**Principle:**

This problem is based on the reverse complement problem, only now you only need the reverse complement of a half site, then check whether it follows said "half site". So, for sites of a given length:

* go through the sequence from beginning to end, taking each subsequence of half this length consequtively
* compute the reverse complement of the half site
* use string.find to check whether the following bases contain the reverse complement of the half-site
* if so (= find does not return -1), add to the list of "restriction sites"
* add 1 to the position to get the normal base counting starting at 1 rather than Python's 0.

**Any advanced information**

This method only finds "restriction sites" that are complete reverse palidromes and thus consist of an even number of bases. In reality, 5-base sites also occur, the middle base is then often either A/G (IUPAC code R) or C/T (IUPAC code Y), i.e. several possible sequences can be cut by such an enzyme.