

Problem PROTEINS: Protein Similarity

Proteins are responsible for almost everything that goes on in our body. All proteins are built up of only twenty amino acids which are chained together in countless variations. It is common to abbreviate the amino acids by a three letter code, e.g. SER for Serin, LEU for Leucin, etc. One of the interesting tasks in bioinformatics is to determine the similarity of two proteins. One way of doing so, is to align the proteins and compute a score for the alignment. Take e.g. the two amino acid sequences SER SER CYS ASP LEU SER CYS and SER CYS CYS ASP ASP LEU CYS SER ASP ASP CYS. One possible alignment is

```
SER CYS CYS ASP ASP LEU CYS SER ASP ASP CYS
|         |         | |         |         |
SER SER CYS ____ ASP LEU ____ SER ____ ____ CYS
```

As you can see, there are amino acids that **match** in both sequences (e.g. SER at the beginning), amino acids that **do not match** (CYS and SER at the second position) and **gaps** in either of the sequences (indicated by ____). Each of the three situations gets a distinct score value. Suppose a match gets a score of 2, a mismatch a score of -1 and a gap a score of -2 (also called *gap penalty*) then the overall score of the alignment above is 3. The higher the score the more similar the two sequences are. Of course there is more than just one alignment for both sequences resulting in different scores. Your task will be to find out the score for the best alignment. Please note that in the final alignment both the shorter and the longer sequence may be filled up with gaps.

Input

The input consists of a bunch of test cases. Each test case is built up of three lines. In the first line the three scores are given as integer values separated by a space (the match score is always non-negative, the other two are always non-positive). The first value is the match score, the second the mismatch score and the third the gap penalty. Then the two proteins follow in the next two lines. They are given as the chain of the three letter codes of their amino acids. There are a maximum of twenty different amino acids. The last test case is terminated by EOF. The sequences will not be longer than 10.000 amino acids.

Output

Your program should output the maximal score for the alignment of each sequence pair as an integer value, each in its own line.

Sample Input 1

```
1 0 0
SERCYSCYASASPSPLEUCYSSERASPCYS
SERSERCYASASPSPLEUSERCYS
2 -1 -2
SERCYSCYASASPSPLEUCYSSERASPCYS
SERSERCYASASPSPLEUSERCYS
```

Sample Output 1

```
6
3
```