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In [2]: testp=Protein('VIKING', 'test', 'unknown', 999)
```

```
In [3]: print(testp)
```

VIKING

```
In [4]: testp.make_kmers(2)
print(testp.kmers)
```

```
['VI', 'IK', 'KI', 'IN', 'NG']
```

```
In [5]: testp.tabulate_amino_acids()
```

```
In [6]: print(testp.aa_counts)
```

```
{'A': 0, 'C': 0, 'D': 0, 'E': 0, 'F': 0, 'G': 1, 'H': 0, 'I': 2, 'K': 1, 'L': 0, 'M': 0, 'N': 1, 'P': 0, 'Q': 0, 'R': 0, 'S': 0, 'T': 0, 'U': 0, 'V': 1, 'W': 0, 'X': 0, 'Y': 0}
```

```
In [7]: x=testp.total_hydro()
print(x)
```

5.3999999999999999

```
In [8]: dat=testp.hydro_scan()
print(dat)
```

```
[4.35, 0.30000000000000004, 0.30000000000000004, 0.5, -1.95]
```