##Original code by Jonathan C Goulding, Adapted to Py3 and Modified by Harrison R S Milton, based on Milton, N.G.N. (2006) Anti-sense Peptides. Protocols 6.39 In Cell Biology Protocols, Eds D. Rickwood, J. Graham & J.R. Harris, Wiley, London, pp 353-358. © J.C. Goulding, H.R.S. Milton & N.G.N. Milton; Neurodelta Ltd.

g=input("Input name: ")

s=input("Input coding mRNA: ")

i=s.replace(' ', '').replace('0', '').replace('1', '').replace('2', '').replace('3', '').replace('4', '').replace('5', '').replace('6', '').replace('7', '').replace('8', '').replace('9', '').replace('A', 'a').replace('C', 'c').replace('G', 'g').replace('T', 't').replace('U', 't').replace('u', 't').replace('\n', '')

def breakdown(data):

array=[]

for i in range(0,len(data),3):

if (i+3>len(data)):

upper = len(data)

else:

upper =i+3

seq=data[i:upper]

try:

array.append(amino\_acids[seq])

except KeyError :

array.append('unknown')

return array

def flip(x):

return x[::-1]

amino\_acids = {'aaa':'K','aac':'N','aag':'K','aat':'N','aca':'T','acc':'T','acg':'T','act':'T','aga':'R','agc':'S','agg':'R','agt':'S','ata':'I','atc':'I','atg':'M','att':'I','caa':'Q','cac':'H','cag':'Q','cat':'H','cca':'P','ccc':'P','ccg':'P','cct':'P','cga':'R','cgc':'R','cgg':'R','cgt':'R','cta':'L','ctc':'L','ctg':'L','ctt':'L','gaa':'E','gac':'D','gag':'E','gat':'D','gca':'A','gcc':'A','gcg':'A','gct':'A','gga':'G','ggc':'G','ggg':'G','ggt':'G','gta':'V','gtc':'V','gtg':'V','gtt':'V','tac':'Y','tat':'Y','tca':'S','tcc':'S','tcg':'S','tct':'S','tgc':'C','tgg':'W','tgt':'C','tta':'L','ttc':'F','ttg':'L','ttt':'F','taa':'\*','tga':'\*','tag':'\*'}

output=breakdown(i)

combined=''

for acid in output:

combined =combined+acid

print ("")

print("SNC -",g,"=",combined)

d=flip(combined)

print ("")

print("SCN -",g,"=",d)

amino\_acids = {'aaa':'F','aac':'L','aag':'F','aat':'L','aca':'C','acc':'W','acg':'C','act':'X','aga':'S','agc':'S','agg':'S','agt':'S','ata':'Y','atc':'X','atg':'Y','att':'X','caa':'V','cac':'V','cag':'V','cat':'V','cca':'G','ccc':'G','ccg':'G','cct':'G','cga':'A','cgc':'A','cgg':'A','cgt':'A','cta':'D','ctc':'E','ctg':'D','ctt':'E','gaa':'L','gac':'L','gag':'L','gat':'L','gca':'R','gcc':'R','gcg':'R','gct':'R','gga':'P','ggc':'P','ggg':'P','ggt':'P','gta':'H','gtc':'Q','gtg':'H','gtt':'Q','tac':'M','tat':'I','tca':'S','tcc':'R','tcg':'S','tct':'R','tgc':'T','tgg':'T','tgt':'T','tta':'N','ttc':'K','ttg':'N','ttt':'K','taa':'\*','tga':'\*','tag':'\*'}

output=breakdown(i)

combined=''

for acid in output:

combined =combined+acid

print ("")

print("AS35NC -",g,"=",combined)

e=flip(combined)

print ("")

print("AS35CN -",g,"=",e)

amino\_acids = {'aaa':'F','aac':'V','aag':'L','aat':'I','aca':'C','acc':'G','acg':'R','act':'S','aga':'S','agc':'A','agg':'P','agt':'T','ata':'Y','atc':'D','atg':'H','att':'N','caa':'L','cac':'V','cag':'L','cat':'M','cca':'W','ccc':'G','ccg':'R','cct':'R','cga':'S','cgc':'A','cgg':'P','cgt':'T','cta':'X','ctc':'E','ctg':'Q','ctt':'K','gaa':'F','gac':'V','gag':'L','gat':'I','gca':'C','gcc':'G','gcg':'R','gct':'S','gga':'S','ggc':'A','ggg':'P','ggt':'T','gta':'Y','gtc':'D','gtg':'H','gtt':'N','tac':'V','tat':'I','tca':'X','tcc':'G','tcg':'R','tct':'R','tgc':'A','tgg':'P','tgt':'T','tta':'X','ttc':'E','ttg':'Q','ttt':'K','taa':'\*','tga':'\*','tag':'\*'}

output=breakdown(i)

combined=''

for acid in output:

combined =combined+acid

print ("")

print("AS53NC -",g,"=",combined)

d=flip(combined)

print ("")

print("AS53CN -",g,"=",d)