#### Task 1

In a file called transcriptic\_test\_1.py define two functions, robotize(well) and humanize(well). These functions should convert well references declared in robot form (each well is represented by an integer, indexed from zero row-wise) to human form (ex: "A1") and vice-versa. Assume a 96-well plate containing 8 rows labeled A-H and 12 columns labeled 1-12. You may also write other helper functions or import packages if you feel the need to. Add assertions and/or tests to make sure all wells are represented.

#### Task 2

In a file called transcriptic\_test\_2.py write a Python script that takes a cDNA sequence of any given length and optionally prints out either its RNA translation or all of the possible in frame sequences that result in a (theoretically) valid protein (including start and stop codon). Your script should take an operation and filename from the command line, and print its output to standard out. For example:

## \$ cat dna.txt

## \$ python transcriptic test 2.py --rna dna.txt

#### \$ python transcriptic test 2.py --genes dna.txt

1 valid protein(s) can be produced from this sequence:

DNA: ATGACGGCTTGTTTCTTTTCTGTGGCTGCGTGA
RNA: AUGACGGCUUGUUUCUUUUCUGUGGCUGCGUGA

amino acid sequence: MTACFFSVAA.

Use the following codon table (next page):

### RNA codon table

	2nd position				
1st position	٦	C	Α	G	3rd position
U	Phe Phe Leu Leu	Ser Ser Ser	Tyr Tyr stop stop	Cys Cys stop Trp	⊃∪∢G
С	Leu Leu Leu	Pro Pro Pro	His His HGIn	Arg Arg Arg Arg	U C A G
Α	ee ee t	Thr Thr Thr Thr	Asn Asn Lys Lys	Ser Ser Arg Arg	<b>⊃</b> ∪ < G
G	Val Val Val	Ala Ala Ala	Asp Asp Glu	Gly Gly Gly	U C ≪ G
	Annual Control Control				

# Amino Acids

Ala: Alanine Arg: Arginine Asn: Asparagine Asp:Aspartic acid Cys:Cysteine Gln: Glutamine Glu: Glutamic acid Gly: Glycine

Gly: Glycine
His: Histidine
Ile: Isoleucine

Leu: Leucine Lys: Lysine Met: Methionine Phe: Phenylalanine Pro: Proline Ser: Serine Thr: Threonine Trp: Tryptophane Tyr: Tyrosisne Val: Valine