C. DNA Alignment

time limit per test: 2 seconds
memory limit per test: 256 megabytes
input: standard input
output: standard output

Vasya became interested in bioinformatics. He's going to write an article about similar cyclic DNA sequences, so he invented a new method for determining the similarity of cyclic sequences.

Let's assume that strings s and t have the same length n, then the function $h(s, t)$ is defined as the number of positions in which the respective symbols of s and t are *the same*. Function $h(s, t)$ can be used to define the function of Vasya distance $\rho(s, t)$:

where is obtained from string s, by applying left circular shift i times. For example,

$$\rho("AGC", "CGT") =$$
$$h("AGC", "CGT") + h("AGC", "GTC") + h("AGC", "TCG") +$$
$$h("GCA", "CGT") + h("GCA", "GTC") + h("GCA", "TCG") +$$
$$h("CAG", "CGT") + h("CAG", "GTC") + h("CAG", "TCG") =$$
$$1 + 1 + 0 + 0 + 1 + 1 + 1 + 0 + 1 = 6$$

Vasya found a string s of length n on the Internet. Now he wants to count how many strings t there are such that the Vasya distance from the string s attains maximum possible value. Formally speaking, t must satisfy the equation: .

Vasya could not try all possible strings to find an answer, so he needs your help. As the answer may be very large, count the number of such strings modulo $10^9 + 7$.

Input

The first line of the input contains a single integer n ($1 \le n \le 10^5$).

The second line of the input contains a single string of length n, consisting of characters "ACGT".

Output

Print a single number — the answer modulo $10^9 + 7$.

Examples

input
1 C
output
1

input
2 AG
output
4

input
3 TTT
output
1

Note

Please note that if for two distinct strings t_1 and t_2 values $\rho(s, t_1)$ и $\rho(s, t_2)$ are maximum among all possible t, then both strings must be taken into account in the answer even if one of them can be obtained by a circular shift of another one.

In the first sample, there is $\rho("C", "C") = 1$, for the remaining strings t of length 1 the value of $\rho(s, t)$ is 0.

In the second sample, $\rho("AG", "AG") = \rho("AG", "GA") = \rho("AG", "AA") = \rho("AG", "GG") = 4.$

In the third sample, $\rho("TTT", "TTT") = 27$