```
with open('dna_sequence-BI.txt','r') as file:
    dna_sequence = file.read().strip()

gc_content = (dna_sequence.count('G') + dna_sequence.count('C'))/len(dna_sequence)*100
print('GC content:',gc_content,'%')

motif_to_find = 'ATG'
motifs_found = [str(i) for i in range(len(dna_sequence)) if dna_sequence.startswith(motif_to_find,i)]
print('Motif',motif_to_find,'found at position:',','.join(motifs_found) if motifs_found else 'Motif'+motif_to_find+'not found in sequence

start_codon = 'ATG'
stop_codon = ['TAA','TAG','TGA']
coding_region = []

for i,codon in enumerate(dna_sequence):
    if dna_sequence[i:i+3] == start_codon:
        for j in range(i+3,len(dna_sequence),3):
            codon = dna_sequence[j:j+3]
            if codon in stop_codon:
                coding_region.append((i,j+3))
                break
        else:
            continue

if coding_region:
    print('Coding regions:')
    for start,end in coding_region:
        print('Start:',start,'End:',end)
else:
    print('No coding region found')
```

    GC content: 49.77777777777778 %
    Motif ATG found at position: 0
    Coding regions:
    Start: 0 End: 27

Start coding or generate with AI.
```
gc_content = (dna_sequence.count('G') + dna_sequence.count('C'))/len(dna_sequence)*100
print('GC content:',gc_content,'%')

motif_to_find = 'ATG'
motifs_found = [str(i) for i in range(len(dna_sequence)) if dna_sequence.startswith(motif_to_find,i)]
print('Motif',motif_to_find,'found at position:',','.join(motifs_found) if motifs_found else 'Motif'+motif_to_find+'not found in sequence
```