Put this file in the same directory as your python script. Change the name of the file in the next line to test your code.

```
In [50]: exec(open("Kelley_OOP_FinalProjectSpr2018.py").read())
```

TEST SEQ CLASS

Make instance of Seq called 's' and test methods

```
In [51]: s=Seq("  gATATAGGACctttaGGACCAC  ","my_gene","H.sapiens")
         s.print_record()
```

```
H.sapiens my_gene: GATATAGGACCTTTAGGACCAC
```

```
In [52]: print(s)
         print(s.gene)
         print(s.species)
```

```
GATATAGGACCTTTAGGACCAC
my_gene
H.sapiens
```

```
In [53]: s.make_kmers(5)
         print(s.kmers)
```

```
['GATAT', 'ATATA', 'TATAG', 'ATAGG', 'TAGGA', 'AGGAC', 'GGACC', 'GACCT', 'ACCTT', 'CCTTT', '
CTTTA', 'TTTAG', 'TTAGG', 'TAGGA', 'AGGAC', 'GGACC', 'GACCA', 'ACCAC']
```

```
In [54]: print(s.fasta())
```

```
>H.sapiens my_gene
GATATAGGACCTTTAGGACCAC
```