Problem 7

Description

One measure of ``unsortedness'' in a sequence is the number of pairs of entries that are out of order with respect to each other. For instance, in the letter sequence ``DAABEC'', this measure is 5, since D is greater than four letters to its right and E is greater than one letter to its right. This measure is called the number of inversions in the sequence. The sequence ``AACEDGG'' has only one inversion (E and D)---it is nearly sorted---while the sequence ``ZWQM'' has 6 inversions (it is as unsorted as can be---exactly the reverse of sorted).

You are responsible for cataloguing a sequence of DNA strings (sequences containing only the four letters A, C, G, and T). However, you want to catalog them, not in alphabetical order, but rather in order of ``sortedness'', from ``most sorted'' to ``least sorted''. All the strings are of the same length.

Input

The first line contains two integers: a positive integer n (0 < n <= 50) giving the length of the strings; and a positive integer m (0 < m <= 100) giving the number of strings. These are followed by m lines, each containing a string of length n.

Output

Output the list of input strings, arranged from ``most sorted'' to ``least sorted''. Since two strings can be equally sorted, then output them according to the original order.

Sample Input

```
10 6
AACATGAAGG
TTTTGGCCAA
TTTGGCCAAA
GATCAGATTT
CCCGGGGGGA
ATCGATGCAT
```

Sample Output

```
CCCGGGGGGA
AACATGAAGG
GATCAGATTT
ATCGATGCAT
TTTTGGCCAA
TTTGGCCAAA
```