

```
# Alineamiento de secuencias
from google.colab import drive
drive.mount("/content/drive")
```

```
with open ("/content/drive/MyDrive/examen.fasta/sequence (1).txt", "r") as archivo:
    secuencia = archivo.read ()
    print (secuencia)
```

```
Mounted at /content/drive
>lcl|MG674053.1_cds_AXR85408.1_1 [protein=beta-tubulin] [frame=3] [protein_id=AXR85408.1] [location=join(<1..13,127..168
GCTGCTTTCTGGCAGCAGATCTCAGGCGAGCACGGCTGGACAGCAATGGCGTGACACGGCACGTCGG
AGCTCCAGCTGGAGCGCATGAGCGTCTACTTCAACGAGGCTTCTGGCAACAAGTACGTCCCGCGTGCTGT
CCTGGTCGATCTCGAGCCGGTACCATGGACGCCGTCGCGCCGGTCTTTCTGGGCCAGCTTTTCCGCCCC
GACAACTTTGTCTTGGCCAGTCGGGTGCTGGCAACAACCTGGGCCAAGGGTCAC
```

```
from google.colab import drive
drive.mount("/content/drive")
```

```
with open ("/content/drive/MyDrive/examen.fasta/sequence (2).txt", "r") as archivo:
    secuencia = archivo.read ()
    print (secuencia)
```

```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=True)
>MZ436942.1 Harringtonia aguacate isolate C2964 large subunit ribosomal RNA gene, partial sequence
CAATAAGCGGAGGAAAGAAACCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAACAGCTCAAA
TTTGAAATCTGGCCCCCGCGGGCCGAGTTGTACTTTGGAGAGGACGCTTCTGGCGCGGCGCGGCCGA
GTGCCCTGGAACGGGCGCGGAGAGGGTGAGAGCCCGTACGGCCGGCCGCTAGCCTCTGCGAAGCTC
CTTCGACGAGTCGAGTAGTTTGGGAATGCTGCTCAAAATGGGAGGTAATTTCTTCTAAAGCTAAATACC
GGCCAGAGACCGATAGCGCACAAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGGGTTAAACA
GTACGTGAAATTGCTGAAAGGGAAGCGCCTGTGGCCAGACTTGCGCCCGCGGACACCCGGCGCCCGCG
CCGGGGCAGCCGCGGGGCGCAGGCCAGCATCGGCTCTCCAGGGGGACAAAGGCCGCGGAACGTAGCG
CCCTCGGGCGTGTTACAGCCCGCGGCCCATGCCCTGGGGGGGCCGAGG
```

```
!pip install biopython
```

```
Collecting biopython
  Downloading biopython-1.84-cp310-cp310-manylinux_2_17_x86_64.manylinux2014_x86_64.whl.metadata (12 kB)
Requirement already satisfied: numpy in /usr/local/lib/python3.10/dist-packages (from biopython) (1.26.4)
Downloading biopython-1.84-cp310-cp310-manylinux_2_17_x86_64.manylinux2014_x86_64.whl (3.2 MB)
3.2/3.2 MB 26.6 MB/s eta 0:00:00
Installing collected packages: biopython
Successfully installed biopython-1.84
```

```
from Bio import pairwise2
from Bio.Seq import Seq
from Bio.pairwise2 import format_alignment
```

```
/usr/local/lib/python3.10/dist-packages/Bio/pairwise2.py:278: BiopythonDeprecationWarning: Bio.pairwise2 has been deprecated, use Bio.pairwise2 module instead
warnings.warn(
```

```
#SECUENCIAS
```

```
seq1 = Seq("atctgtgggatcccgagaac")
seq2 = Seq("atgggttctcgggatccac")
```

```
alignments = pairwise2.align.globalxx(seq1, seq2)
```

```
for match in alignments:
    print(match)
```

```
Alignment(seqA='atctg--t---gggatcccgagaac', seqB='a--tgggttctcgggatccc---ac', score=14.0, start=0, end=26)
Alignment(seqA='atctg--t---gggatcccgagaac', seqB='at--gggttctcgggatccc---ac', score=14.0, start=0, end=26)
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