Alien DNA (prob11)

An alien species has a strange genome with a DNA sequence of only two types of nucleotides: A and B. A valid DNA sequence must also obey the constraint that no two A's can be adjacent in the sequence. For example, ABBAB is a valid sequence and BAABA is invalid. Such a DNA sequence has a natural orientation, so the reverse of a sequence is not necessarily the same as the original. For example, ABBAB and BABBA are considered two distinct sequences.

Dr. Watson is studying the alien DNA and he is interested in the number of possible sequences. Because the length n of a DNA sequence can be extremely large, it may be difficult to use the total number $f(n)$ of valid sequences directly. Instead, Dr. Watson would like to know the remainder of the number of sequences modulo m. (In a project for a future date but *not* today, using the Chinese Remainder Theorem, he should be able to recover the total number with properly chosen moduli.) You are to write a program to compute $f(n)$ mod m, the number of valid alien DNA sequences of a given length modulo m.

Input

There will be several sets of input. Each set will consist of two integers on a single line:
    n m

The first number, n ($1 \leq n \leq 8{,}000{,}000{,}000{,}000{,}000{,}000$), represents the length of a DNA sequence. The

second number, m ($1 \leq m \leq 2{,}000{,}000{,}000$), is the modulus for the operation. The input will be terminated by a line with two 0's.

Output

For each input set, print a single line containing one integer, specifying the number of valid DNA sequences modulo m. There should be no blank lines between outputs.

Sample Input

```
1 10
2 10
5 10
6 8
0 0
```

Sample Output

```
2
3
3
5
```