**#Q2.1**

ARTICLE: [The complete genome sequence of Escherichia coli K-12](http://science.sciencemag.org/content/277/5331/1453.short?casa_token=cWnCgCj9FnsAAAAA:LcomRi-vwqrT6QjAnjEI_QCplhsu57bNkXMb-wHi9qj9byXws84d7ra9fIh4QeviBqgVtemwFjkXVg)

CITE: Blattner, Frederick R., et al. "The complete genome sequence of Escherichia coli K-12." *science* 277.5331 (1997): 1453-1462.

LINK:<https://scholar.google.com/scholar?q=the+complete+genome+sequence+of+escherichia+coli+k-12+google+scholar&hl=en&as_sdt=0&as_vis=1&oi=scholart>

1)E. coli is studied because E. coli is easy to obtain and maintain in laboratory. It is a simple organism to study.

2) The M13 Janus shotgun strategy was used in sequencing project.

3) E.coli is a small and compact organism. The genomic sequence study also suggests absence of introns leading to a small genome size. Also, there are overlapping genes present which accounts for its compactness.

4.5) The two facts of interest are-

1)The genome of E.Coli consist of 4,639,221 bp of circular duplex DNA.

2) A radial plot shows E. coli's local similarity to sequenced bacteriophage genes.

**#Q2.2**

indices = [22, 0, 39, -6, 14, 8, 30, -22]

l=len(indices) #length of indices

sequence = "IF WE KNEW WHAT WE WERE DOING IT WOULD NOT BE CALLED RESEARCH"

for i in range(l):

print(indices[i],"", sequence[indices[i]]) #printing numbers and corresponding character

**#Q2.3**

seq="DELGCFVGTA"

hy=['A','V','I','L','M','F','Y','W'] #hy contains list of all hydrophobic elements

for ch in seq:

if ch in hy : #check for hydrophobic elements

print(ch,"hydrophobic")

else:

print(ch,"not hydrophobic")