
Aminoacid Triplets U47389_en

Write a program that processes a sequence of cases. Each case consists of three names of aminoacid types A, B, C, followed by a protein (a sequence of aminoacid codes) ended with the word `END`. For each case, the program must list the triplets of consecutive amioacids in the protein such as the first one belongs to type A, the second to type B, and the third to type C. The total amount of found triplets for each protein must also be printed.

The known aminoacid codes are: `ala` (alanine), `arg` (arginine), `asn` (asparagine), `asp` (aspartic acid), `cys` (cysteine), `gln` (glutamine), `glu` (glutamic acid), `gly` (glycine), `his` (histidine), `ile` (isoleucine), `leu` (leucine), `lys` (lysine), `met` (methionine), `phe` (phenylalanine), `pro` (proline), `ser` (serine), `thr` (threonine), `trp` (tryptophan), `tyr` (tyrosine), `val` (valine).

The aminoacid types are:

```
aliphatic: ['ala', 'gly', 'ile', 'leu', 'pro', 'val']
aromatic: ['phe', 'trp', 'tyr']
acidic: ['asp', 'glu']
basic: ['arg', 'his', 'lys']
hydroxylic: ['ser', 'thr']
sulphur: ['cys', 'met']
amidic: ['asn', 'gln']
```

Input

The input is a sequence of cases. Each case starts with three aminoacid types. Then, a sequence of aminoacid codes follows, ended with the word `END`. There are no restrictions on the length of the protein.

Output

The output is, for each case, the list of consecutive triplets matching the three given types, plus the total number of found triplets. Print a blank line after each case. Follow the format of the examples.

Sample input 1

```
basic sulphur aliphatic
   phe lys leu tyr val lys met ala val val lys asn his
   arg cys gly ala ala END
sulphur basic acidic
   lys cys his asp ile glu val pro END
hydroxylic hydroxylic sulphur
   thr lys glu asp leu gln thr cys thr cys cys tyr thr
   phe asp his met ser ser END
amidic acidic amidic
   gln glu gln asn asp asn trp gly pro pro asn val
   asn glu asn ile ala gln asp gln END
basic basic basic
   his his arg phe arg lys lys pro END
sulphur hydroxylic aliphatic
   trp gln trp met thr leu cys asn glu lys glu ala met
   asn phe ser lys pro trp lys thr asp met ser gly val
   thr glu thr tyr phe END
```

Sample output 1

```
Triplets basic-sulphur-aliphatic in protein 1:
lys met ala
arg cys gly
Total: 2

Triplets sulphur-basic-acidic in protein 2:
cys his asp
Total: 1

Triplets hydroxylic-hydroxylic-sulphur in protein 3:
Total: 0

Triplets amidic-acidic-amidic in protein 4:
gln glu gln
asn asp asn
asn glu asn
gln asp gln
Total: 4

Triplets basic-basic-basic in protein 5:
his his arg
arg lys lys
Total: 2

Triplets sulphur-hydroxylic-aliphatic in protein 6:
met thr leu
met ser gly
Total: 2
```

Sample input 2

```
aliphatic aromatic aliphatic
   ala phe gly trp ile tyr leu phe pro trp val tyr gly END
aliphatic aliphatic aliphatic
   ala ala gly ile ala ala pro asp gln END
```

Sample output 2

```
Triplets aliphatic-aromatic-aliphatic in protein 1:
ala phe gly
gly trp ile
ile tyr leu
leu phe pro
pro trp val
val tyr gly
Total: 6

Triplets aliphatic-aliphatic-aliphatic in protein 2:
ala ala gly
ala gly ile
gly ile ala
ile ala ala
ala ala pro
Total: 5
```

Sample input 3

```
aliphatic hydroxylic acidic
   gly gly ile ser glu lys trp trp lys pro trp ser thr gly val thr his END
hydroxylic acidic aromatic
   thr tyr END
basic hydroxylic aromatic
   gln END
basic basic hydroxylic
   glu tyr cys pro lys tyr his his END
amidic amidic basic
   END
```

Sample output 3

```
Triplets aliphatic-hydroxylic-acidic in protein 1:
ile ser glu
Total: 1

Triplets hydroxylic-acidic-aromatic in protein 2:
Total: 0

Triplets basic-hydroxylic-aromatic in protein 3:
Total: 0

Triplets basic-basic-hydroxylic in protein 4:
Total: 0

Triplets amidic-amidic-basic in protein 5:
Total: 0
```

Observation

Note 1: You can use any data structure you find useful to store which aminoacids belong to which group.

Note 2: Solutions storing the whole aminoacid sequence will receive a severe score penalty.

Problem information

Author: Lluís Padró

Generation: 2026-01-25T13:00:41.950Z