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#####
#                                     #
# Solution of TPC2, 23 April 2025    #
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#                                     #
#####
```

```
.macro print (%ttt)
    li $v0, 4
    la $a0, %ttt
    syscall
.end_macro
```

```
.data
```

```
filename: .asciiz "dna.txt"
searchstring: .asciiz "TGGGTGCGTTTGCCACACGCCTTTTATTTGTCTAGCCGTAACCAGAA"
foundstring: .asciiz ">>>> FOUND!"
notfoundstring: .asciiz "NOT FOUND!!!!"
buffer: .space 256
```

```
.text
```

```
    la $a0, filename
    li $a1, 0
    li $a2, 0
    li $v0, 13
    syscall
    move $t9, $v0
```

```
readname:
```

```
    move $a0, $t9
    la $a1, buffer
    li $a2, 1
    li $v0, 14
    syscall                # read 1 char from file

    blez $v0, exiterror    # if read error then exit
    li $v0, 11
    lb $a0, buffer
    syscall                # print char
    beq $a0, 10, newline
    j readname
```

```
newline:
```

```
    move $t0, $zero        # $t0: match counter; how many letters are correct
```

```
readDNA:
```

```
    move $a0, $t9
    la $a1, buffer
    li $a2, 1
    li $v0, 14
    syscall                # read 1 char
    blez $v0, exiterror    # if read error then exit

    lb $t2, buffer         # in $t2 we have letter of sequence in file
    beq $t2, 10, readname  # if newline, we have a new name
    blez $t2, exitprogram  # if EoF end program
    la $a0, searchstring
    add $a0, $a0, $t0
    lb $t1, ($a0)          # in $t1 we now have letter char[$t0] of searchstring
    beqz $t1, match        # if end of searchstring we have found the sequence!
```

```

    bne $t2, $t1, mismatch # if mismatch then goto mismatch
    addi $t0, $t0, 1       # so far so good. $t0++
    j readDNA

mismatch:
    move $t0, $zero        # reset $t0 counter
    j readDNA              # continue

match:
    print foundstring      # print "FOUND!"

exitprogram:
    li $v0, 16
    move $a0, $t9
    syscall                # close file
terminate:
    li $v0, 10 # return(0)
    syscall

exiterror:
    print notfoundstring
    j exitprogram

```