1334 – Genes in DNA

Your friend is a biologist. He has just sequenced a DNA and wants to know about contribution of different genes in that DNA. Both Gene and DNA can be represented by a sequence of letters or strings. Given the sequence of a DNA **D** and a Gene **G**; your friend uses following method to calculate the contribution.

1. Generate a list **P** of proper non-empty prefixes of **G** and another **S** of proper non-empty suffixes of **G** [1]. Additionally let the **L** is list of all strings that is concatenation of a prefix and a suffix. So if **G = ACCT** then **P = A, AC, ACC** and **S = T, CT, CCT** and **L = AT, ACT, ACCT, ACT, ACCT, ACCCT, ACCT, ACCCT, ACCCCT**. If **|G| = n** then it is obvious that size of **L** is $(n - 1)^2$.
2. For each element of **L**, count number of times it occurs as substring in **D**. Contribution of Gene **G** in DNA **D** is total of these values. For example if **D = ACTACCTACCCCT** then

AT	0
ACT	1
ACCT	1
ACT	1
ACCT	1
ACCCT	0
ACCT	1
ACCCT	0
ACCCCT	1
Total	**6**

As this process is very clumsy he wants to automate this process. As he is not a programmer, he needs your help. He will be very grateful if you kindly write him a program which will read the sequence of the DNA and the Gene, and will calculate contribution of the Gene in the DNA.

Input

Input starts with an integer **T (≤ 20)**, denoting the number of test cases.

Each case contains two lines. The first line contains a string denoting the sequence of DNA, and the second line contains another string denoting the Gene. The length of each string is less than **50000** and consists of only **A, C, T** and **G**.

Output

For each case, print the case number and the contribution, as described above.

Sample Input	Output for Sample Input
3 ACTACCTACCCCT ACCT AAA AAAA AAAA AAA	Case 1: 6 Case 2: 4 Case 3: 8

Note

1. Proper prefix (suffix) of a string **S** is a prefix (suffix) of length smaller than **|S|**. Here **|S|** denotes length of **S**.
2. Dataset is huge, use faster I/O methods.