

In [1]:

```
# This is done in Jupyter notebook. Any online python compiler would work
# e.g. copy the code and run it at https://www.online-python.com/

# assign your target amino acid sequence to input_AA as a string, between the ""
## spaces in amino acid sequence are allowed
## stop codon must be a '*'

#target amino acid sequence
input_AA = "MVKSGEAVIKFEFMRFKVH MEGSMNGHEFEIE GEG EG*"

input_AA = input_AA.replace(" ", "")
dna = []
d_codon_10 = {'A': 'GCT',
              'C': 'TGC',
              'D': 'GAT',
              'E': 'GAG',
              'F': 'TTC',
              'G': 'GGA',
              'H': 'CAT',
              'I': 'ATC',
              'K': 'AAG',
              'L': 'CTC',
              'M': 'ATG',
              'N': 'AAT',
              'P': 'CCT',
              'Q': 'CAG',
              'R': 'AGA',
              'S': 'TCT',
              'T': 'ACT',
              'V': 'GTG',
              'W': 'TGG',
              'Y': 'TAC',
              '*': 'TGA'}

for i in input_AA.strip():
    dna.append(d_codon_10[i])
opt_dna = ''.join(dna)

print("optimized Pristionchus top 10% highest used codons\n", opt_dna , sep='\n')

# Improving transgenesis efficiency and CRISPR-associated tools
# through codon optimization and native intron addition in
# Pristionchus nematodes. Z Han, WS Lo et al.,... - Genetics, 2020
```

optimized Pristionchus top 10% highest used codons

```
ATGGTGTCTAAGGGAGAGGCTGTGATCAAGGAGTTCATGAGATTCAAGGTGCATATGGAGGGATCTATGAATGGACATGAGTTCTGA
GATCGAGGGAGAGGGAGAGGGAAGACCTTACGAGGGAACTCAGACTGCTAAGCTCAAGGTGACTAAGGGAGGAACTTCTCATAATG
AGGATTACACTGTGGTGGAGCAGTACGAGAGATCTGAGGGAAGACATTCTACTGGAGGAATGGATGAGCTCTACAAGTGA
```