

Complete the Python script below that asks the user to enter a number and prints the name of the sequence in dna2.fasta with length closest to that number (10 pts). For example if dna.txt contains

```
>human
ACACCGGTACCAG
>mouse
ACCAGAGGGGGTTTTAAACCACAGCG
>cat
AGTGTATGA
>dog
GTA
```

and the user entered 5 then the program should print **>dog** because its sequence has length closest to 5. If the user enters 9 then the program should print **>cat** because the **>cat** sequence has length exactly 9. Your program should work for any set of sequences in dna.fasta and not just for the example provided.

```
myfile = open("dna2.fasta", "r")
data=myfile.readlines()
for i in range(0, len(data), 1):
    data[i] = data[i].rstrip('\n')

userlength = input("Please enter sequence length ")
```