

Problem H

DNA Reconstruction

Time limit: 2s
Memory limit: 256MB

In bioinformatics, scientists often study DNA through short pieces of equal length, called K -mers. A DNA string is a string consisting only of the four characters A, C, G and T.

A DNA string of length $L \geq K$ yields $L - K + 1$ contiguous substrings of length K , starting at positions $1, 2, \dots, L - K + 1$. For example, for $K = 3$ the string ACGTA yields three K -mers: ACG, CGT and GTA.

After a sequencing experiment, the scientists obtained N pairwise distinct DNA fragments $S_1, S_2, \dots, S_N$, each of length exactly K . They want to reconstruct a shortest DNA string from these fragments.

A DNA string T is called *valid* if both of the following conditions hold:

- every S_i ($1 \leq i \leq N$) occurs at least once as a contiguous substring of T ;
- every contiguous substring of T of length K belongs to the set $\{S_1, S_2, \dots, S_N\}$.

Thus a fragment S_i may occur in T several times, but no K -mer outside the given list may occur in T .

Moreover, because of storage limits, the length of T must not exceed

$$N + K - 1 + R,$$

where R is a given non-negative integer.

Find the minimum length of a valid DNA string whose length does not exceed this limit. If no such string exists, print -1 .

Input

- The first line contains three integers N , K and R ($1 \leq N \leq 2 \cdot 10^5$, $2 \leq K \leq 12$, $0 \leq R \leq 15$).
- The i -th of the next N lines contains the string S_i , which has length exactly K and consists only of the characters A, C, G and T.

The strings $S_1, S_2, \dots, S_N$ are pairwise distinct.

Output

Print a single integer: the minimum length of a valid DNA string whose length is at most $N + K - 1 + R$, or -1 if no such string exists.

Sample Input	Sample Output
5 2 1 AC AG AT CG GA	7
5 2 0 AC AG AT CG GA	-1
2 3 9 ACT GGA	-1

Notes

In the first example, the string **ACGAGAT** has length 7 and contains all five given fragments; the fragment **GA** occurs in it twice. There is no valid string of length 6.

In the second example, at least 7 characters are needed to form a valid string, while the length limit is $5 + 2 - 1 + 0 = 6$.

In the third example, no string can contain both given fragments without also containing a 3-mer that is not in the list.