RNA Origami

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C++ — 2 SEC — 512 MB

A team of biologists is analysing how a single strand of RNA folds in solution. The RNA strand is comprised of four different molecules, called bases: Adenine (A), Cytosine (C), Guanine (G), and Uracil (U). These bases interact with each other, forming bonds between specific pairs. Adenine can only interact with Uracil and Guanine can only interact with Cytosine. Each base can only be involved with exactly one bonding interaction.

The specific set of bonding interactions determines how the RNA strand folds. A *perfect* folding has every base involved in a bonding interaction. Further, to prevent the RNA from knotting itself, no two bonding interactions are allowed to cross, as demonstrated in the SAMPLE. For an RNA strand to possess a *perfect* folding, it must have an equal number of Adenine and Uracil bases, and an equal number of Cytosine and Guanine bases.

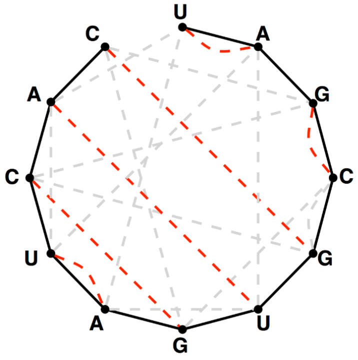
In order to determine how a given RNA strand folds, the biologists want to count the number of *perfect* foldings.

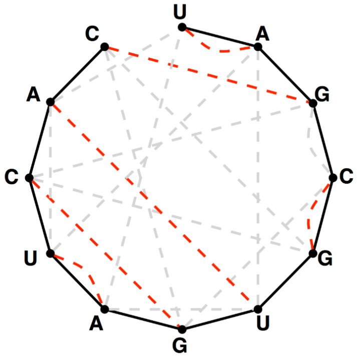
INPUT You will be given a string of length **n**, representing an RNA strand. It will contain the same number of occurrences of A as U, and the same number of occurrences of C as G.

$1 \leq \mathbf{n} \leq 3000$

OUTPUT Output a single integer, **p**, giving the number of different *perfect* foldings possessed by the RNA strand.

SAMPLE For example, consider the RNA strand `UAGCGUGAUCAC`. This strand possesses only 2 *perfect* foldings (all bases involved in a bonding interaction and no bonding interactions crossing), shown below.





INPUT	**OUTPUT**
`UAGCGUGAUCAC`	2
`AUCUCGCGAGAU`	4
`AAGCGCGCCGUUACGGGCCU`	10