

## 4250 MCS

In modern molecular biology the genome of an organism is its hereditary information encoded in DNA. The genome includes both the genes and the non-coding sequences of the DNA. In the view of computer science, the genome can be regarded as a very long string consisting of only four letters  $\{A,G,T,C\}$ .

In order to study specific genetic diseases, it is very important to examine if there are DNA (substring) patterns which appear more frequently than others in a whole genome. Especially we are intended in finding “*compositionally equivalent*” substrings. A string  $P$  is said to be compositionally equivalent to a string  $Q$  if the number of 4 letters  $\{A,G,T,C\}$  appearing in  $P$  and  $Q$  is exactly the same. For example,  $P=“ATTATGC”$  is compositionally equivalent to  $Q=“GTATCTA”$  since the number of ‘A’, ‘G’, ‘C’ and ‘T’ in  $P$  is exactly same to that in  $Q$ , respectively. In the other hand, “TTGCA” is not compositionally equivalent to “TGCCA”.

In this problem we want to find the  $k$ -Major Composition Substring ( $k$ -MCS for short). For a genome string given,  $k$ -MCS is defined as the most frequently appearing substring of length  $k$  up to compositionally equivalence. Since the  $k$ -MCS for a given input genome is not necessarily unique, two or more different  $k$ -MCS could be possible. In the following,  $k$ -substring means a substring of length  $k$ .

Let us show one example. We have a genome string  $W=“GCAGGAGCGCCAGG”$  with length 14. There are many different compositionally equivalent 3-substrings such as GCA, CAG, GGA, GAG, . . . , CAG and AGG. In  $W$  it is easy to find that “AGG” is a 3-MCS which appears four times as AGG, GGA, GAG and AGG, since there is no other 3-substring (up to compositionally equivalence) which appears more than 4 times in  $W$ .

### Input

The input consists of  $T$  test cases. The number of test cases  $T$  is given in the first line of the input. Each test case (input genome) starts with the value  $k$  for  $k$ -MCS and the genome string  $W$ , where  $1 \leq k \leq 600$ . The length of the input genome string,  $|W|$ , is bounded by  $10 \leq |W| \leq 60000$ .

### Output

Your program is to write the number of occurrence of a  $k$ -MCS appearing in each genome string, on a line by itself.

### Sample Input

```
3
3 GCAGGAGCGCCAGG
4 AGTCCTTAGAG
5 GGGAGGGGGGTGGGGGGGT
```

### Sample Output

```
4
2
7
```