```python
#!/usr/bin/env python3
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#ss will be replaced with the file, this class puts the restriction enzymes from a
file into a key value pair
def file_view(ss):
    fileRead = open(ss, "r")
    file = {}
    yes = 3
    key = ''
    value = ''
    for line in fileRead:
    # When file is created with the restriction enzype sequence to name then we can
finish the rest putting the key value pair into the dictionary file
        if yes == 0:
            key = line
            yes += 1
        elif yes == 1:
            value = line
            file[str(key)] = str(value)
            yes += 1
        elif 'yes' in line:
            yes = 0
    return file


# this function allows us to filnd all of the instances of a substring within a
string
def find_all(a_str, sub):
    start = 0
    while True:
        start = a_str.find(sub, start)
        if start == -1: return
        yield start
        # use start += 1 to find overlapping matches
        start += len(sub)


#This function finds which restriction enzymes are in the given sequence and their
positions
def combination(nucSeq, file):
    # this will include the restriction enzyme and its position
    enzymes = {}
    enzOrder = {}
    key_list = list(file.keys())
    val_list = list(file.values())
    # amend enzymes so it has the key as name and the value as its frequency
(number of times) and its position(s)
    for i in file.values():
        place = ""
        position = val_list.index(i)

        if i.strip() in nucSeq:
            position = val_list.index(i)
            #calls function made earlier
            find1 = find_all(nucSeq, i.strip())
            place1 = ""
            for j in find1:
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                place1 = place1 + str(j) + ', '
            place = place + place1

        n = nucSeq.count(i.strip())
        if n > 0:
            # number of times the restriction enzyme is found and their positions
            val = "Number of times found: " + str(n) + " positions:  " + str(place)
            val = val[:-1]
            val = val[:-1]
            enzymes[key_list[position]] =  val
            enzOrder[key_list[position]] = n

    return enzymes, enzOrder
#file_view and combination will be called here
def main():
    c = 0
    while True:
        #name of the file that ill output
        f = 'restriction_enzyme_result.txt'
        f1 = f
        #keeps track of outputted interations of this loop, adds a number to every
new output file created
        if c > 0:
            f = str(c) + f1
        inp = input("hello, please enter the nucleotide sequence you want searched
for restriction enzymes or enter 'e' to exit!")
        inp = inp.upper()
        if inp == 'E':
            return "Goodbye (:"
        else:
            #placeholder for file name, ss will be replaced
            file = file_view("restriction_enzymes_list.txt") #placeholder for file
name, ss will be replaced
            enzymes, enzOrder = combination(inp, file)

            #dict ordered by nymber of occurences of each enzyme
            enzOrder2 = dict(sorted(enzOrder.items(), key=lambda kv: kv[1]))

            with open(f, 'w') as f:
                f.write('Nucleotide Sequence: '+ inp + "\n Restriction Enzymes
Present: \n")
                for i in enzOrder2:
                    f.write(i.strip() + ': ' + enzymes[i] + '\n')
                f.write('Credit for for restriction enzyme list is due to
http://rebase.neb.com/rebase/azlist.re2.cy.html.\nSuppliers for these restriction
enzymes can also be found at that link.')
            # Here we ficure out what to do with the enzymes and their pisitions.
        #adds one to the iteration
        c +=1


main()
```