

Objective: Identify segments of DNA which code for a specific amino acid.

Background Information: Open Reading Frames is a tactic for determining which segments of DNA actually code for a protein and therefore might be genes. There are three nucleotide triplets that don't have a corresponding tRNA, and therefore do not code for an amino acid: TAA, TAG, & TGA. The other 61 codons do have corresponding tRNAs in the cytoplasm and therefore code for an amino acid. If one was to randomly generate a sequence of G's, A's, C's, and T's, the chances of encountering a TAA, TAG, or TGA, would be 3/64, or about 1 in 20. It would be unlikely to find a random sequence of more than 50-60 nucleotides without encountering three nucleotides in a row that specify a stop codon.

Materials:

- 12 lettered beads
- Twine
- Nucleotide/amino acid table

Procedure:

1. Randomly select 12 lettered beads.
2. Cut twine to fit wrist.
3. Randomly thread beads through twine and have a partner help tie onto your wrist.
4. Using the nucleotide/amino acid table, identify possible reading frames on your bracelet.

	T	C	A	G
T	TTT Phe (F) TTC " TTA Leu (L) TTG "	TCT Ser (S) TCC " TCA " TCG "	TAT Tyr (Y) TAC TAA Stop TAG Stop	TGT Cys (C) TGC TGA Stop TGG Trp (W)
C	CTT Leu (L) CTC " CTA " CTG "	CCT Pro (P) CCC " CCA " CCG "	CAT His (H) CAC " CAA Gln (Q) CAG "	CGT Arg (R) CGC " CGA " CGG "
A	ATT Ile (I) ATC " ATA " ATG Met (M)	ACT Thr (T) ACC " ACA " ACG "	AAT Asn (N) AAC " AAA Lys (K) AAG "	AGT Ser (S) AGC " AGA Arg (R) AGG "
G	GTT Val (V) GTC " GTA " GTG "	GCT Ala (A) GCC " GCA " GCG "	GAT Asp (D) GAC " GAA Glu (E) GAG "	GGT Gly (G) GGC " GGA " GGG "

