* **At first,**I have chosen a FASTA file which includes the DNA sequences of **MAG: Alteromonas macleodii isolate SRR3965586\_bin.4\_MetaWRAP\_v1.3\_MAG ERZ505278.11097, whole genome shotgun sequence**

Source of FASTA File:<https://www.ncbi.nlm.nih.gov/nuccore/NZ_CATLUL010000280.1?report=fasta>

* **Secondly,**I have downloaded this fast file and uploaded it on my python script and copied the path of FASTA File to find the promoter and Start Codon.The promoter and Start Codon came out as this:

**Sequence\_NZ\_CATLUL010000280.1 Promoter:** GCATCAGTAAAAGGGCTAGTATCTCCGCCATTGGGGGCGATAGAGCCTGATTTGAAGGCAATGCCCGGCTGGTCGTTATACTCCATGGCTGCGCGCGCAATGATTTCAAGCTGATCGTAATTCGCTCGCCATGTTGCACGTAGTGCTTGTACTGAAACACCCTGAAGATCTTCGCTGTTGCACGGCACTTCTTCACCAAG

**Start Codon: TTG**

Before running this code, I installed bio python running the cell **pip install biopython.**

* **Thirdly, I** tried to find the start codon within the 30 bases of promoter sequence through python script, giving the necessary information in input.Unfortunately,after running the code it gives output as

**Start codon not found within 30 bases of the promoter sequence.**

* **At last,** After the start codon, I tried to look for at least 50 consecutive amino acids before a stop codon which may found or not through python script,where I added a codon table to translate the dna sequences into amino acid sequence first to get the output.Finally,it came as False and printed print **Gene not found.**