

## Finding Substrings

You are given two DNA strings of length **N**. You are then given **Q** substrings of length **K**. You need to check whether those substrings exist in the two strings given to you.

### Input

The first line of the input contains two integers **N** ( $1 \leq N \leq 500$ ) and **K** ( $1 \leq K \leq 6$ ), where **N** is the length of those strings and **K** is the length of the substring that we are interested in. The second line contains the first string of length **N**. The third line contains the second string of length **N**. The next line contains an integer **Q** ( $1 \leq Q \leq 1,000$ ), denoting the number of substrings that we are interested in. The next **Q** lines contain the substrings of length **K**.

### Output

Print a single integer, each in a new line, for each substring:

- Print 0 if the substring does not belong to both strings.
- Print 1 if the substring is in first string but not second string.
- Print 2 if the substring is in second string but not first string.
- Print 3 if the substring is in both strings.

The last line of output should contain a newline character.

### Sample Input

```
6 2
ACGTAC
ACTGCA
6
AC
CG
AT
GT
TA
CA
```

### Sample Output

```
3
1
0
2
1
2
```

### Explanation

Find AC : ACGTAC ACTGCA  
 Find CG : ACGTAC ACTGCA  
 Find AT : ACGTAC ACTGCA (none)  
 Find GC : ACGTAC ACTGCA  
 Find TA : ACGTAC ACTGCA  
 Find CA : ACGTAC ACTGCA

### Skeleton

You are given the skeleton file **Find.java**

### Note

1. Your solution must be able to answer each query in **O(K)** time to pass all the given test cases, OK?