA-
-----A

Sequence Identity = 0.8840579710144928

Score = 281

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 60

Length :69

Bitscore = 9.825633635028398
p-value = 5.40482368556362e-05
e-value = 0.3333695249255641

Alignment - 10 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTA----
-----T

Sequence Identity = 0.855072463768116

Score = 273

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 59

Length :69

Bitscore = 9.60426156336257

p-value = 6.744072032428942e-05

e-value = 0.41597436296021717

Alignment - 11 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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|

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGT----
-----A

Sequence Identity = 0.855072463768116

Score = 265

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 58

Length :69

Bitscore = 9.399729859242958

p-value = 8.274641571703596e-05

e-value = 0.5103798921426778

Alignment - 12 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 i

solate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAG-----
-----T

Sequence Identity = 0.8260869565217391

Score = 257

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 57

Length :69

Bitscore = 9.21548337403942

p-value = 9.948702005285248e-05

e-value = 0.6136359396859941

Alignment - 13 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCA-----
-----G

Sequence Identity = 0.8115942028985508

Score = 249

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 56

Length :69

Bitscore = 9.047689917808375

p-value = 0.00011766253333173899

e-value = 0.7257425055901661

Alignment - 14 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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|

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGC-----
-----A

Sequence Identity = 0.8115942028985508

Score = 241

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 55

Length :69

Bitscore = 8.893539237981116

p-value = 0.0001372729555536955

e-value = 0.8466995898551938

Alignment - 15 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACG-----
-----C

Sequence Identity = 0.782608695652174

Score = 233

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 54

Length :69

Bitscore = 8.750903078363676

p-value = 0.00015831828671872196

e-value = 0.9765071924810771

Alignment - 16 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
-----G

Sequence Identity = 0.7681159420289855

Score = 225

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 53

Length :69

Bitscore = 8.615485248658311

p-value = 0.0001812768298078418
e-value = 1.1181154862547682

Alignment - 17 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTCA-----
----C

Sequence Identity = 0.7536231884057971

Score = 217

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 52

Length :69

Bitscore = 8.48923624505313

p-value = 0.00020567028184003157

e-value = 1.2685742983893147

Alignment - 18 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTCA-----
----A

Sequence Identity = 0.7536231884057971

Score = 209

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 51

Length :69

Bitscore = 8.370936547024106

p-value = 0.00023149864281529135

e-value = 1.427883628884717

Alignment - 19 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
-----C

Sequence Identity = 0.7246376811594203

Score = 201

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 50

Length :69

Bitscore = 8.259602174894257

p-value = 0.0002587619127336211

e-value = 1.5960434777409749

Alignment - 20 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
-----T

Sequence Identity = 0.7101449275362319

Score = 193

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 49

Length :69

Bitscore = 8.154426519205531

p-value = 0.00028746009159502086

e-value = 1.7730538449580886

Alignment - 21 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----

-----C

Sequence Identity = 0.6956521739130435
Score = 185
Dtabase sequence range: 71 - 138
Query sequence range: 1 - 48
Length :69
Bitscore = 8.053234413084883
p-value = 0.00031807148238051396
e-value = 1.9618649033230102

Alignment - 22 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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|

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGC-----
-----A

Sequence Identity = 0.6956521739130435
Score = 177
Dtabase sequence range: 71 - 138
Query sequence range: 1 - 47
Length :69
Bitscore = 7.957240939779426
p-value = 0.000350117782109077
e-value = 2.159526480048787

Alignment - 23 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGC-----
-----C

Sequence Identity = 0.6666666666666666
Score = 169
Dtabase sequence range: 71 - 138
Query sequence range: 1 - 46
Length :69
Bitscore = 7.865912845874224
p-value = 0.00038359899078071005

e-value = 2.3660385751354194

Alignment - 24 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGT-----
-----G

Sequence Identity = 0.6521739130434783

Score = 161

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 45

Length :69

Bitscore = 7.778797567383124

p-value = 0.0004185151083954131

e-value = 2.581401188582908

Alignment - 25 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGT-----
-----T

Sequence Identity = 0.6376811594202898

Score = 153

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 44

Length :69

Bitscore = 7.695507391195347

p-value = 0.0004548661349531861

e-value = 2.805614320391252

Alignment - 26 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTA-----
----G

Sequence Identity = 0.6231884057971014

Score = 145

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 43

Length :69

Bitscore = 7.614736969723778

p-value = 0.0004931303734350525

e-value = 3.0416281433474035

Alignment - 27 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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|

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTT-----
----A

Sequence Identity = 0.6231884057971014

Score = 137

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 42

Length :69

Bitscore = 7.537309033253509

p-value = 0.0005328295208599888

e-value = 3.286492484664411

Alignment - 28 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTT-----
----T

Sequence Identity = 0.5942028985507246
Score = 129
Dtabase sequence range: 71 - 138
Query sequence range: 1 - 41
Length :69
Bitscore = 7.462944617964646
p-value = 0.000573963577227995
e-value = 3.5402073443422735

Alignment - 29 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGC-----
-----T

Sequence Identity = 0.5797101449275363
Score = 121
Dtabase sequence range: 71 - 138
Query sequence range: 1 - 40
Length :69
Bitscore = 7.391399450801551
p-value = 0.0006165325425390713
e-value = 3.802772722380992

Alignment - 30 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATG-----
-----C

Sequence Identity = 0.5652173913043478
Score = 113
Dtabase sequence range: 71 - 138
Query sequence range: 1 - 39
Length :69
Bitscore = 7.322458300331445
p-value = 0.0006605364167932176
e-value = 4.074188618780567

Alignment - 31 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA
|||||||||||||||||||||||||||||||||||||
:
sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCAT-----
-----G

Sequence Identity = 0.5507246376811594
Score = 105
Dtabase sequence range: 71 - 138
Query sequence range: 1 - 38
Length :69
Bitscore = 7.255253171209358
p-value = 0.0007064535029714572
e-value = 4.3574052063279485

Alignment - 32 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA
|||||||||||||||||||||||||||||||||
:
sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCA-----
-----T

Sequence Identity = 0.5362318840579711
Score = 97
Dtabase sequence range: 71 - 138
Query sequence range: 1 - 37
Length :69
Bitscore = 7.190376183322914
p-value = 0.0007538054980927669
e-value = 4.649472312236186

Alignment - 33 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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|

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGC-----
-----A

Sequence Identity = 0.5362318840579711

Score = 89

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 36

Length :69

Bitscore = 7.127663566713586

p-value = 0.0008025924021571464

e-value = 4.950389936505279

Alignment - 34 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGC-----
-----C

Sequence Identity = 0.5072463768115942

Score = 81

Dtabase sequence range: 71 - 138

Query sequence range: 1 - 35

Length :69

Bitscore = 7.0669688358775975

p-value = 0.000852814215164596

e-value = 5.260158079135228

Alignment - 35 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGC-----
-----G

Sequence Identity = 0.4927536231884058
Score = 73
Dtabase sequence range: 71 - 138
Query sequence range: 1 - 34
Length :69
Bitscore = 7.00816038508228
p-value = 0.0009044709371151155
e-value = 5.578776740126033

Alignment - 36 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGC-----
-----T

Sequence Identity = 0.4782608695652174
Score = 65
Dtabase sequence range: 71 - 138
Query sequence range: 1 - 33
Length :69
Bitscore = 6.950620118074919
p-value = 0.0009580408709897284
e-value = 5.909196092264645

Alignment - 37 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAAT-A

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|||| |

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.9855072463768116
Score = 337
Dtabase sequence range: 71 - 137
Query sequence range: 1 - 68
Length :69
Bitscore = 13.166727092620848
p-value = 1.913211924093317e-06
e-value = 0.011800691147807579

Alignment - 38 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGG-----
----C

Sequence Identity = 0.47058823529411764

Score = 60

Dtabase sequence range: 71 - 137

Query sequence range: 1 - 32

Length :68

Bitscore = 6.915787064951266

p-value = 0.0009920003826423848

e-value = 6.118658360138229

Alignment - 39 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAA--T

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||| :

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.9565217391304348

Score = 329

Dtabase sequence range: 71 - 136

Query sequence range: 1 - 68

Length :69

Bitscore = 12.250436360746692

p-value = 4.7830298102332925e-06

e-value = 0.02950172786951895

Alignment - 40 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT

TA---A

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.9565217391304348

Score = 321

Dtabase sequence range: 71 - 135

Query sequence range: 1 - 68

Length :69

Bitscore = 11.608582474574298

p-value = 9.087756639443255e-06

e-value = 0.056053282952085996

Alignment - 41 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
T----A

|| | |||||||||||||||||||||||||||||||||||

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.9420289855072463

Score = 313

Dtabase sequence range: 71 - 134

Query sequence range: 1 - 68

Length :69

Bitscore = 11.119034249255591

p-value = 1.4827392411723206e-05

e-value = 0.09145535639550874

Alignment - 42 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCG-----
-G

Sequence Identity = 0.47692307692307695

Score = 61
Dtabase sequence range: 71 - 134
Query sequence range: 1 - 31
Length :65
Bitscore = 6.9230457467129485
p-value = 0.000984825837927035
e-value = 6.074405768333952

Alignment - 43 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
-----T

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.9130434782608695

Score = 305
Dtabase sequence range: 71 - 133
Query sequence range: 1 - 68
Length :69
Bitscore = 10.70287385203068
p-value = 2.2480240108096473e-05
e-value = 0.13865812098673905

Alignment - 44 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAA-
-----T

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.8985507246376812

Score = 297
Dtabase sequence range: 71 - 132
Query sequence range: 1 - 68
Length :69
Bitscore = 10.363366711714312
p-value = 3.156799674753973e-05
e-value = 0.19471140393882505

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.8840579710144928

Score = 281

Dtabase sequence range: 71 - 130

Query sequence range: 1 - 68

Length :69

Bitscore = 9.825633635028398

p-value = 5.40482368556362e-05

e-value = 0.3333695249255641

Alignment - 48 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTA-----

-----T

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sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.855072463768116

Score = 273

Dtabase sequence range: 71 - 129

Query sequence range: 1 - 68

Length :69

Bitscore = 9.60426156336257

p-value = 6.744072032428942e-05

e-value = 0.41597436296021717

Alignment - 49 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTAT

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sequence2: CGAACTTAAAATCTGTGGCTGTCACT-----C

Sequence Identity = 0.4833333333333334

Score = 60

Dtabase sequence range: 71 - 129

Query sequence range: 1 - 29

Length :60

Bitscore = 6.915787064951266

p-value = 0.0009920003826423848

e-value = 6.118658360138229

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCA-----
-----G

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCA GTATAAT
TAATAA

Sequence Identity = 0.8115942028985508

Score = 249

Dtabase sequence range: 71 - 126

Query sequence range: 1 - 68

Length :69

Bitscore = 9.047689917808375

p-value = 0.00011766253333173899

e-value = 0.7257425055901661

Alignment - 53 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCAC-----T

Sequence Identity = 0.49122807017543857

Score = 61

Dtabase sequence range: 71 - 126

Query sequence range: 1 - 28

Length :57

Bitscore = 6.9230457467129485

p-value = 0.000984825837927035

e-value = 6.074405768333952

Alignment - 54 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCA-----
-----A

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCA GTATAAT
TAATAA

Sequence Identity = 0.8115942028985508

Score = 241

Dtabase sequence range: 71 - 125

Query sequence range: 1 - 68
Length :69
Bitscore = 8.893539237981116
p-value = 0.000137272955536955
e-value = 0.8466995898551938

Alignment - 55 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACG-----
-----C

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.782608695652174
Score = 233
Dtabase sequence range: 71 - 124
Query sequence range: 1 - 68
Length :69
Bitscore = 8.750903078363676
p-value = 0.00015831828671872196
e-value = 0.9765071924810771

Alignment - 56 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCAC-----
-----G

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.7681159420289855
Score = 225
Dtabase sequence range: 71 - 123
Query sequence range: 1 - 68
Length :69
Bitscore = 8.615485248658311
p-value = 0.0001812768298078418
e-value = 1.1181154862547682

Alignment - 57 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACG

||||||||||||||||||||| : -----C

sequence2: CGAACTTTAAAATCTGTGTGGCTGTC-----C

Sequence Identity = 0.5
Score = 62
Dtabase sequence range: 71 - 123
Query sequence range: 1 - 27
Length :54
Bitscore = 6.929868385263836
p-value = 0.0009781295961927084
e-value = 6.033103349316625

Alignment - 58 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACG-----C

||||||||||||||||||||| : -----C

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCA GTATAA TAATAA

Sequence Identity = 0.7536231884057971
Score = 217
Dtabase sequence range: 71 - 122
Query sequence range: 1 - 68
Length :69
Bitscore = 8.48923624505313
p-value = 0.00020567028184003157
e-value = 1.2685742983893147

Alignment - 59 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACG-----A

||||||||||||||||||||| : -----A

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCA GTATAA TAATAA

TAATAA

Sequence Identity = 0.7536231884057971
Score = 209
Dtabase sequence range: 71 - 121
Query sequence range: 1 - 68
Length :69
Bitscore = 8.370936547024106
p-value = 0.00023149864281529135
e-value = 1.427883628884717

Alignment - 60 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTC-----A

Sequence Identity = 0.5192307692307693
Score = 60
Dtabase sequence range: 71 - 121
Query sequence range: 1 - 26
Length :52
Bitscore = 6.915787064951266
p-value = 0.0009920003826423848
e-value = 6.118658360138229

Alignment - 61 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
-----C

||||||||||||||||||||| |

:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACCGCAGTATAAT
TAATAA

Sequence Identity = 0.7246376811594203
Score = 201
Dtabase sequence range: 71 - 120
Query sequence range: 1 - 68
Length :69
Bitscore = 8.259602174894257
p-value = 0.0002587619127336211
e-value = 1.5960434777409749

Alignment - 62 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----

-----T

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.7101449275362319

Score = 193

Dtabase sequence range: 71 - 119

Query sequence range: 1 - 68

Length :69

Bitscore = 8.154426519205531

p-value = 0.00028746009159502086

e-value = 1.7730538449580886

Alignment - 63 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----

-----C

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6956521739130435

Score = 185

Dtabase sequence range: 71 - 118

Query sequence range: 1 - 68

Length :69

Bitscore = 8.053234413084883

p-value = 0.00031807148238051396

e-value = 1.9618649033230102

Alignment - 64 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC

||||||||||||||||||||||| |
sequence2: CGAACTTTAAAATCTGTGTGGCTGT-----C

Sequence Identity = 0.5306122448979592
Score = 61
Dtabase sequence range: 71 - 118
Query sequence range: 1 - 25
Length :49
Bitscore = 6.9230457467129485
p-value = 0.000984825837927035
e-value = 6.074405768333952

Alignment - 65 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGC-----
-----A

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|

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6956521739130435
Score = 177
Dtabase sequence range: 71 - 117
Query sequence range: 1 - 68
Length :69
Bitscore = 7.957240939779426
p-value = 0.000350117782109077
e-value = 2.159526480048787

Alignment - 66 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGC-----
-----C

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6666666666666666
Score = 169
Dtabase sequence range: 71 - 116
Query sequence range: 1 - 68
Length :69

Bitscore = 7.865912845874224
p-value = 0.00038359899078071005
e-value = 2.3660385751354194

Alignment - 67 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGT-----
-----G

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6521739130434783

Score = 161

Dtabase sequence range: 71 - 115

Query sequence range: 1 - 68

Length :69

Bitscore = 7.778797567383124

p-value = 0.0004185151083954131

e-value = 2.581401188582908

Alignment - 68 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTG

||||||||||||||||||||| : |

sequence2: CGAACTTTAAAATCTGTGTGGCTG-----T

Sequence Identity = 0.5217391304347826

Score = 62

Dtabase sequence range: 71 - 115

Query sequence range: 1 - 24

Length :46

Bitscore = 6.929868385263836

p-value = 0.0009781295961927084

e-value = 6.033103349316625

Alignment - 69 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAG-----
-----T

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6376811594202898

Score = 153

Dtabase sequence range: 71 - 114

Query sequence range: 1 - 68

Length :69

Bitscore = 7.695507391195347

p-value = 0.0004548661349531861

e-value = 2.805614320391252

Alignment - 70 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTA-----
-----G

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6231884057971014

Score = 145

Dtabase sequence range: 71 - 113

Query sequence range: 1 - 68

Length :69

Bitscore = 7.614736969723778

p-value = 0.0004931303734350525

e-value = 3.0416281433474035

Alignment - 71 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAG

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sequence2: CGAACTTTAAAATCTGTGTGGCT-----G

Sequence Identity = 0.5454545454545454

Score = 60

Dtabase sequence range: 71 - 113

Query sequence range: 1 - 23
Length :44
Bitscore = 6.915787064951266
p-value = 0.0009920003826423848
e-value = 6.118658360138229

Alignment - 72 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTT-----
-----A

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6231884057971014

Score = 137

Dtabase sequence range: 71 - 112

Query sequence range: 1 - 68

Length :69

Bitscore = 7.537309033253509

p-value = 0.0005328295208599888

e-value = 3.286492484664411

Alignment - 73 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTT-----
-----T

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.5942028985507246

Score = 129

Dtabase sequence range: 71 - 111

Query sequence range: 1 - 68

Length :69

Bitscore = 7.462944617964646

p-value = 0.000573963577227995

e-value = 3.5402073443422735

Alignment - 74 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGC-----
-----T

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.5797101449275363

Score = 121

Dtabase sequence range: 71 - 110

Query sequence range: 1 - 68

Length :69

Bitscore = 7.391399450801551

p-value = 0.0006165325425390713

e-value = 3.802772722380992

Alignment - 75 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCT

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sequence2: CGAACTTTAAAATCTGTGTGGC-----T

Sequence Identity = 0.5609756097560976

Score = 61

Dtabase sequence range: 71 - 110

Query sequence range: 1 - 22

Length :41

Bitscore = 6.9230457467129485

p-value = 0.000984825837927035

e-value = 6.074405768333952

Alignment - 76 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATG-----
-----C

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT

TAATAA

Sequence Identity = 0.5652173913043478
Score = 113
Dtabase sequence range: 71 - 109
Query sequence range: 1 - 68
Length :69
Bitscore = 7.322458300331445
p-value = 0.0006605364167932176
e-value = 4.074188618780567

Alignment - 77 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCAT-----
----G

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
TACGCAGTATAAT
TAATAA

Sequence Identity = 0.5507246376811594
Score = 105
Dtabase sequence range: 71 - 108
Query sequence range: 1 - 68
Length :69
Bitscore = 7.255253171209358
p-value = 0.0007064535029714572
e-value = 4.3574052063279485

Alignment - 78 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCA-----
----T

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
TACGCAGTATAAT
TAATAA

Sequence Identity = 0.5362318840579711
Score = 97
Dtabase sequence range: 71 - 107
Query sequence range: 1 - 68
Length :69
Bitscore = 7.190376183322914
p-value = 0.0007538054980927669

e-value = 4.649472312236186

Alignment - 79 -----

--
Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCAT

||||||||||||||||||| :
sequence2: CGAACTTTAAAATCTGTGTGG-----C

Sequence Identity = 0.5526315789473685

Score = 62

Dtabase sequence range: 71 - 107

Query sequence range: 1 - 21

Length :38

Bitscore = 6.929868385263836

p-value = 0.0009781295961927084

e-value = 6.033103349316625

Alignment - 80 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGC-----
-----A

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACCGCAGTATAATTAAATAA

Sequence Identity = 0.5362318840579711

Score = 89

Dtabase sequence range: 71 - 106

Query sequence range: 1 - 68

Length :69

Bitscore = 7.127663566713586

p-value = 0.0008025924021571464

e-value = 4.950389936505279

Alignment - 81 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTG-----
-----C

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.5072463768115942

Score = 81

Dtabase sequence range: 71 - 105

Query sequence range: 1 - 68

Length :69

Bitscore = 7.0669688358775975

p-value = 0.000852814215164596

e-value = 5.260158079135228

Alignment - 82 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGC

||||||||||||||||| : -----

sequence2: CGAACTTTAAAATCTGTGTG-----G

Sequence Identity = 0.5555555555555556

Score = 60

Dtabase sequence range: 71 - 105

Query sequence range: 1 - 20

Length :36

Bitscore = 6.915787064951266

p-value = 0.0009920003826423848

e-value = 6.118658360138229

Alignment - 83 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTG-----
-----G

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.4927536231884058

Score = 73

Dtabase sequence range: 71 - 104

Query sequence range: 1 - 68

Length :69

Bitscore = 7.00816038508228
p-value = 0.0009044709371151155
e-value = 5.578776740126033

Alignment - 84 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGC-----
-----T

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.4782608695652174

Score = 65

Dtabase sequence range: 71 - 103

Query sequence range: 1 - 68

Length :69

Bitscore = 6.950620118074919

p-value = 0.0009580408709897284

e-value = 5.909196092264645

Alignment - 85 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGG-----
----C

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATA

Sequence Identity = 0.47058823529411764

Score = 60

Dtabase sequence range: 71 - 102

Query sequence range: 1 - 67

Length :68

Bitscore = 6.915787064951266

p-value = 0.0009920003826423848

e-value = 6.118658360138229

Alignment - 86 -----
--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 i

solate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGC

||||||||||||||||||| :

sequence2: CGAACTTTAAAATCTGTGT-----G

Sequence Identity = 0.57575757575758

Score = 61

Dtabase sequence range: 71 - 102

Query sequence range: 1 - 19

Length :33

Bitscore = 6.9230457467129485

p-value = 0.000984825837927035

e-value = 6.074405768333952

Alignment - 87 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGG-----

-G

||||||||||||||||||||||| :

:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAATTA

Sequence Identity = 0.47692307692307695

Score = 61

Dtabase sequence range: 71 - 101

Query sequence range: 1 - 64

Length :65

Bitscore = 6.9230457467129485

p-value = 0.000984825837927035

e-value = 6.074405768333952

Alignment - 88 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTC-----G

||||||||||||||||||| :

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAA

Sequence Identity = 0.4838709677419355

Score = 62

Dtabase sequence range: 71 - 100

Query sequence range: 1 - 61
Length :62
Bitscore = 6.929868385263836
p-value = 0.0009781295961927084
e-value = 6.033103349316625

Alignment - 89 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACT-----C

||||||||||||||||||||||||| :

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACGCACTCACGCAGTAT

Sequence Identity = 0.4833333333333334

Score = 60

Dtabase sequence range: 71 - 99

Query sequence range: 1 - 59

Length :60

Bitscore = 6.915787064951266

p-value = 0.0009920003826423848

e-value = 6.118658360138229

Alignment - 90 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTC

||||||||||||||||| :

sequence2: CGAACTTTAAAATCTGTG-----T

Sequence Identity = 0.6

Score = 62

Dtabase sequence range: 71 - 99

Query sequence range: 1 - 18

Length :30

Bitscore = 6.929868385263836

p-value = 0.0009781295961927084

e-value = 6.033103349316625

Alignment - 91 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCAC-----T

|||||||||||||||||||||||||

:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAG

Sequence Identity = 0.49122807017543857

Score = 61

Dtabase sequence range: 71 - 98

Query sequence range: 1 - 56

Length :57

Bitscore = 6.9230457467129485

p-value = 0.000984825837927035

e-value = 6.074405768333952

Alignment - 92 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTC-----C

|||||||||||||||||||||||||

:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCATGCTTAGTGCAC

Sequence Identity = 0.5

Score = 62

Dtabase sequence range: 71 - 97

Query sequence range: 1 - 53

Length :54

Bitscore = 6.929868385263836

p-value = 0.0009781295961927084

e-value = 6.033103349316625

Alignment - 93 -----

--

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCAC

||||||||||||||| :

sequence2: CGAACTTAAAATCTGT-----G

Sequence Identity = 0.6071428571428571

Score = 60

Dtabase sequence range: 71 - 97

Query sequence range: 1 - 17

Length :28

Bitscore = 6.915787064951266

p-value = 0.0009920003826423848

e-value = 6.118658360138229

sequence1: CGAACTTTAAAATCTGTGTGGC-----T

||||||||||||||||| |

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCT

Sequence Identity = 0.5609756097560976

Score = 61

Dtabase sequence range: 71 - 92

Query sequence range: 1 - 40

Length :41

Bitscore = 6.9230457467129485

p-value = 0.000984825837927035

e-value = 6.074405768333952

Alignment - 100 -----

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGG-----C

||||||||||||||||| : |

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCAT

Sequence Identity = 0.5526315789473685

Score = 62

Dtabase sequence range: 71 - 91

Query sequence range: 1 - 37

Length :38

Bitscore = 6.929868385263836

p-value = 0.0009781295961927084

e-value = 6.033103349316625

Alignment - 101 -----

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGC

||||||||| : |

sequence2: CGAACTTTAAAATCT-----G

Sequence Identity = 0.6818181818181818

Score = 62

Dtabase sequence range: 71 - 91

Query sequence range: 1 - 15

Length :22

Bitscore = 6.929868385263836

p-value = 0.0009781295961927084

e-value = 6.033103349316625

Score = 60
Dtabase sequence range: 71 - 89
Query sequence range: 1 - 14
Length :20
Bitscore = 6.915787064951266
p-value = 0.0009920003826423848
e-value = 6.118658360138229

Alignment - 105 -----

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTG-----T

||||||| :
.....

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCAC

Sequence Identity = 0.6
Score = 62
Dtabase sequence range: 71 - 88
Query sequence range: 1 - 29
Length :30
Bitscore = 6.929868385263836
p-value = 0.0009781295961927084
e-value = 6.033103349316625

Alignment - 106 -----

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGT-----G

||||||| :
.....

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCAC

Sequence Identity = 0.6071428571428571
Score = 60
Dtabase sequence range: 71 - 87
Query sequence range: 1 - 27
Length :28
Bitscore = 6.915787064951266
p-value = 0.0009920003826423848
e-value = 6.118658360138229

Alignment - 107 -----

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTG-----T

||||||||||||||| |

sequence2: CGAACTTTAAAATCTGTGTGGCTGT

Sequence Identity = 0.68

Score = 61

Dtabase sequence range: 71 - 86

Query sequence range: 1 - 24

Length :25

Bitscore = 6.9230457467129485

p-value = 0.000984825837927035

e-value = 6.074405768333952

Alignment - 108 -----

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGT

||||||||||||| :

sequence2: CGAACTTTAAAAT---C

Sequence Identity = 0.7647058823529411

Score = 61

Dtabase sequence range: 71 - 86

Query sequence range: 1 - 13

Length :17

Bitscore = 6.9230457467129485

p-value = 0.000984825837927035

e-value = 6.074405768333952

Alignment - 109 -----

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCT-----G

||||||||||||| :

sequence2: CGAACTTTAAAATCTGTGTGGC

Sequence Identity = 0.6818181818181818

Score = 62

Dtabase sequence range: 71 - 85

Query sequence range: 1 - 21

Length :22

Bitscore = 6.929868385263836

p-value = 0.0009781295961927084

e-value = 6.033103349316625

Alignment - 110 -----

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATC-----T

||||||| : :

sequence2: CGAACTTTAAAATCTGTGTG

Sequence Identity = 0.7

Score = 60

Dtabase sequence range: 71 - 84

Query sequence range: 1 - 19

Length :20

Bitscore = 6.915787064951266

p-value = 0.0009920003826423848

e-value = 6.118658360138229

Alignment - 111 -----

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAAT---C

||||||| : :

sequence2: CGAACTTTAAAATCTGT

Sequence Identity = 0.7647058823529411

Score = 61

Dtabase sequence range: 71 - 83

Query sequence range: 1 - 16

Length :17

Bitscore = 6.9230457467129485

p-value = 0.000984825837927035

e-value = 6.074405768333952

Alignment - 112 -----

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATC

||||||| : :

sequence2: CGAACTTTAAAA-T

```
Sequence Identity = 0.8571428571428571
Score = 62
Database sequence range: 71 - 83
Query sequence range: 1 - 12
Length :14
Bitscore = 6.929868385263836
p-value = 0.0009781295961927084
e-value = 6.033103349316625
```

Alignment - 113 -----

- - -

Sequence 1 = >MN908947.3 Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAA-T

⋮

sequence2: CGAACTTTAAAATC

Sequence Identity = 0.8571428571428571

Score = 62

Dtabase sequence range: 71 - 82

Query sequence range: 1 - 13

Length :14

Bitscore = 6.929868385263836

p-value = 0.0009781295961927084

e-value = 6.033103349316625

Alignment - 114 -----

- - -

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTACGCAGTATAATTAA

1

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAATTAAATA

Sequence Identity = 1.0

Score = 345

Database sequence range: 39 - 106

Query sequence range: 1 - 68

Query sequence
Length: 69

Bitscore = 14.550812803641515

p-value = 4.79346171831635e-07

p-value = 4.793481718210333e-07
q-value = 0.0038566071877958466

ϵ -value = 0.0029500071877958400

Alignment - 115 -----

-

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

||||| : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
||||| |

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAAT-A

Sequence Identity = 0.9855072463768116

Score = 337

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 67

Length :69

Bitscore = 13.164548442521625

p-value = 1.917384687286541e-06

e-value = 0.011826428751183386

Alignment - 116 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

||||| : |||||||||||||||||||||||||||||||||||||||||||||||||
||| :

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAA--T

Sequence Identity = 0.9565217391304348

Score = 329

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 66

Length :69

Bitscore = 12.24825771064747

p-value = 4.793461718216353e-06

e-value = 0.029566071877958462

Alignment - 117 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

||||| : |||||||||||||||||||||||||||||||||||||||||

|| |

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TA---A

Sequence Identity = 0.9565217391304348

Score = 321

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 65

Length :69

Bitscore = 11.606403824475075

p-value = 9.107577264611071e-06

e-value = 0.05617553656812109

Alignment - 118 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

| |

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
T----A

Sequence Identity = 0.9420289855072463

Score = 313

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 64

Length :69

Bitscore = 11.11685559915637

p-value = 1.4859731326470693e-05

e-value = 0.09165482282167124

Alignment - 119 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

:

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sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
-----T

Sequence Identity = 0.9130434782608695

Score = 305

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 63

Length :69
Bitscore = 10.700695201931456
p-value = 2.252927007561686e-05
e-value = 0.1389605378264048

Alignment - 120 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAA-
-----T

Sequence Identity = 0.8985507246376812

Score = 297

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 62

Length :69

Bitscore = 10.36118806161509

p-value = 3.163684734022793e-05

e-value = 0.19513607439452588

Alignment - 121 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||||||||||||||||||

|

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAA--
-----A

Sequence Identity = 0.8985507246376812

Score = 289

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 61

Length :69

Bitscore = 10.073505989163309

p-value = 4.21824631203039e-05

e-value = 0.2601814325260345

Alignment - 122 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||||||||||||||||||||||

|

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTAT---
-----A

Sequence Identity = 0.8840579710144928

Score = 281

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 60

Length :69

Bitscore = 9.823454984929175

p-value = 5.416611741584479e-05

e-value = 0.3340966122209307

Alignment - 123 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||||||||||

:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTA---
-----T

Sequence Identity = 0.855072463768116

Score = 273

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 59

Length :69

Bitscore = 9.602082913263347

p-value = 6.758781022685058e-05

e-value = 0.4168816134792144

Alignment - 124 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||||||

|

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGT-----
-----A

Sequence Identity = 0.855072463768116

Score = 265

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 58

Length :69

Bitscore = 9.397551209143737

p-value = 8.29268877251429e-05

e-value = 0.5114930434886814

Alignment - 125 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||||||||||||||||||||||

:

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGT-----
-----T

Sequence Identity = 0.8260869565217391

Score = 257

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 57

Length :69

Bitscore = 9.213304723940198

p-value = 9.970400373890015e-05

e-value = 0.6149742950615361

Alignment - 126 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||||||||||

:

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCA-----
-----G

Sequence Identity = 0.8115942028985508

Score = 249

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 56

Length :69

Bitscore = 9.045511267709152
p-value = 0.00011791915826812227
e-value = 0.7273253681977782

Alignment - 127 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||||||||||||||||||

|

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGC-----
-----A

Sequence Identity = 0.8115942028985508

Score = 241

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 55

Length :69

Bitscore = 8.891360587881895

p-value = 0.00013757235131280933

e-value = 0.848546262897408

Alignment - 128 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||||||||||

:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACG-----
-----C

Sequence Identity = 0.782608695652174

Score = 233

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 54

Length :69

Bitscore = 8.748724428264453

p-value = 0.0001586635828729613

e-value = 0.9786369791604252

Alignment - 129 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 i

solate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||||||||||||||

:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
-----G

Sequence Identity = 0.7681159420289855

Score = 225

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 53

Length :69

Bitscore = 8.61330659855909

p-value = 0.00018167219912039977

e-value = 1.1205541241746257

Alignment - 130 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||||||

:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
-----C

Sequence Identity = 0.7536231884057971

Score = 217

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 52

Length :69

Bitscore = 8.487057594953908

p-value = 0.00020611885388330318

e-value = 1.271341090752214

Alignment - 131 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

|||||||||||||||||||||||||||||||||

|

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
----A

Sequence Identity = 0.7536231884057971

Score = 209

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 51

Length :69

Bitscore = 8.368757896924883

p-value = 0.0002320035471616715

e-value = 1.4309978788931896

Alignment - 132 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
TAATAA

|||||||||||||||||||||||||||||||||||||||||||||||||

:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
----C

Sequence Identity = 0.7246376811594203

Score = 201

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 50

Length :69

Bitscore = 8.257423524795033

p-value = 0.0002593262789555047

e-value = 1.5995244885975528

Alignment - 133 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
TAATAA

|||||||||||||||||||||||||||||||||||||

:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
----T

Sequence Identity = 0.7101449275362319

Score = 193

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 49

Length :69

Bitscore = 8.152247869106308

p-value = 0.0002880870492648028
e-value = 1.7769209198653038

Alignment - 134 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGC-----
-----C

Sequence Identity = 0.6956521739130435

Score = 185

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 48

Length :69

Bitscore = 8.051055762985662

p-value = 0.00031876520426138747

e-value = 1.9661437798842378

Alignment - 135 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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|

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGC-----
-----A

Sequence Identity = 0.6956521739130435

Score = 177

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 47

Length :69

Bitscore = 7.955062289680204

p-value = 0.000350881397773437

e-value = 2.1642364614665595

Alignment - 136 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTG-----
----C

Sequence Identity = 0.6666666666666666

Score = 169

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 46

Length :69

Bitscore = 7.8637341957750015

p-value = 0.0003844356298009515

e-value = 2.371198964612269

Alignment - 137 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGT----
----G

Sequence Identity = 0.6521739130434783

Score = 161

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 45

Length :69

Bitscore = 7.776618917283901

p-value = 0.00041942790034393086

e-value = 2.5870312893213656

Alignment - 138 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGT----

-----T

Sequence Identity = 0.6376811594202898
Score = 153
Dtabase sequence range: 39 - 106
Query sequence range: 1 - 44
Length :69
Bitscore = 7.693328741096125
p-value = 0.00045585820940237517
e-value = 2.81173343559385

Alignment - 139 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTA-----
-----G

Sequence Identity = 0.6231884057971014
Score = 145
Dtabase sequence range: 39 - 106
Query sequence range: 1 - 43
Length :69
Bitscore = 7.612558319624556
p-value = 0.000494205903148106
e-value = 3.0482620106175173

Alignment - 140 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTA-----
-----A

Sequence Identity = 0.6231884057971014
Score = 137
Dtabase sequence range: 39 - 106
Query sequence range: 1 - 42
Length :69
Bitscore = 7.535130383154287
p-value = 0.0005339916354093017

e-value = 3.293660407204573

Alignment - 141 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCT-----

-----T

Sequence Identity = 0.5942028985507246

Score = 129

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 41

Length :69

Bitscore = 7.460765967865424

p-value = 0.0005752154061859624

e-value = 3.547928625355016

Alignment - 142 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCT-----

-----T

Sequence Identity = 0.5797101449275363

Score = 121

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 40

Length :69

Bitscore = 7.389220800702328

p-value = 0.0006178772154780879

e-value = 3.8110666650688465

Alignment - 143 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATG-----
-----C

Sequence Identity = 0.5652173913043478

Score = 113

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 39

Length :69

Bitscore = 7.320279650232224

p-value = 0.0006619770632856784

e-value = 4.083074526346064

Alignment - 144 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATG-----
-----G

Sequence Identity = 0.5507246376811594

Score = 105

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 38

Length :69

Bitscore = 7.253074521110136

p-value = 0.0007079942957805553

e-value = 4.366908816374465

Alignment - 145 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCA-----
-----T

Sequence Identity = 0.5362318840579711
Score = 97
Dtabase sequence range: 39 - 106
Query sequence range: 1 - 37
Length :69
Bitscore = 7.188197533223692
p-value = 0.0007554495667908973
e-value = 4.659612927966254

Alignment - 146 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGC-----
-----A

Sequence Identity = 0.5362318840579711
Score = 89
Dtabase sequence range: 39 - 106
Query sequence range: 1 - 36
Length :69
Bitscore = 7.125484916614364
p-value = 0.000804342876316704
e-value = 4.96118686112143

Alignment - 147 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTG-----
-----C

Sequence Identity = 0.5072463768115942
Score = 81
Dtabase sequence range: 39 - 106
Query sequence range: 1 - 35
Length :69
Bitscore = 7.064790185778375
p-value = 0.0008546742243579757
e-value = 5.271630615839994

Alignment - 148 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCT-----

-----G

Sequence Identity = 0.4927536231884058

Score = 73

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 34

Length :69

Bitscore = 7.005981734983059

p-value = 0.0009064436109147123

e-value = 5.590944192121945

Alignment - 149 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCT-----

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Sequence Identity = 0.4782608695652174

Score = 65

Dtabase sequence range: 39 - 106

Query sequence range: 1 - 33

Length :69

Bitscore = 6.948441467975697

p-value = 0.0009601303821587354

e-value = 5.922084197155081

Alignment - 150 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAAT-A

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.9855072463768116

Score = 337

Dtabase sequence range: 39 - 105

Query sequence range: 1 - 68

Length :69

Bitscore = 13.164548442521625

p-value = 1.917384687286541e-06

e-value = 0.011826428751183386

Alignment - 151 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGG-----
----C

Sequence Identity = 0.47058823529411764

Score = 60

Dtabase sequence range: 39 - 105

Query sequence range: 1 - 32

Length :68

Bitscore = 6.913608414852043

p-value = 0.0009941639603580717

e-value = 6.132003307488586

Alignment - 152 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAA--T

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.9565217391304348
Score = 329
Dtabase sequence range: 39 - 104
Query sequence range: 1 - 68
Length :69
Bitscore = 12.24825771064747
p-value = 4.793461718216353e-06
e-value = 0.029566071877958462

Alignment - 153 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TA---A

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.9565217391304348
Score = 321
Dtabase sequence range: 39 - 103
Query sequence range: 1 - 68
Length :69
Bitscore = 11.606403824475075
p-value = 9.107577264611071e-06
e-value = 0.05617553656812109

Alignment - 154 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
T---A

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.9420289855072463
Score = 313
Dtabase sequence range: 39 - 102
Query sequence range: 1 - 68
Length :69
Bitscore = 11.11685559915637
p-value = 1.4859731326470693e-05
e-value = 0.09165482282167124

Alignment - 155 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TA

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sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCG-----
-G

Sequence Identity = 0.47692307692307695

Score = 61

Dtabase sequence range: 39 - 102

Query sequence range: 1 - 31

Length :65

Bitscore = 6.920867096613726

p-value = 0.0009869737677807471

e-value = 6.087654199671648

Alignment - 156 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
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sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.9130434782608695

Score = 305

Dtabase sequence range: 39 - 101

Query sequence range: 1 - 68

Length :69

Bitscore = 10.700695201931456

p-value = 2.252927007561686e-05

e-value = 0.1389605378264048

Alignment - 157 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAA-

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.8985507246376812

Score = 297

Dtabase sequence range: 39 - 100

Query sequence range: 1 - 68

Length :69

Bitscore = 10.36118806161509

p-value = 3.163684734022793e-05

e-value = 0.19513607439452588

Alignment - 158 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAA--

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.8985507246376812

Score = 289

Dtabase sequence range: 39 - 99

Query sequence range: 1 - 68

Length :69

Bitscore = 10.073505989163309

p-value = 4.21824631203039e-05

e-value = 0.2601814325260345

Alignment - 159 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAA

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTC-----G

Sequence Identity = 0.4838709677419355

Score = 62

Dtabase sequence range: 39 - 99

Query sequence range: 1 - 30

Length :62
Bitscore = 6.927689735164614
p-value = 0.000980262921375244
e-value = 6.046261699042505

Alignment - 160 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTAT---
-----A

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.8840579710144928

Score = 281

Dtabase sequence range: 39 - 98

Query sequence range: 1 - 68

Length :69

Bitscore = 9.823454984929175

p-value = 5.416611741584479e-05

e-value = 0.3340966122209307

Alignment - 161 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTA---
-----T

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.855072463768116

Score = 273

Dtabase sequence range: 39 - 97

Query sequence range: 1 - 68

Length :69

Bitscore = 9.602082913263347

p-value = 6.758781022685058e-05

e-value = 0.4168816134792144

Alignment - 162 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTAT

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACT-----C

Sequence Identity = 0.4833333333333334

Score = 60

Dtabase sequence range: 39 - 97

Query sequence range: 1 - 29

Length :60

Bitscore = 6.913608414852043

p-value = 0.0009941639603580717

e-value = 6.132003307488586

Alignment - 163 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTAT-----
----A

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.855072463768116

Score = 265

Dtabase sequence range: 39 - 96

Query sequence range: 1 - 68

Length :69

Bitscore = 9.397551209143737

p-value = 8.29268877251429e-05

e-value = 0.5114930434886814

Alignment - 164 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTAT-----
----T

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.8260869565217391
Score = 257
Dtabase sequence range: 39 - 95
Query sequence range: 1 - 68
Length :69
Bitscore = 9.213304723940198
p-value = 9.970400373890015e-05
e-value = 0.6149742950615361

Alignment - 165 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCA-----
-----G

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCA GTATAAT
TAATAA

Sequence Identity = 0.8115942028985508
Score = 249
Dtabase sequence range: 39 - 94
Query sequence range: 1 - 68
Length :69
Bitscore = 9.045511267709152
p-value = 0.00011791915826812227
e-value = 0.7273253681977782

Alignment - 166 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAG

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sequence2: CGAACTTTAAAATCTGTGTGGCTGTCAC-----T

Sequence Identity = 0.49122807017543857
Score = 61
Dtabase sequence range: 39 - 94
Query sequence range: 1 - 28
Length :57
Bitscore = 6.920867096613726
p-value = 0.0009869737677807471
e-value = 6.087654199671648

Alignment - 167 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGC-----
-----A

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sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.8115942028985508

Score = 241

Dtabase sequence range: 39 - 93

Query sequence range: 1 - 68

Length :69

Bitscore = 8.891360587881895

p-value = 0.00013757235131280933

e-value = 0.848546262897408

Alignment - 168 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACG-----
-----C

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sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.782608695652174

Score = 233

Dtabase sequence range: 39 - 92

Query sequence range: 1 - 68

Length :69

Bitscore = 8.748724428264453

p-value = 0.0001586635828729613

e-value = 0.9786369791604252

Alignment - 169 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----
-----G

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.7681159420289855

Score = 225

Dtabase sequence range: 39 - 91

Query sequence range: 1 - 68

Length :69

Bitscore = 8.61330659855909

p-value = 0.00018167219912039977

e-value = 1.1205541241746257

Alignment - 170 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACG

||||||||||||||||||||||||| :-----

sequence2: CGAACTTAAAATCTGTGTGGCTGTCA-----C

Sequence Identity = 0.5

Score = 62

Dtabase sequence range: 39 - 91

Query sequence range: 1 - 27

Length :54

Bitscore = 6.927689735164614

p-value = 0.000980262921375244

e-value = 6.046261699042505

Alignment - 171 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTC

-----C

|||||||||||||||||||||||||-----

:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.7536231884057971

Score = 217

Dtabase sequence range: 39 - 90

Query sequence range: 1 - 68

Length :69

Bitscore = 8.487057594953908

p-value = 0.00020611885388330318
e-value = 1.271341090752214

Alignment - 172 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTC-----
-----A

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|

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.7536231884057971

Score = 209

Dtabase sequence range: 39 - 89

Query sequence range: 1 - 68

Length :69

Bitscore = 8.368757896924883

p-value = 0.0002320035471616715

e-value = 1.4309978788931896

Alignment - 173 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTC

||||||||||||||||||||| |

sequence2: CGAACTTTAAAATCTGTGTGGCTGTC-----A

Sequence Identity = 0.5192307692307693

Score = 60

Dtabase sequence range: 39 - 89

Query sequence range: 1 - 26

Length :52

Bitscore = 6.913608414852043

p-value = 0.0009941639603580717

e-value = 6.132003307488586

Alignment - 174 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTC-----

-----C

|||||||||||||||||||||||||||||||||||||||||

:

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.7246376811594203

Score = 201

Dtabase sequence range: 39 - 88

Query sequence range: 1 - 68

Length :69

Bitscore = 8.257423524795033

p-value = 0.0002593262789555047

e-value = 1.5995244885975528

Alignment - 175 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----

-----T

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:

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.7101449275362319

Score = 193

Dtabase sequence range: 39 - 87

Query sequence range: 1 - 68

Length :69

Bitscore = 8.152247869106308

p-value = 0.0002880870492648028

e-value = 1.7769209198653038

Alignment - 176 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC-----

-----C

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:

sequence2: CGAACTTAAAATCTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6956521739130435

Score = 185
Dtabase sequence range: 39 - 86
Query sequence range: 1 - 68
Length :69
Bitscore = 8.051055762985662
p-value = 0.00031876520426138747
e-value = 1.9661437798842378

Alignment - 177 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC

||||||||||||||||||||| |

sequence2: CGAACTTTAAAATCTGTGTGGCTGT-----C

Sequence Identity = 0.5306122448979592
Score = 61
Dtabase sequence range: 39 - 86
Query sequence range: 1 - 25
Length :49
Bitscore = 6.920867096613726
p-value = 0.0009869737677807471
e-value = 6.087654199671648

Alignment - 178 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGC-----
-----A

||||||||||||||||||||| |

|
sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACGCAGTATAATTAAATAA

Sequence Identity = 0.6956521739130435
Score = 177
Dtabase sequence range: 39 - 85
Query sequence range: 1 - 68
Length :69
Bitscore = 7.955062289680204
p-value = 0.000350881397773437
e-value = 2.1642364614665595

Alignment - 179 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTG-----
-----C

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6666666666666666

Score = 169

Dtabase sequence range: 39 - 84

Query sequence range: 1 - 68

Length :69

Bitscore = 7.8637341957750015

p-value = 0.0003844356298009515

e-value = 2.371198964612269

Alignment - 180 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTG-----
-----G

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6521739130434783

Score = 161

Dtabase sequence range: 39 - 83

Query sequence range: 1 - 68

Length :69

Bitscore = 7.776618917283901

p-value = 0.00041942790034393086

e-value = 2.5870312893213656

Alignment - 181 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTG

||||||||||||||||||||| : |

sequence2: CGAACTTTAAAATCTGTGTGGCTG-----T

Sequence Identity = 0.5217391304347826
Score = 62
Dtabase sequence range: 39 - 83
Query sequence range: 1 - 24
Length :46
Bitscore = 6.927689735164614
p-value = 0.000980262921375244
e-value = 6.046261699042505

Alignment - 182 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAG-----
-----T

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6376811594202898
Score = 153
Dtabase sequence range: 39 - 82
Query sequence range: 1 - 68
Length :69
Bitscore = 7.693328741096125
p-value = 0.00045585820940237517
e-value = 2.81173343559385

Alignment - 183 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTA-----
-----G

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.6231884057971014
Score = 145
Dtabase sequence range: 39 - 81
Query sequence range: 1 - 68
Length :69
Bitscore = 7.612558319624556
p-value = 0.000494205903148106
e-value = 3.0482620106175173

Alignment - 184 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAG

|||||||||||||||||||||| |

sequence2: CGAACTTTAAAATCTGTGTGGCT-----G

Sequence Identity = 0.5454545454545454

Score = 60

Dtabase sequence range: 39 - 81

Query sequence range: 1 - 23

Length :44

Bitscore = 6.913608414852043

p-value = 0.0009941639603580717

e-value = 6.132003307488586

Alignment - 185 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTT-----

-----A

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|

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTACGCAGTATAATTAA

Sequence Identity = 0.6231884057971014

Score = 137

Dtabase sequence range: 39 - 80

Query sequence range: 1 - 68

Length :69

Bitscore = 7.535130383154287

p-value = 0.0005339916354093017

e-value = 3.293660407204573

Alignment - 186 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTT-----

-----T

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.5942028985507246

Score = 129

Dtabase sequence range: 39 - 79

Query sequence range: 1 - 68

Length :69

Bitscore = 7.460765967865424

p-value = 0.0005752154061859624

e-value = 3.547928625355016

Alignment - 187 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGC-----

-----T

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.5797101449275363

Score = 121

Dtabase sequence range: 39 - 78

Query sequence range: 1 - 68

Length :69

Bitscore = 7.389220800702328

p-value = 0.0006178772154780879

e-value = 3.8110666650688465

Alignment - 188 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCT

||||||||||||||||||||| |

sequence2: CGAACTTAAAATCTGTGTGGC-----T

Sequence Identity = 0.5609756097560976

Score = 61

Dtabase sequence range: 39 - 78

Query sequence range: 1 - 22

Length :41

Bitscore = 6.920867096613726

p-value = 0.0009869737677807471
e-value = 6.087654199671648

Alignment - 189 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATG-----
-----C

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.5652173913043478

Score = 113

Dtabase sequence range: 39 - 77

Query sequence range: 1 - 68

Length :69

Bitscore = 7.320279650232224

p-value = 0.0006619770632856784

e-value = 4.083074526346064

Alignment - 190 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATG-----
-----G

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.5507246376811594

Score = 105

Dtabase sequence range: 39 - 76

Query sequence range: 1 - 68

Length :69

Bitscore = 7.253074521110136

p-value = 0.0007079942957805553

e-value = 4.366908816374465

Alignment - 191 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCA-----

----T

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:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.5362318840579711

Score = 97

Dtabase sequence range: 39 - 75

Query sequence range: 1 - 68

Length :69

Bitscore = 7.188197533223692

p-value = 0.0007554495667908973

e-value = 4.659612927966254

Alignment - 192 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCAT

||||||||||||||||||| : |

sequence2: CGAACTTAAAATCTGTGTGG-----C

Sequence Identity = 0.5526315789473685

Score = 62

Dtabase sequence range: 39 - 75

Query sequence range: 1 - 21

Length :38

Bitscore = 6.927689735164614

p-value = 0.000980262921375244

e-value = 6.046261699042505

Alignment - 193 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGC-----

----A

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|

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.5362318840579711

Score = 89
Dtabase sequence range: 39 - 74
Query sequence range: 1 - 68
Length :69
Bitscore = 7.125484916614364
p-value = 0.000804342876316704
e-value = 4.96118686112143

Alignment - 194 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTG-----
-----C

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACGCAGTATAATTAAATAA

Sequence Identity = 0.5072463768115942

Score = 81
Dtabase sequence range: 39 - 73
Query sequence range: 1 - 68
Length :69
Bitscore = 7.064790185778375
p-value = 0.0008546742243579757
e-value = 5.271630615839994

Alignment - 195 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGC

||||||||||||||||||| : -----

sequence2: CGAACTTTAAAATCTGTGTG-----G

Sequence Identity = 0.5555555555555556

Score = 60
Dtabase sequence range: 39 - 73
Query sequence range: 1 - 20
Length :36
Bitscore = 6.913608414852043
p-value = 0.0009941639603580717
e-value = 6.132003307488586

Alignment - 196 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCT-----
----G

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.4927536231884058

Score = 73

Dtabase sequence range: 39 - 72

Query sequence range: 1 - 68

Length :69

Bitscore = 7.005981734983059

p-value = 0.0009064436109147123

e-value = 5.590944192121945

Alignment - 197 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCT-----
----T

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:

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAAT
TAATAA

Sequence Identity = 0.4782608695652174

Score = 65

Dtabase sequence range: 39 - 71

Query sequence range: 1 - 68

Length :69

Bitscore = 6.948441467975697

p-value = 0.0009601303821587354

e-value = 5.922084197155081

Alignment - 198 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTCGG-----
----C

|||||||||||||||||||||

:

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCCAGTATAAT
TAATA

Sequence Identity = 0.47058823529411764

Score = 60

Dtabase sequence range: 39 - 70

Query sequence range: 1 - 67

Length :68

Bitscore = 6.913608414852043

p-value = 0.0009941639603580717

e-value = 6.132003307488586

Alignment - 199 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCGGC

||||||||||||||||||| : -----

sequence2: CGAACTTAAAATCTGTGT-----G

Sequence Identity = 0.5757575757575758

Score = 61

Dtabase sequence range: 39 - 70

Query sequence range: 1 - 19

Length :33

Bitscore = 6.920867096613726

p-value = 0.0009869737677807471

e-value = 6.087654199671648

Alignment - 200 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCACTCG-----
-G

||||||||||||||||||||||| :

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCCAGTATAAT
TA

Sequence Identity = 0.47692307692307695

Score = 61

Dtabase sequence range: 39 - 69

Query sequence range: 1 - 64

Length :65

Bitscore = 6.920867096613726

p-value = 0.0009869737677807471

e-value = 6.087654199671648

Alignment - 201 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTC-----G

||||||||||||||||||||||||| :

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAA

Sequence Identity = 0.4838709677419355

Score = 62

Dtabase sequence range: 39 - 68

Query sequence range: 1 - 61

Length :62

Bitscore = 6.927689735164614

p-value = 0.000980262921375244

e-value = 6.046261699042505

Alignment - 202 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTC-----C

||||||||||||||||||||| :

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTAT

Sequence Identity = 0.4833333333333334

Score = 60

Dtabase sequence range: 39 - 67

Query sequence range: 1 - 59

Length :60

Bitscore = 6.913608414852043

p-value = 0.0009941639603580717

e-value = 6.132003307488586

Alignment - 203 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCACTC

||||||||||||| :

sequence2: CGAACTTTAAAATCTGTG-----T

Sequence Identity = 0.6
Score = 62
Dtabase sequence range: 39 - 67
Query sequence range: 1 - 18
Length :30
Bitscore = 6.927689735164614
p-value = 0.000980262921375244
e-value = 6.046261699042505

Alignment - 204 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCAC-----T

||||||||||||||||||||||| : |||||

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAG

Sequence Identity = 0.49122807017543857
Score = 61
Dtabase sequence range: 39 - 66
Query sequence range: 1 - 56
Length :57
Bitscore = 6.920867096613726
p-value = 0.0009869737677807471
e-value = 6.087654199671648

Alignment - 205 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGTCAC-----C

||||||||||||||||||||||| : |||||

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACG

Sequence Identity = 0.5
Score = 62
Dtabase sequence range: 39 - 65
Query sequence range: 1 - 53
Length :54
Bitscore = 6.927689735164614
p-value = 0.000980262921375244
e-value = 6.046261699042505

Alignment - 206 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTCAC

||||||||||||||||| :

sequence2: CGAACTTAAAATCTGT-----G

Sequence Identity = 0.6071428571428571

Score = 60

Dtabase sequence range: 39 - 65

Query sequence range: 1 - 17

Length :28

Bitscore = 6.913608414852043

p-value = 0.0009941639603580717

e-value = 6.132003307488586

Alignment - 207 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTC-----A

||||||||||||||||| |

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC

Sequence Identity = 0.5192307692307693

Score = 60

Dtabase sequence range: 39 - 64

Query sequence range: 1 - 51

Length :52

Bitscore = 6.913608414852043

p-value = 0.0009941639603580717

e-value = 6.132003307488586

Alignment - 208 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTAAAATCTGTGTGGCTGTC-----C

||||||||||||| |

sequence2: CGAACTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCAC

Sequence Identity = 0.5306122448979592

Score = 61

Dtabase sequence range: 39 - 63

Query sequence range: 1 - 48

Length :49

Bitscore = 6.920867096613726

p-value = 0.0009869737677807471

e-value = 6.087654199671648

Alignment - 209 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTG-----T

||||||| :
|

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTG

Sequence Identity = 0.5217391304347826

Score = 62

Dtabase sequence range: 39 - 62

Query sequence range: 1 - 45

Length :46

Bitscore = 6.927689735164614

p-value = 0.000980262921375244

e-value = 6.046261699042505

Alignment - 210 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTGT

||||||| |

sequence2: CGAACTTTAAAATCTG-----T

Sequence Identity = 0.68

Score = 61

Dtabase sequence range: 39 - 62

Query sequence range: 1 - 16

Length :25

Bitscore = 6.920867096613726

p-value = 0.0009869737677807471

e-value = 6.087654199671648

Alignment - 211 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGCTG-----G

||||||| |

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAG

Sequence Identity = 0.5454545454545454
Score = 60
Dtabase sequence range: 39 - 61
Query sequence range: 1 - 43
Length :44
Bitscore = 6.913608414852043
p-value = 0.0009941639603580717
e-value = 6.132003307488586

Alignment - 212 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGC-----T

|||||||||||||||||| |

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCT

Sequence Identity = 0.5609756097560976
Score = 61
Dtabase sequence range: 39 - 60
Query sequence range: 1 - 40
Length :41
Bitscore = 6.920867096613726
p-value = 0.0009869737677807471
e-value = 6.087654199671648

Alignment - 213 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGG-----C

|||||||||||||||||| : |

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCAT

Sequence Identity = 0.5526315789473685
Score = 62
Dtabase sequence range: 39 - 59
Query sequence range: 1 - 37
Length :38
Bitscore = 6.927689735164614
p-value = 0.000980262921375244
e-value = 6.046261699042505

Alignment - 214 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 i

solate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTGGC

||||||| :

sequence2: CGAACTTTAAAATCT-----G

Sequence Identity = 0.6818181818181818

Score = 62

Dtabase sequence range: 39 - 59

Query sequence range: 1 - 15

Length :22

Bitscore = 6.927689735164614

p-value = 0.000980262921375244

e-value = 6.046261699042505

Alignment - 215 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTG-----G

||||||| :

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGC

Sequence Identity = 0.5555555555555556

Score = 60

Dtabase sequence range: 39 - 58

Query sequence range: 1 - 35

Length :36

Bitscore = 6.913608414852043

p-value = 0.0009941639603580717

e-value = 6.132003307488586

Alignment - 216 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTG-----G

||||||| :

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTCGGC

Sequence Identity = 0.5757575757575758

Score = 61

Dtabase sequence range: 39 - 57

Query sequence range: 1 - 32

Length :33

Bitscore = 6.920867096613726

p-value = 0.0009869737677807471
e-value = 6.087654199671648

Alignment - 217 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTGTG

||||||| :

sequence2: CGAACTTTAAAATC----T

Sequence Identity = 0.7
Score = 60
Dtabase sequence range: 39 - 57
Query sequence range: 1 - 14
Length :20
Bitscore = 6.913608414852043
p-value = 0.0009941639603580717
e-value = 6.132003307488586

Alignment - 218 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGTG-----T

||||||| :

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCACTC

Sequence Identity = 0.6
Score = 62
Dtabase sequence range: 39 - 56
Query sequence range: 1 - 29
Length :30
Bitscore = 6.927689735164614
p-value = 0.000980262921375244
e-value = 6.046261699042505

Alignment - 219 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGT-----G

||||||| :

sequence2: CGAACTTTAAAATCTGTGTGGCTGTCAC

Sequence Identity = 0.6071428571428571

Score = 60

Dtabase sequence range: 39 - 55

Query sequence range: 1 - 27

Length :28

Bitscore = 6.913608414852043

p-value = 0.0009941639603580717

e-value = 6.132003307488586

Alignment - 220 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTG-----T

||||||| | ||||| | |

sequence2: CGAACTTTAAAATCTGTGTGGCTGT

Sequence Identity = 0.68

Score = 61

Dtabase sequence range: 39 - 54

Query sequence range: 1 - 24

Length :25

Bitscore = 6.920867096613726

p-value = 0.0009869737677807471

e-value = 6.087654199671648

Alignment - 221 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCTGT

||||||| | | | | | :

sequence2: CGAACTTTAAAAT---C

Sequence Identity = 0.7647058823529411

Score = 61

Dtabase sequence range: 39 - 54

Query sequence range: 1 - 13

Length :17

Bitscore = 6.920867096613726

p-value = 0.0009869737677807471

e-value = 6.087654199671648

Alignment - 222 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATCT-----G

||||||| :

sequence2: CGAACTTTAAAATCTGTGTGGC

Sequence Identity = 0.6818181818181818

Score = 62

Dtabase sequence range: 39 - 53

Query sequence range: 1 - 21

Length :22

Bitscore = 6.927689735164614

p-value = 0.000980262921375244

e-value = 6.046261699042505

Alignment - 223 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATC-----T

||||||| :

sequence2: CGAACTTTAAAATCTGTGTG

Sequence Identity = 0.7

Score = 60

Dtabase sequence range: 39 - 52

Query sequence range: 1 - 19

Length :20

Bitscore = 6.913608414852043

p-value = 0.0009941639603580717

e-value = 6.132003307488586

Alignment - 224 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome

Sequence 2 = Query sequence

sequence1: CGAACTTTAAAAT---C

||||||| :

sequence2: CGAACTTTAAAATCTGT

Sequence Identity = 0.7647058823529411

Score = 61

Dtabase sequence range: 39 - 51

Query sequence range: 1 - 16

Length :17

Bitscore = 6.920867096613726
p-value = 0.0009869737677807471
e-value = 6.087654199671648

Alignment - 225 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAATC

||||||| :

sequence2: CGAACTTTAAAA-T

Sequence Identity = 0.8571428571428571
Score = 62
Dtabase sequence range: 39 - 51
Query sequence range: 1 - 12
Length :14
Bitscore = 6.927689735164614
p-value = 0.000980262921375244
e-value = 6.046261699042505

Alignment - 226 -----

Sequence 1 = >MN938384.1 Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-SZ-002a_2020, complete genome
Sequence 2 = Query sequence

sequence1: CGAACTTTAAAA-T

||||||| :

sequence2: CGAACTTTAAAATC

Sequence Identity = 0.8571428571428571
Score = 62
Dtabase sequence range: 39 - 50
Query sequence range: 1 - 13
Length :14
Bitscore = 6.927689735164614
p-value = 0.000980262921375244
e-value = 6.046261699042505

Total number of allignments in complete database = 226
Execution time : 1.0462868213653564 Seconds