



## **IT 257 BIOINFORMATICS**

**SUBMITTED BY**

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to the

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## Task 1: Reading and Understanding a GenBank File

```
from Bio import SeqIO

# Path to the GenBank file file_path
= "sequence.gb"

# Read and process the sequence record
= SeqIO.read(file_path, "genbank")

# Print required details print("ID:", record.id) print("Sequence length:", len(record.seq))
print("Organism:", record.annotations.get("organism", "Unknown")) # Extracting
organism print("First 50 nucleotides:", record.seq[:50]) # Print first 50 bases
```

## Task 2: Modifying and Saving a Sequence

```
from Bio import SeqIO from
Bio.SeqRecord import SeqRecord
from Bio.Seq import Seq

# Path to the original GenBank file file_path
= "student_sequence.gb"

record = SeqIO.read(file_path, "genbank")

# Modify the sequence: remove the last 20 nucleotides and add an artificial tail
modified_seq = record.seq[:-20] + "AGCTAGCTAG"
```

```
# Create a new SeqRecord object with the modified
sequence modified_record = SeqRecord(
    Seq(modified_seq),
    id=record.id,
    name=record.name,
    description=record.description,
    annotations=record.annotations
)

# Path to the modified GenBank file modified_file_path
= "modified_sequence.gb"

# Save the modified sequence to a new file
SeqIO.write(modified_record, modified_file_path, "genbank")

# Print the new sequence and its length
print("Modified Sequence Length:", len(modified_seq))
print("New Sequence (first 50 bases):", modified_seq[:50])
```