



## How to Translate DNA to its Amino Acid Chain

**Description:** This algorithm takes in a strand of DNA as its input and returns the first amino acid chain that can be found within the strand. The program will iterate through a valid DNA strand and look at each codon until the codon ATG is found, which will start the amino acid chain. After that, the amino acid that corresponds to the next codon is added to the output list, until one of the END codons (TAA, TGA, or TAG) is found. The program ends with the chain of amino acids being printed out.

**Step 1:** User inputs a valid strand of DNA

- a. Valid strand of DNA:
  - i. Contains only A's, C's, T's, and G's
  - ii. Has no spaces, numbers, or other letters
  - iii. Must contain at least 3 bases
  - iv. Examples of invalid DNA strands:
    1. ACGT AGTCTCGTA
    2. ASDJASDJASDPROAJAGF
    3. AC
    4. ASDJASCJ#\$\*%R&JQ@@@J
    5. 2jsdajhd364r6v92hv

**Step 2:** Begin to iterate through the DNA strand by looking at groups of 3 bases to find the first occurrence of ATG

**Step 3:** Once ATG is found, add "Met" to the output list.

**Step 4:** Advance to the next codon and add the corresponding amino acid to the output list.

**Step 5:** Once either TAA, TGA, or TAG, or the DNA strand ends, end the process and the output list will contain the first chain of amino acids for the DNA strand.

