

```
1 #Exercise 1
2
3 def nt_id(seq):
4     if 'U' in seq:
5         return 'RNA'
6     elif 'T' in seq:
7         return 'DNA'
8     else:
9         return 'unk'
10
11 # if __name__ == '__main__':
12 #     seq = input('Enter a sequence: ')
13 #     print(nt_id(seq))
14
15
16 # Exercise 2
17
18 def stop_codon(seq):
19     if 'UGA' in seq or 'UAA' in seq or 'UAG' in seq :
20         return True
21     else:
22         return False
23
24 # if __name__ == '__main__':
25
26
27 # Exercise 3
28
29 def peptide_length(seq):
30     return len(seq) // 3
31
32 if __name__ == '__main__':
33     seq = input('Enter a sequence: ')
34     print(peptide_length(seq))
35
36
37 # Exercise 4
38
39 def cube_root(n):
40     try:
41         return float(n)**(1/3)
42     except:
43         return 'Invalid entry'
44
45 # if __name__ == '__main__':
```

```
46 # num = input('Enter a number: ')
47 # print(cube_root(num))
48
49
50 # Exercise 5
51
52 def sum_num(n1 = 0, n2 = 0, n3 = 0, n4 = 0):
53     return n1 + n2 + n3 + n4
54
55 # if __name__ == '__main__':
56 #     print(sum_num(5,6,7))
57
58
59 # Exercise 6
60
61 import assignment2
62 if assignment2.stop_codon(input('Enter an RNA sequence: ')) == True:
63     print('The sequence contains a stop codon.')
64 else:
65     print('The sequence does not contain a stop codon.')
66
```