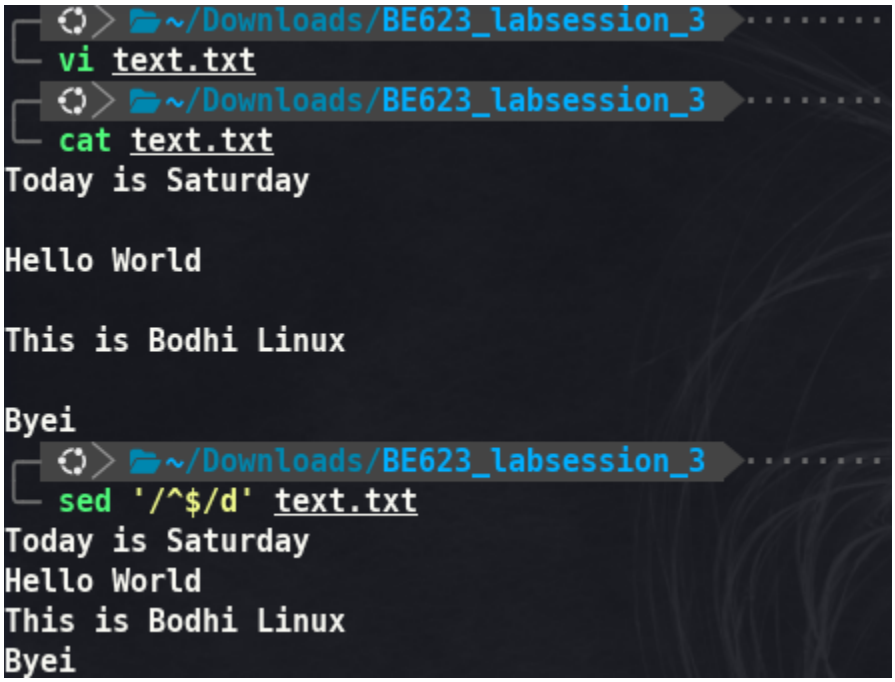
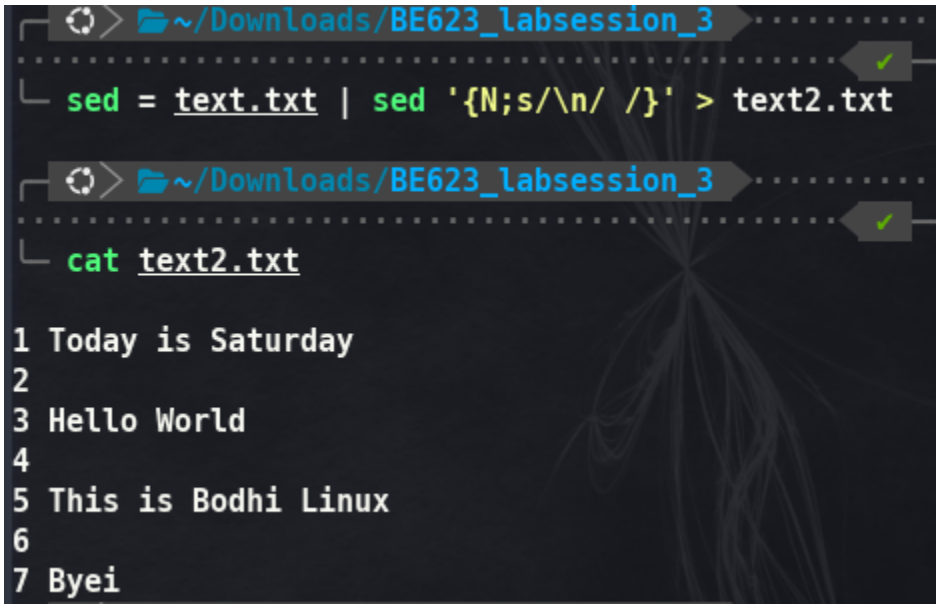
BE623-Lab-3 Assignment (By - Bibhu Prasad Sahoo, 25210036)

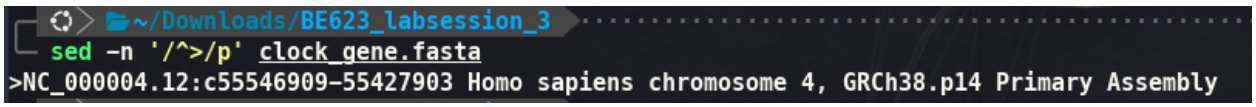
1.



2.



3.



4.

```
~/Downloads/BE623_labsession_3
sed -n '/^>.*CLOCK/p' protein.fasta
>seq1|Homo_sapiens|CLOCK_protein
```

5.

```
~/Downloads/BE623_labsession_3
sed -n '/CC/p' protein.fasta
MTEYKLVVVGAGCCGKSALTIQLInhfgFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAG
MADQLTEEQIAEFKEAFSLFDKDGDGTCCTKELGTVMRSCCQNPTEAELQDMINEVDADGNGQ
```

6. Used chatgpt

```
~/Downloads/BE623_labsession_3
grep -v "^>" protein.fasta | grep -o "G" | wc -l
51
```

7.

```
~/Downloads/BE623_labsession_3
sed -n '5,28 p' clock_gene.fasta
GTGGAGGAGGGGAAGGGAAGGGAGGGGGAGGAGGAGCTGGCCACAGGAGCGGCGAATTTTTGGGGGGGTG
GGTGGGGGGCGCCACTCACAGCCCCAGGTGCTGCTGGAGGTGGGAGCCGCGGCGCCTCCTGGACACAGGC
GGGGTAGTGGTTCCGAGTCACCGCAGCGGGAGACCTGGGTGGGGGAGGGAAGAAGCCGGAGCCGCCGCAA
GCCACACGGTGAGGGCGCGGGGAAGGGGAGGGAGCGGGGGGCGGCGTGTGTGGGGCCGGGGGGCGGCGGC
CAAGGGTGGGGAAGGCGGGAGCTGAAGCCCAAGTTTGGCGTGTCGTTCTAGTGTGTCTTTTCCCGGGACT
TCGGGCCGAGGCCCGCCCTGCCTGAGAGGCCCTCTGGGGCAGCTGGGGTTACCTGCGGGGCAGGGGCGGG
AGTGGGGTGCACGGCGGGGCCGGGCGGCTTGAGGGCGCCCGGAGCTGCGGCCGATTCCAGCAGCTGGGAG
GCGGGGAAAGACGGGGACCGGGTGCCGAGAGAGCTTTCGCTGGGGACCCGCTAGGCCTTGTGACCCACTT
```

8. Used Chatgpt

```
~/Downloads/BE623_labsession_3
sed -n 's/^>\(.*\)/\1/p' protein.fasta
seq1|Homo_sapiens|CLOCK_protein
seq2|Mus_musculus|PER_protein
seq3|Drosophila_melanogaster|TIM_protein
seq4|Danio_rerio|BMAL_protein
seq5|Arabidopsis_thaliana|LHY_protein
seq6|Saccharomyces_cerevisiae|CYC_protein
seq7|Caenorhabditis_elegans|CLK_protein
seq8|Gallus_gallus|CRY_protein
seq9|Escherichia_coli|RecA_protein
seq10|Xenopus_laevis|REV-ERB_protein
```

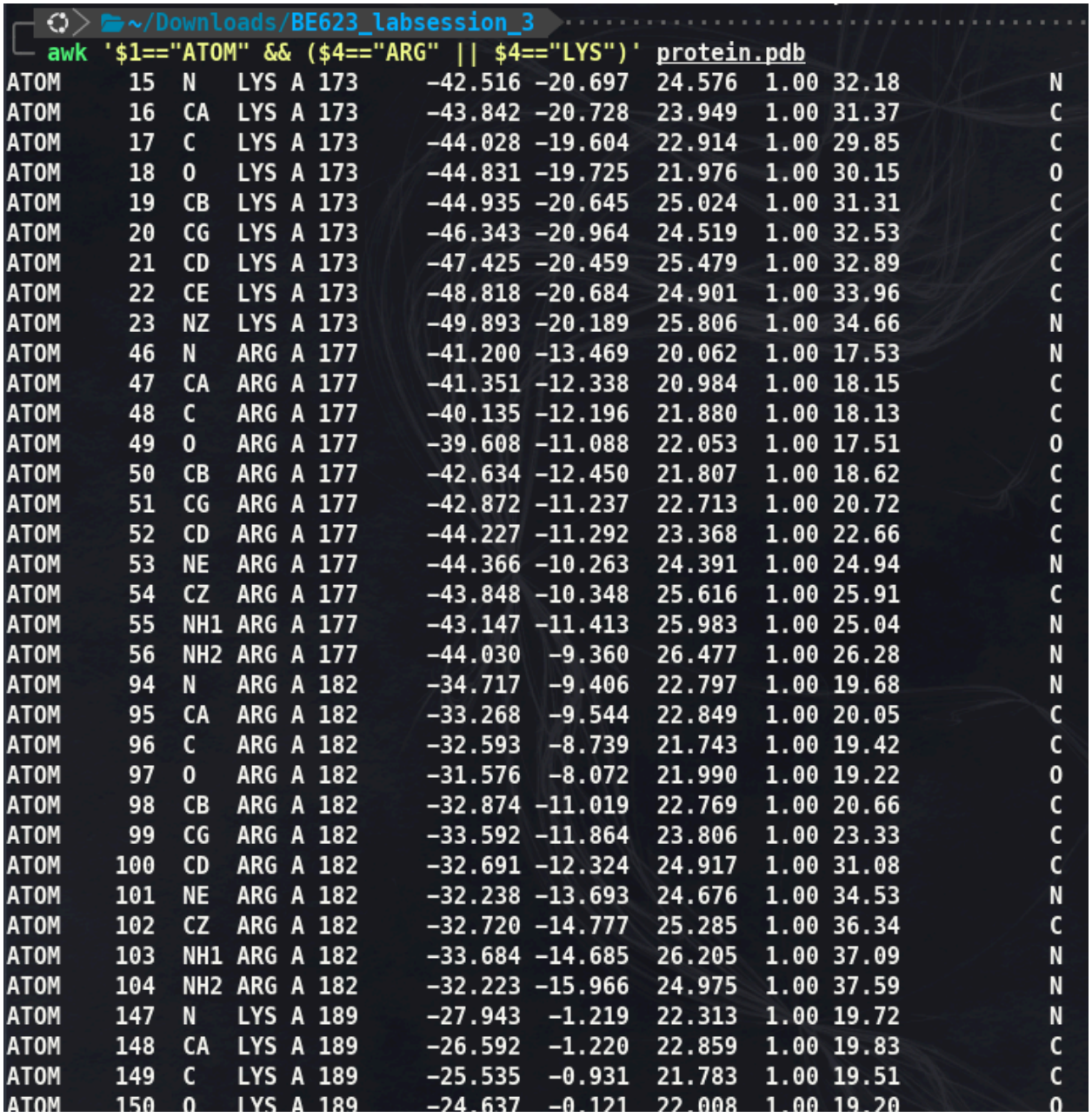
9.

```
~/Downloads/BE623_labsession_3
sed -n '/^M.*Q$/p' protein.fasta
MADQLTEEQIAEFKEAFSLFDKDGDGTCCTKELGTVMRSCCQNPTEAELQDMINEVDADGNGQ
MADSQRRLLQNVINKAAGKSSTLLPVDGDKILVVTTGGQVVQSNVLEAMKELLQ
```

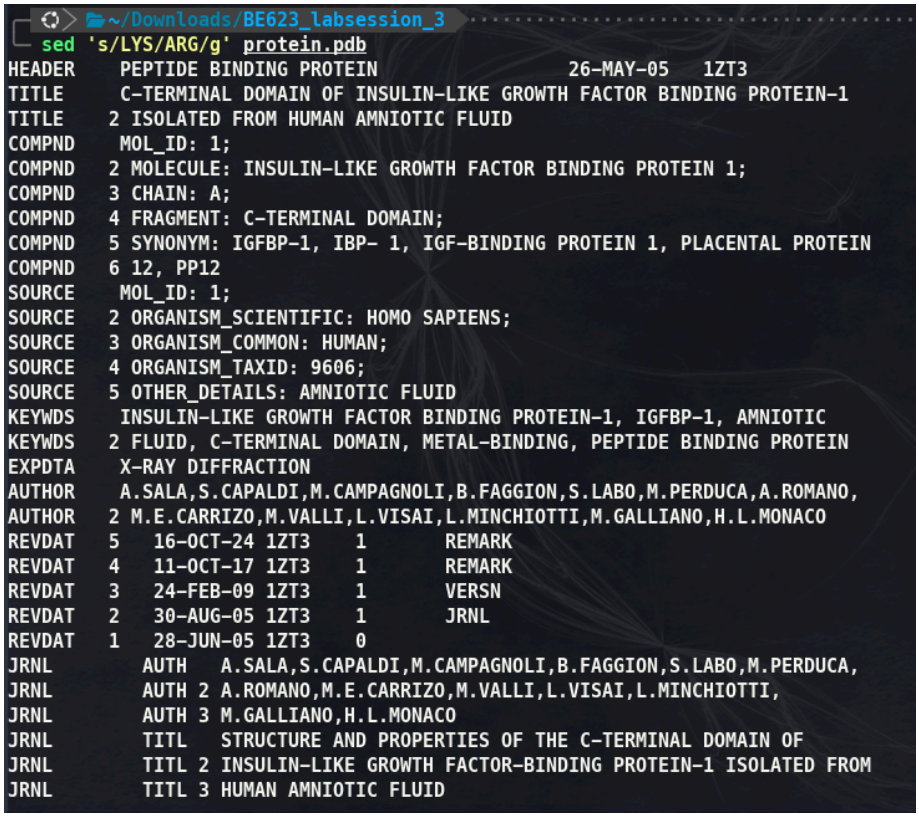
11.

```
~/Downloads/BE623_labsession_3
awk '$1=="ATOM" && $5=="A"' protein.pdb
ATOM      1  N   TRP A 172     -39.136 -21.997  24.415  1.00 34.43           N
ATOM      2  CA  TRP A 172     -40.108 -20.907  24.729  1.00 34.28           C
ATOM      3  C   TRP A 172     -41.403 -21.065  23.944  1.00 33.46           C
ATOM      4  O   TRP A 172     -41.385 -21.496  22.789  1.00 33.48           O
ATOM      5  CB  TRP A 172     -39.506 -19.534  24.418  1.00 35.12           C
ATOM      6  CG  TRP A 172     -38.161 -19.292  25.025  1.00 36.34           C
ATOM      7  CD1 TRP A 172     -37.773 -19.568  26.306  1.00 37.69           C
ATOM      8  CD2 TRP A 172     -37.032 -18.693  24.384  1.00 37.47           C
ATOM      9  NE1 TRP A 172     -36.465 -19.190  26.497  1.00 37.97           N
ATOM     10  CE2 TRP A 172     -35.985 -18.650  25.334  1.00 37.83           C
ATOM     11  CE3 TRP A 172     -36.799 -18.192  23.097  1.00 37.57           C
ATOM     12  CZ2 TRP A 172     -34.725 -18.128  25.037  1.00 37.51           C
ATOM     13  CZ3 TRP A 172     -35.545 -17.671  22.802  1.00 37.85           C
ATOM     14  CH2 TRP A 172     -34.523 -17.646  23.769  1.00 37.43           C
ATOM     15  N   LYS A 173     -42.516 -20.697  24.576  1.00 32.18           N
ATOM     16  CA  LYS A 173     -43.842 -20.728  23.949  1.00 31.37           C
ATOM     17  C   LYS A 173     -44.028 -19.604  22.914  1.00 29.85           C
ATOM     18  O   LYS A 173     -44.831 -19.725  21.976  1.00 30.15           O
ATOM     19  CB  LYS A 173     -44.935 -20.645  25.024  1.00 31.31           C
ATOM     20  CG  LYS A 173     -46.343 -20.964  24.519  1.00 32.53           C
ATOM     21  CD  LYS A 173     -47.425 -20.459  25.479  1.00 32.89           C
ATOM     22  CE  LYS A 173     -48.818 -20.684  24.901  1.00 33.96           C
ATOM     23  NZ  LYS A 173     -49.893 -20.189  25.806  1.00 34.66           N
ATOM     24  N   GLU A 174     -43.280 -18.518  23.090  1.00 27.67           N
ATOM     25  CA  GLU A 174     -43.337 -17.366  22.191  1.00 25.77           C
ATOM     26  C   GLU A 174     -41.922 -17.014  21.728  1.00 23.54           C
ATOM     27  O   GLU A 174     -41.381 -15.977  22.138  1.00 23.23           O
ATOM     28  CB  GLU A 174     -43.933 -16.148  22.913  1.00 25.76           C
ATOM     29  CG  GLU A 174     -45.376 -16.258  23.359  1.00 26.89           C
ATOM     30  CD  GLU A 174     -45.777 -15.061  24.206  1.00 27.42           C
ATOM     31  OE1 GLU A 174     -46.102 -14.001  23.639  1.00 29.42           O
ATOM     32  OE2 GLU A 174     -45.756 -15.182  25.445  1.00 30.63           O
ATOM     33  N   PRO A 175     -41.313 -17.867  20.872  1.00 21.55           N
ATOM     34  CA  PRO A 175     -39.891 -17.705  20.564  1.00 20.10           C
ATOM     35  C   PRO A 175     -39.565 -16.385  19.866  1.00 18.58           C
ATOM     36  O   PRO A 175     -38.520 -15.781  20.142  1.00 18.18           O
ATOM     37  CB  PRO A 175     -39.594 -18.893  19.632  1.00 20.52           C
ATOM     38  CG  PRO A 175     -40.909 -19.247  19.043  1.00 19.77           C
```

12.


~/Downloads/BE623_labsession_3
awk '$1=="ATOM" && ($4=="ARG" || $4=="LYS")' protein.pdb
ATOM 15 N LYS A 173 -42.516 -20.697 24.576 1.00 32.18 N
ATOM 16 CA LYS A 173 -43.842 -20.728 23.949 1.00 31.37 C
ATOM 17 C LYS A 173 -44.028 -19.604 22.914 1.00 29.85 C
ATOM 18 O LYS A 173 -44.831 -19.725 21.976 1.00 30.15 O
ATOM 19 CB LYS A 173 -44.935 -20.645 25.024 1.00 31.31 C
ATOM 20 CG LYS A 173 -46.343 -20.964 24.519 1.00 32.53 C
ATOM 21 CD LYS A 173 -47.425 -20.459 25.479 1.00 32.89 C
ATOM 22 CE LYS A 173 -48.818 -20.684 24.901 1.00 33.96 C
ATOM 23 NZ LYS A 173 -49.893 -20.189 25.806 1.00 34.66 N
ATOM 46 N ARG A 177 -41.200 -13.469 20.062 1.00 17.53 N
ATOM 47 CA ARG A 177 -41.351 -12.338 20.984 1.00 18.15 C
ATOM 48 C ARG A 177 -40.135 -12.196 21.880 1.00 18.13 C
ATOM 49 O ARG A 177 -39.608 -11.088 22.053 1.00 17.51 O
ATOM 50 CB ARG A 177 -42.634 -12.450 21.807 1.00 18.62 C
ATOM 51 CG ARG A 177 -42.872 -11.237 22.713 1.00 20.72 C
ATOM 52 CD ARG A 177 -44.227 -11.292 23.368 1.00 22.66 C
ATOM 53 NE ARG A 177 -44.366 -10.263 24.391 1.00 24.94 N
ATOM 54 CZ ARG A 177 -43.848 -10.348 25.616 1.00 25.91 C
ATOM 55 NH1 ARG A 177 -43.147 -11.413 25.983 1.00 25.04 N
ATOM 56 NH2 ARG A 177 -44.030 -9.360 26.477 1.00 26.28 N
ATOM 94 N ARG A 182 -34.717 -9.406 22.797 1.00 19.68 N
ATOM 95 CA ARG A 182 -33.268 -9.544 22.849 1.00 20.05 C
ATOM 96 C ARG A 182 -32.593 -8.739 21.743 1.00 19.42 C
ATOM 97 O ARG A 182 -31.576 -8.072 21.990 1.00 19.22 O
ATOM 98 CB ARG A 182 -32.874 -11.019 22.769 1.00 20.66 C
ATOM 99 CG ARG A 182 -33.592 -11.864 23.806 1.00 23.33 C
ATOM 100 CD ARG A 182 -32.691 -12.324 24.917 1.00 31.08 C
ATOM 101 NE ARG A 182 -32.238 -13.693 24.676 1.00 34.53 N
ATOM 102 CZ ARG A 182 -32.720 -14.777 25.285 1.00 36.34 C
ATOM 103 NH1 ARG A 182 -33.684 -14.685 26.205 1.00 37.09 N
ATOM 104 NH2 ARG A 182 -32.223 -15.966 24.975 1.00 37.59 N
ATOM 147 N LYS A 189 -27.943 -1.219 22.313 1.00 19.72 N
ATOM 148 CA LYS A 189 -26.592 -1.220 22.859 1.00 19.83 C
ATOM 149 C LYS A 189 -25.535 -0.931 21.783 1.00 19.51 C
ATOM 150 O LYS A 189 -24.637 -0.121 22.008 1.00 19.20 O

13.


~/Downloads/BE623_labsession_3
sed 's/LYS/ARG/g' protein.pdb
HEADER   PEPTIDE BINDING PROTEIN   26-MAY-05   1ZT3
TITLE   C-TERMINAL DOMAIN OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-1
TITLE   2 ISOLATED FROM HUMAN AMNIOTIC FLUID
COMPND   MOL_ID: 1;
COMPND   2 MOLECULE: INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1;
COMPND   3 CHAIN: A;
COMPND   4 FRAGMENT: C-TERMINAL DOMAIN;
COMPND   5 SYNONYM: IGFBP-1, IBP- 1, IGF-BINDING PROTEIN 1, PLACENTAL PROTEIN
COMPND   6 12, PP12
SOURCE   MOL_ID: 1;
SOURCE   2 ORGANISM_SCIENTIFIC: HOMO SAPIENS;
SOURCE   3 ORGANISM_COMMON: HUMAN;
SOURCE   4 ORGANISM_TAXID: 9606;
SOURCE   5 OTHER_DETAILS: AMNIOTIC FLUID
KEYWDS   INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-1, IGFBP-1, AMNIOTIC
KEYWDS   2 FLUID, C-TERMINAL DOMAIN, METAL-BINDING, PEPTIDE BINDING PROTEIN
EXPDTA   X-RAY DIFFRACTION
AUTHOR   A.SALA,S.CAPALDI,M.CAMPAGNOLI,B.FAGGION,S.LABO,M.PERDUCA,A.ROMANO,
AUTHOR   2 M.E.CARRIZO,M.VALLI,L.VISAI,L.MINCHIOTTI,M.GALLIANO,H.L.MONACO
REVDAT   5   16-OCT-24 1ZT3   1   REMARK
REVDAT   4   11-OCT-17 1ZT3   1   REMARK
REVDAT   3   24-FEB-09 1ZT3   1   VERSN
REVDAT   2   30-AUG-05 1ZT3   1   JRNL
REVDAT   1   28-JUN-05 1ZT3   0
JRNL   AUTH   A.SALA,S.CAPALDI,M.CAMPAGNOLI,B.FAGGION,S.LABO,M.PERDUCA,
JRNL   AUTH 2 A.ROMANO,M.E.CARRIZO,M.VALLI,L.VISAI,L.MINCHIOTTI,
JRNL   AUTH 3 M.GALLIANO,H.L.MONACO
JRNL   TITL   STRUCTURE AND PROPERTIES OF THE C-TERMINAL DOMAIN OF
JRNL   TITL 2 INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-1 ISOLATED FROM
JRNL   TITL 3 HUMAN AMNIOTIC FLUID

14.
```
~/Downloads/BE623_labsession_3
awk '$1=="ATOM" {print $9}' protein.pdb
24.415
24.729
23.944
22.789
24.418
25.025
26.306
24.384
26.497
25.334
23.097
25.037
22.802
23.769
24.576
23.949
22.914
21.976
25.024
24.519
25.479
24.901
25.806
23.090
22.191
```

15.
```
~/Downloads/BE623_labsession_3
grep -c "GLY" protein.pdb
33
```

16.
```
~/Downloads/BE623_labsession_3
awk '/^ATOM/ && $3=="CA"  && ($4=="ALA" || $4=="GLY") {print $0}' protein.pdb
ATOM    143  CA  ALA A 188     -29.906  -0.273  21.249  1.00 19.62           C
ATOM    157  CA  ALA A 190     -24.689  -1.402  19.528  1.00 20.13           C
ATOM    193  CA  GLY A 195     -19.179   3.890  13.965  1.00 34.45           C
ATOM    315  CA  GLY A 210     -45.353 -14.753  19.536  1.00 18.56           C
ATOM    422  CA  GLY A 223     -36.815   5.170   1.658  1.00 21.58           C
ATOM    435  CA  ALA A 225     -37.186  -1.492   0.463  1.00 20.30           C
ATOM    440  CA  GLY A 226     -35.705  -3.955   2.980  1.00 18.85           C
ATOM    526  CA  GLY A 236     -37.957 -18.276  12.295  1.00 18.22           C
ATOM    565  CA  GLY A 241     -34.199 -22.463  -1.334  1.00 28.67           C
ATOM    610  CA  GLY A 247     -40.259  -7.039  -1.851  1.00 24.01           C
```

17.
```
~/Downloads/BE623_labsession_3
awk -n '/^ATOM/ && $3=="C"' protein.pdb | wc -l
80
```

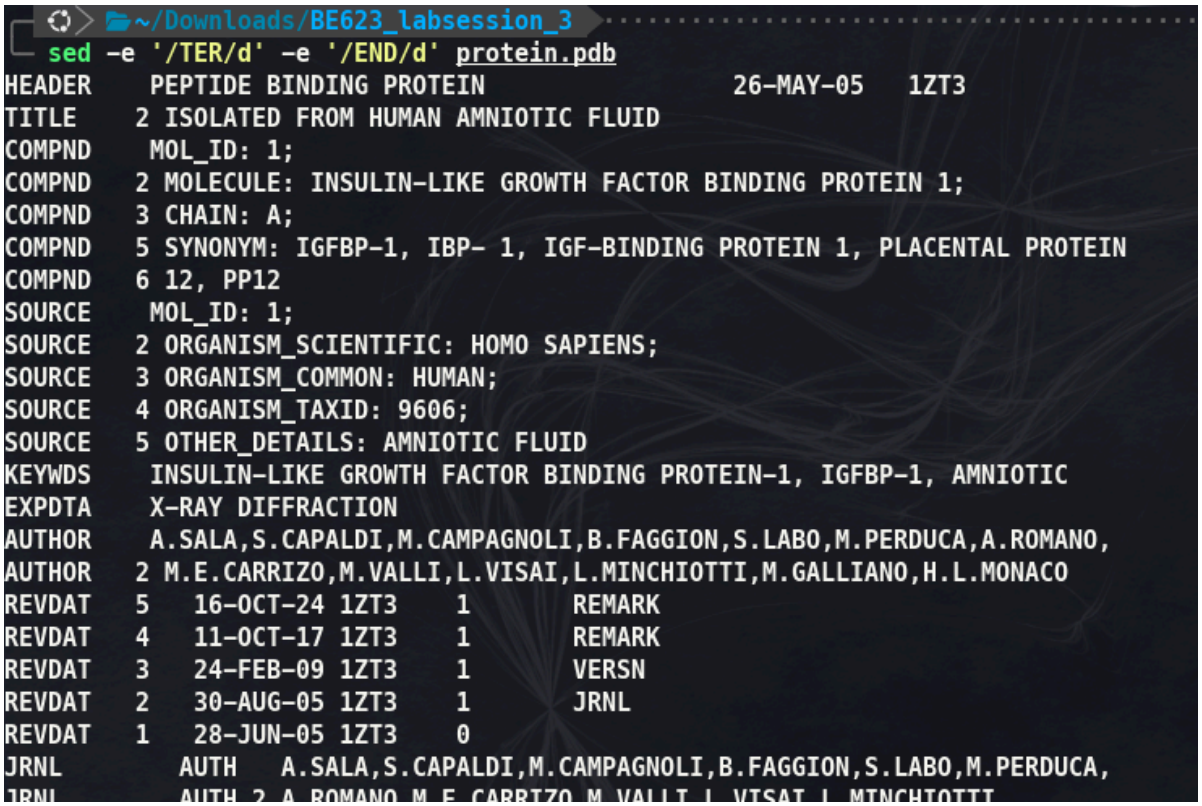
18.

```
~/Downloads/BE623_labsession_3
sed -n '/^HETATM/p' protein.pdb
HETATM  644  C1  DIO A 400     -29.064  -6.946  17.132  1.00 36.16           C
HETATM  645  C2  DIO A 400     -28.073  -9.061  16.720  1.00 36.92           C
HETATM  646  C1' DIO A 400     -27.687  -6.281  17.202  1.00 35.99           C
HETATM  647  C2' DIO A 400     -26.684  -8.437  16.825  1.00 36.68           C
HETATM  648  O1  DIO A 400     -28.996  -8.072  16.254  1.00 36.78           O
HETATM  649  O1' DIO A 400     -26.726  -7.251  17.629  1.00 36.28           O
HETATM  650  O   HOH A   1     -37.255  -6.228  10.647  1.00 14.97           O
HETATM  651  O   HOH A   2     -22.012  -0.788  22.336  1.00 20.64           O
HETATM  652  O   HOH A   3     -38.877  -3.391   4.471  1.00 20.33           O
HETATM  653  O   HOH A   4     -34.212 -23.871   7.998  1.00 18.39           O
HETATM  654  O   HOH A   5     -20.730  -0.315  24.894  1.00 20.65           O
HETATM  655  O   HOH A   6     -44.936 -13.438   1.965  1.00 28.30           O
HETATM  656  O   HOH A   7     -48.895 -18.702  15.563  1.00 27.48           O
HETATM  657  O   HOH A   8     -21.393  -0.854  17.811  1.00 24.13           O
HETATM  658  O   HOH A   9     -32.124   5.776   0.506  1.00 29.82           O
HETATM  659  O   HOH A  10     -46.186 -13.792   6.539  1.00 23.52           O
HETATM  660  O   HOH A  11     -29.575  -1.996  25.245  1.00 28.23           O
HETATM  661  O   HOH A  12     -45.642 -11.444  19.694  1.00 25.61           O
HETATM  662  O   HOH A  13     -49.384 -20.064  17.570  1.00 29.28           O
HETATM  663  O   HOH A  14     -30.137  -4.552   3.329  1.00 27.31           O
HETATM  664  O   HOH A  15     -42.693  -7.945  15.244  1.00 19.76           O
HETATM  665  O   HOH A  16     -35.906 -28.174   5.866  1.00 31.98           O
HETATM  666  O   HOH A  17     -44.171  -7.687  17.621  1.00 22.18           O
HETATM  667  O   HOH A  18     -47.265 -12.454  21.564  1.00 29.40           O
HETATM  668  O   HOH A  19     -36.430   3.094  -3.026  1.00 25.02           O
HETATM  669  O   HOH A  20     -29.553  -5.969  12.150  1.00 34.06           O
HETATM  670  O   HOH A  21     -42.686  -4.398  27.240  1.00 25.96           O
HETATM  671  O   HOH A  22     -43.889  -9.382  19.695  1.00 29.00           O
HETATM  672  O   HOH A  23     -43.476  -6.477  -2.563  1.00 30.73           O
```

19.

```
~/Downloads/BE623_labsession_3
awk -n '/^ATOM/ {print $4}p' protein.pdb | grep "E$" | sort -u
ILE
PHE
```

20.


~/Downloads/BE623_labsession_3
sed -e '/TER/d' -e '/END/d' protein.pdb
HEADER PEPTIDE BINDING PROTEIN 26-MAY-05 1ZT3
TITLE 2 ISOLATED FROM HUMAN AMNIOTIC FLUID
COMPND MOL_ID: 1;
COMPND 2 MOLECULE: INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1;
COMPND 3 CHAIN: A;
COMPND 5 SYNONYM: IGFBP-1, IBP- 1, IGF-BINDING PROTEIN 1, PLACENTAL PROTEIN
COMPND 6 12, PP12
SOURCE MOL_ID: 1;
SOURCE 2 ORGANISM_SCIENTIFIC: HOMO SAPIENS;
SOURCE 3 ORGANISM_COMMON: HUMAN;
SOURCE 4 ORGANISM_TAXID: 9606;
SOURCE 5 OTHER_DETAILS: AMNIOTIC FLUID
KEYWDS INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-1, IGFBP-1, AMNIOTIC
EXPDTA X-RAY DIFFRACTION
AUTHOR A.SALA,S.CAPALDI,M.CAMPAGNOLI,B.FAGGION,S.LABO,M.PERDUCA,A.ROMANO,
AUTHOR 2 M.E.CARRIZO,M.VALLI,L.VISAI,L.MINCHIOTTI,M.GALLIANO,H.L.MONACO
REVDAT 5 16-OCT-24 1ZT3 1 REMARK
REVDAT 4 11-OCT-17 1ZT3 1 REMARK
REVDAT 3 24-FEB-09 1ZT3 1 VERSN
REVDAT 2 30-AUG-05 1ZT3 1 JRNL
REVDAT 1 28-JUN-05 1ZT3 0
JRNL AUTH A.SALA,S.CAPALDI,M.CAMPAGNOLI,B.FAGGION,S.LABO,M.PERDUCA,

21.

```
~/Downloads/BE623_labsession_3
awk -n '/^ATOM/ && $4!="ARG"' protein.pdb
ATOM      1  N   TRP A 172     -39.136 -21.997  24.415  1.00 34.43           N
ATOM      2  CA  TRP A 172     -40.108 -20.907  24.729  1.00 34.28           C
ATOM      3  C   TRP A 172     -41.403 -21.065  23.944  1.00 33.46           C
ATOM      4  O   TRP A 172     -41.385 -21.496  22.789  1.00 33.48           O
ATOM      5  CB  TRP A 172     -39.506 -19.534  24.418  1.00 35.12           C
ATOM      6  CG  TRP A 172     -38.161 -19.292  25.025  1.00 36.34           C
ATOM      7  CD1 TRP A 172     -37.773 -19.568  26.306  1.00 37.69           C
ATOM      8  CD2 TRP A 172     -37.032 -18.693  24.384  1.00 37.47           C
ATOM      9  NE1 TRP A 172     -36.465 -19.190  26.497  1.00 37.97           N
ATOM     10  CE2 TRP A 172     -35.985 -18.650  25.334  1.00 37.83           C
ATOM     11  CE3 TRP A 172     -36.799 -18.192  23.097  1.00 37.57           C
ATOM     12  CZ2 TRP A 172     -34.725 -18.128  25.037  1.00 37.51           C
ATOM     13  CZ3 TRP A 172     -35.545 -17.671  22.802  1.00 37.85           C
ATOM     14  CH2 TRP A 172     -34.523 -17.646  23.769  1.00 37.43           C
ATOM     15  N   LYS A 173     -42.516 -20.697  24.576  1.00 32.18           N
ATOM     16  CA  LYS A 173     -43.842 -20.728  23.949  1.00 31.37           C
ATOM     17  C   LYS A 173     -44.028 -19.604  22.914  1.00 29.85           C
ATOM     18  O   LYS A 173     -44.831 -19.725  21.976  1.00 30.15           O
ATOM     19  CB  LYS A 173     -44.935 -20.645  25.024  1.00 31.31           C
ATOM     20  CG  LYS A 173     -46.343 -20.964  24.519  1.00 32.53           C
ATOM     21  CD  LYS A 173     -47.425 -20.459  25.479  1.00 32.89           C
ATOM     22  CE  LYS A 173     -48.818 -20.684  24.901  1.00 33.96           C
```

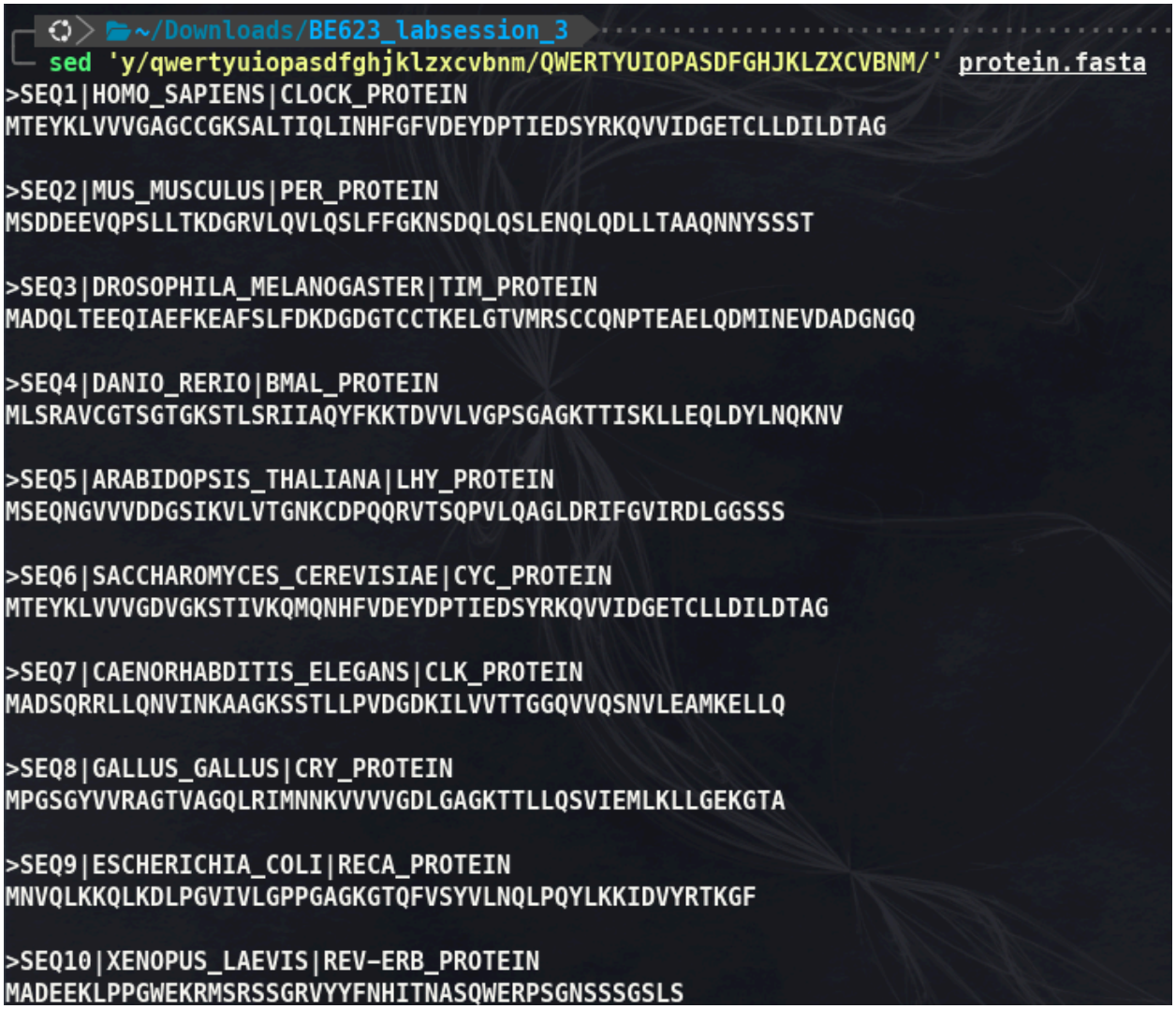
22. Used chatgpt to get the uniq part of the command

```
~/Downloads/BE623_labsession_3
awk '$1=="ATOM" && $5=="A" {print $4}' protein.pdb | sort | uniq -c
     15 ALA
     55 ARG
     40 ASN
     16 ASP
     37 CYS
     18 GLN
     81 GLU
     28 GLY
     10 HIS
     32 ILE
     32 LEU
     45 LYS
      8 MET
     22 PHE
     42 PRO
     36 SER
     14 THR
     42 TRP
     48 TYR
     21 VAL
```

23.

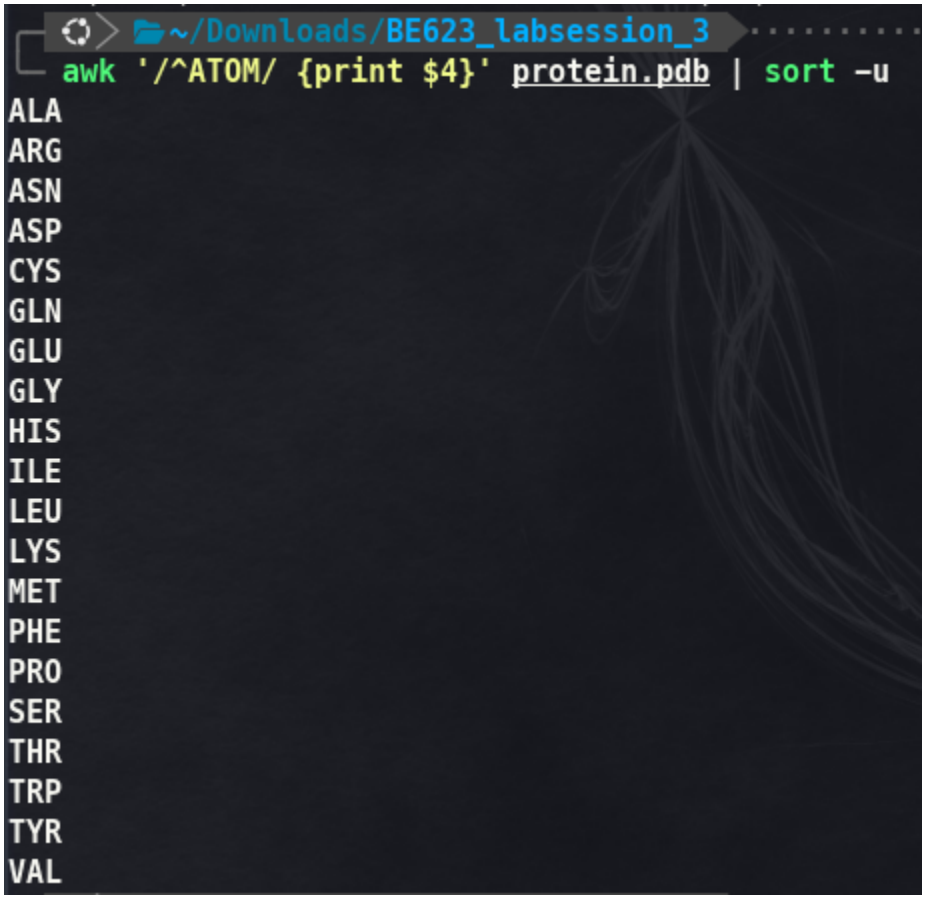

~/Downloads/BE623_labsession_3
awk '/^ATOM/ {print $3", "$4", "$5}' protein.pdb
N, TRP, A
CA, TRP, A
C, TRP, A
O, TRP, A
CB, TRP, A
CG, TRP, A
CD1, TRP, A
CD2, TRP, A
NE1, TRP, A
CE2, TRP, A
CE3, TRP, A
CZ2, TRP, A
CZ3, TRP, A
CH2, TRP, A
N, LYS, A
CA, LYS, A
C, LYS, A
O, LYS, A
CB, LYS, A

24.


~/Downloads/BE623_labsession_3
sed 'y/qwertyuiopasdfghjklzxcvbnm/QWERTYUIOPASDFGHJKLZXCVBNM/' protein.fasta
>SEQ1|HOMO_SAPIENS|CLOCK_PROTEIN
MTEYKLVVVGAGCCGKSALTIQLINHFGFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAG
>SEQ2|MUS_MUSCULUS|PER_PROTEIN
MSDDEEVQPSLLTKDGRVLQVLQSLFFGKNSDQLQSLENQLQDLLTAAQNNYSSST
>SEQ3|DROSOPHILA_MELANOGASTER|TIM_PROTEIN
MADQLTEEQIAEFKEAFSLFDKDGDGTCCTKELGTVMRSCCQNPTEAELQDMINEVDADGNGQ
>SEQ4|DANIO_RERIO|BMAL_PROTEIN
MLSRAVCGTSGTGKSTLSRIIAQYFKKTDVVLVGPSGAGKTTISKLLEQLDYLNQKNV
>SEQ5|ARABIDOPSIS_THALIANA|LHY_PROTEIN
MSEQNGVVVDDGSIKVLVTGNKCDPQQRVTSQPVLQAGLDRIFGVIRDLGGSSS
>SEQ6|SACCHAROMYCES_CEREVISIAE|CYC_PROTEIN
MTEYKLVVVGDVGKSTIVKQMQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAG
>SEQ7|CAENORHABDITIS_ELEGANS|CLK_PROTEIN
MADSQRRLLQNVINKAAGKSSTLLPVDGDKILVVTTGGQVVQSNVLEAMKELLQ
>SEQ8|GALLUS_GALLUS|CRY_PROTEIN
MPGSGYVVRAGTVAGQLRIMNNKVVVVGDLGAGKTTLLQSVIEMLKLLGEKGTA
>SEQ9|ESCHERICHIA_COLI|RECA_PROTEIN
MNVQLKKQLKDLPGVIVLGPPGAGKGTQFVSYVLNQLPQYLKKIDVYRTKGF
>SEQ10|XENOPUS_LAEVIS|REV-ERB_PROTEIN
MADEEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSGSLS

25.

26.


~/Downloads/BE623_labsession_3
awk '/^ATOM/ {print $4}' protein.pdb | sort -u
ALA
ARG
ASN
ASP
CYS
GLN
GLU
GLY
HIS
ILE
LEU
LYS
MET
PHE
PRO
SER
THR
TRP
TYR
VAL

27.

28.