

Task: SUB

Count the Subsequences

UFAM Workshop, contest #5. Source file sub.* Available memory: 512 MB.

You have a DNA string $s[1..n]$ consisting of n characters from the set $\{\text{A, C, G, T}\}$, and you want to obtain answers to some q queries.

Each query is of form (l_i, r_i) and asks for the number of different nonempty subsequences that can be found in substring $s[l_i..r_i]$.

Input

In the first line of the input there are two integers n and q ($1 \leq n, q \leq 500\,000$). In the second line there is a string consisting of n characters from the set $\{\text{A, C, G, T}\}$. The following q lines contains queries; the i -th of these lines contains two integers l_i and r_i ($1 \leq l_i \leq r_i \leq n$) specifying the i -th query.

Output

Your program should output exactly q lines; the i -th line should contain one integer specifying the number of different nonempty subsequences in substring $s[l_i..r_i]$. Since these numbers can be quite big, output them modulo $10^9 + 7$.

Example

For the input data:

```
11 5
ACGAAATATAC
7 9
2 4
4 6
5 10
7 7
```

the correct result is:

```
6
7
3
27
1
```

Explanation of the example: For the first query substring TAT has 6 different nonempty subsequences: A, T, AT, TA, TT and TAT.