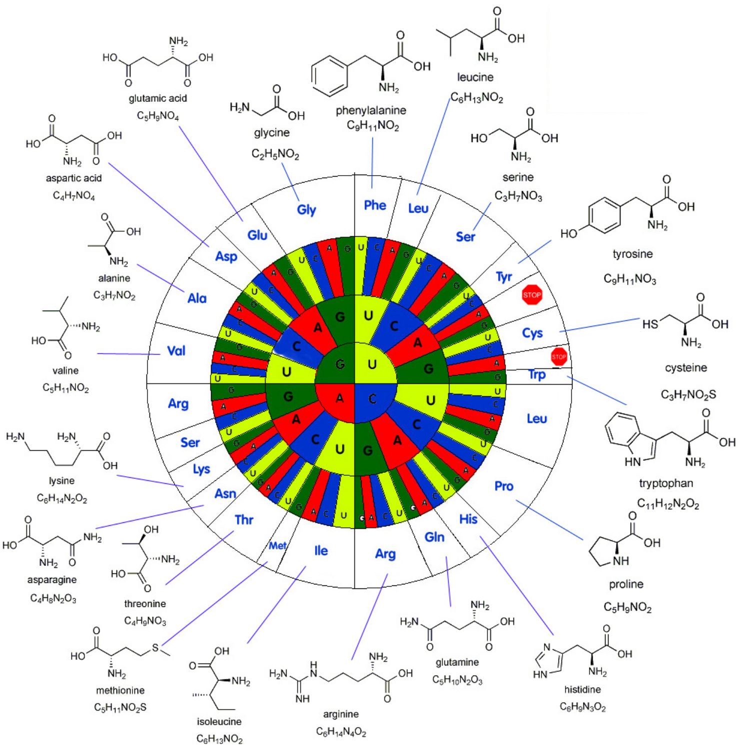
Genetic code P36671_en

Write a program that converts chains of messenger RNA (derived sequences of DNA) to proteins using the genetic code.

The genetic code is a set of rules that translates the sequences of messenger RNA to proteins. A sequence of messenger RNA is a sequence of bases. There are four possible bases: @A@, @C@, @G@ and @U@. The bases of genes are grouped in threes forming codons. Every codon corresponds to an amino acid. A protein is a sequence of amino acids.

The following figure shows the genetic code. It can be seen, for instance, that the codon @GGA@ corresponds to glycine and that the codon @AUC@ corresponds to isoleucine. There are also three special codons, marked with the stop symbol, that do not encode any amino acid, but indicate the end of codification. Once a stop codon is found, the gene is finished (an AUG does not have to be searched after). Moreover, proteins only start to be synthesized from the first appearance of the codon @AUG@. Thus, an imaginari gene @GCCAAUGACUAAGGCCUAAAGA@ would correspond to the protein @ThrLysAla@.



Input

Input is a gene obtained from the GeneBank, a genome bank that can be consulted on the Internet. This gene consists of a brief finished in ‘:’ followed by the sequence of messenger RNA bases corresponding to this gene. It always appears a @AUG@ codon before a Stop codon.

Output

The output must be the protein synthesized by this gene according the previous rules of the genetic code. Your program must print the sequence using the standard names of three letters for each amino acid. For each line, print 26 amino acids, except the last one, that may contain less.

Sample input 1

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Small test:
GCCAAUGACUAAGGCCUAAAGA
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Sample output 1

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ThrLysAla
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Sample input 2

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Hepatitis C virus, partial genome:
UUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCCGGGAGGUCUCGUAGACCGUGCACCAUGAGCACG
AAUCCUAAACCUCAAAGAAAAACCAAACGUAACACCAACCGUCGCCCACAGGACGUCAAGUUCCCGGGUG
GCGGUCAGAUCGUUGGUGGAGUUUACUUGUUGCCGCGCAGGGGCCCUAGAUUGGGUGUGCGCGCGACGAG
GAAGACUUCCGAGCGGUCGCAACCUCGAGGUAGACGUCAGCCUAUCCCCAAGGCACGUCGGCCCGAGGGC
AGGACCUGGGCUCAGCCCGGGUACCCUUGGCCCCUCUAUGGCAAUGAGGGUUGCGGGUGGGCGGGAUGGC
UCCUGUCUCCCCGUGGCUCUCGGCCUAGCUGGGGCCCCACAGACCCCCGGCGUAGGUCGCGCAAUUUGGG
UAAGGUCAUCGAUACCCUUACGUGCGGCUUCGCCGACCUCAUGGGGUACAUACCGCUCGUCGGCGCCCCU
CUUGGAGGCGCUGCCAGGGCCCUGGCGCAUGGCGUCCGGGUUCUGGAAGACGGCGUGAACUAUGCAACAG
GGAACCUUCCUGGUUGCUCUUUCUCUAUCUUCCUUCUGGCCCUGCUCUCUUGCCUGACUGUGCCCGCUUC
AGCGUUGGUGGUAGCUCAGCUGCUCCGGAUCCCACAAGCCAUCAUGGACAUGAUCGCUGGUGCUCACUGG
GGAGUCCUGGCGGGCAUAGCGUAUUUCUCCAUGGUGGGGAACUGGGCGAAGGUCCUGGUAGUGCUGCUGC
UAUUUGCCGGCGUCGACGCGGAAACCCACGUCACCGGGGGAAGUGCCGGCCGCACCACGGCUGGGCUUGU
UGGUCUCCUUACACCAGGCGCCAAGCAGAACAUCCAACUGAUCAACACCAACGGCAGUUGGCACAUCAAU
AGCACGGCCUUGAACUGCAAUGAAAGCCUUAACACCGGCUGGUUAGCAGGGCUCUUCUAUCAGCACAAAU
UCAACUCUUCAGGCUGUCCUGAGAGGUUGGCCAGCUGCCGACGCCUUACCGAUUUUGCCCAGGGCUGGGG
UCCUAUCAGUUAUGCCAACGGAAGCGGCCUCGACGAACGCCCCUACUGCUGGCACUAACCUCCAAGACCU
```

Sample output 2

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SerThrAsnProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPheProGlyGly
GlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeuGlyValArgAlaThrArgLysThrSer
GluArgSerGlnProArgGlyArgArgGlnProIleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnPro
GlyTyrProTrpProLeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArgPro
SerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysValIleAspThrLeuThrCysGlyPheAla
AspLeuMetGlyTyrIleProLeuValGlyAlaProLeuGlyGlyAlaAlaArgAlaLeuAlaHisGlyValArgVal
LeuGluAspGlyValAsnTyrAlaThrGlyAsnLeuProGlyCysSerPheSerIlePheLeuLeuAlaLeuLeuSer
CysLeuThrValProAlaSerAlaLeuValValAlaGlnLeuLeuArgIleProGlnAlaIleMetAspMetIleAla
GlyAlaHisTrpGlyValLeuAlaGlyIleAlaTyrPheSerMetValGlyAsnTrpAlaLysValLeuValValLeu
LeuLeuPheAlaGlyValAspAlaGluThrHisValThrGlyGlySerAlaGlyArgThrThrAlaGlyLeuValGly
LeuLeuThrProGlyAlaLysGlnAsnIleGlnLeuIleAsnThrAsnGlySerTrpHisIleAsnSerThrAlaLeu
AsnCysAsnGluSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrGlnHisLysPheAsnSerSerGlyCysPro
GluArgLeuAlaSerCysArgArgLeuThrAspPheAlaGlnGlyTrpGlyProIleSerTyrAlaAsnGlySerGly
LeuAspGluArgProTyrCysTrpHis
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Observation

The second instance is an artificial extract of genome of hepatitis C virus.The private test datas contain the complete genome (10 kilobases).

Problem information

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Generation: 2026-01-25T10:29:54.603Z