```python
# input and out file read and write

fd1 = open("proteinSeq", "r")

fd2 = open("mutationAAC", "r")

fd3 = open("mutateseq.fsa", "w+")

#line defining and counting from the inputfile fd2

Lines = fd2.readlines()

# read mutation one by one

for line in Lines:

        #print ("Lines{}:{}".format (count, line.strip()))

        #print (line.strip())

        mut = line.strip()

        pos = ""

        for i in mut:

                if i.isdigit():

            pos = pos + i

        exist_aa = mut[0]

        mutate_aa = mut[len(mut)-1]

        #print (exist_aa, mutate_aa)

        pos = int(pos)

        pos = pos-1

        #print (pos)

#finding seq position from the fd1 and definding from the mutated position required numbe writting the 17 mer fasta file as wt and mt to mutateseq.fsa

        fd1.seek(pos, 0)

        if (fd1.read(1) == exist_aa):

                fd1.seek(pos-8, 0)

                str = fd1.read(17)

                fd3.write(">WT")

                fd3.write(mut)
```

```python
fd3.write("\n")
fd3.write(str)
fd3.write("\n")
str = list(str)
str[9] = mutate_aa
str = ''.join(str)
fd3.write(">MT")
fd3.write(mut)
fd3.write("\n")
fd3.write(str)
fd3.write("\n")
```