George Apostolidis – C1 Exercise Bioinformatics

**Q1: In which directory do you enter the server?**

/home/apost005

**Q2: which directories are present in the directory “data\_c1”?**

Pdb, scripts and tomato

**Q3: What is the output of the script?**

Hello!

**Q4: What is the output of the script now?**

Again, its Hello!

Hello !

C:\Users\geoap\Documents\WUR\msc\_bioinformatics\_and\_systems\_biology\period\_2\advanced\_bioinformatics

You are running this script with Python version: 3.13.3 (tags/v3.13.3:6280bb5, Apr 8 2025, 14:47:33) [MSC v.1943 64 bit (AMD64)]

**Q5: What kind of crystal structure is stored in the file 1EHZ.pdb?**

CRYSTAL STRUCTURE OF YEAST PHENYLALANINE TRANSFER RNA

**Q6: What is the difference in resolution between the structure in1EHZ.pdb and 1EVV.pdb? You can find this info in the first few lines of the file.**

1EHZ has 1.93 resolution while 1EVV has 2.

**Q7: how many lines start with the word ATOM in the file 1EHZ.pdb?**

1346 (grep "ATOM" 1EHZ.pdb | wc -l)

**Q8: what are the lowest and highest x-coordinates that are found in thelist of coordinates for all ATOM lines? Use the documentation on thePDB format to figure out where the x-coordinate is in the line. (hint,with the cut command you can select specific character positions in aline and the sort command allows you to sort lines)**

Lowest X: 32.161 Highest X: 84.715

**Q9: how many amino acids are there in your protein?**

171

**Q10: what is the molecular weight of your protein?**

Molecular weight = 18764.84

**Q11: what is the percent identity of the alignment?**

100.0%