1. Write a bash script that prints the following five string variables (1 pt) and the length of all of the variables added together (1 pt).

- **Methionine**
- **Leucine**
- **Cysteine**
- **Alanine**
- **Valine**

nano Lab4question1.sh

```
#!/bin/bash

m="Methionine"
l="Leucine"
c="Cysteine"
a="Alanine"
v="Valine"

echo $m $l $c $a $v

allAdded=$((${#m} + ${#l} + ${#c} + ${#a} + ${#v}))

echo "The length of all of the variables added together is:" $allAdded
```

bash Lab4question1.sh

2. Write a bash script to count the number of start codons (ATG) (1 pt) and stop codons (TAA, TAG, TGA) (1 pt) from the example2.fasta file.

- **Please use variables for the start and stop codons and print out the count in a meaningful way.**
- **Remember that start codons only occur at the beginning of sequences and stop codons only occur at the end of sequences.**

```
#!/bin/bash


string_start="^ATG"

string_stop="TAA$|TAG$|TGA$"

egrep "$string_start" example2.fasta | wc -l

egrep "$string_stop" example2.fasta | wc -l
```

3. Write a bash script that prints the following:

- **Username (0.25 pt)**
- **Current directory (0.25 pt)**
- **Location of root directory (0.25 pt)**
- **Date/time (0.25 pt)**

```
nano lab4question3.sh

#!/bin/bash


whoami

echo $USER

echo $ROOT

date


Bash lab4question3.sh
```

4. Do the following commands compress or uncompress a file?

- **gunzip file.gz (0.25 pt)**

Compresses

- **tar -zxvf file.tar.gz (0.25 pt)**

  Uncompresses

- **zip file.zip file.txt file1.txt (0.25 pt)**

  Compresses

- **tar -zcvf file.tar.gz file.txt file1.txt (0.25 pt)**

  Compresses

5. Write an array in bash that contains these amino acids (0.25 pt):

- **Methionine**
- **Leucine**
- **Cysteine**
- **Alanine**
- **Valine**
- **Tyrosine**
- **Proline**

```
#!/bin/bash


array=("Methionine" "Leucine" "Cysteine" "Alanine" "Valine" "Tyrosine" "Proline")
```

Give the command to delete Alanine (0.25 pt)

```
unset 'array[3]'
```

Give the command to have print the aminos from Cysteine to Tyrosine (0.25 pt)

```
echo ${array[@]:2:3}
```

Give the command to add Histidine to the array (0.25 pt)

```
array+=('Histidine')

echo ${array[@]}
```

6. Give the command to count how many times the name 'abdul' is left to the name 'chi' in doppelganger_names.txt (0.5 pt). What is the count (0.5 pt)?

```
grep -cP "abdul\tchi" doppelganger_names.txt
```

The count is 8

7. Give an example of a legal variable name (0.5 pt) and an illegal variable name (0.5 pt).

Legal = myvar

Illegal = 1myvar

8. What are the commands to compile (0.5 pt) and run a bash script (0.5 pt)?

Chmod 777 script.sh

Bash script.sh

Bonus I (3 pts): Write a BASH code to iterate through the amino acid array.

- **Methionine**
- **Leucine**
- **Cysteine**
- **Alanine**
- **Valine**
- **Tyrosine**
- **Proline**