Indian Institute of Technology Gandhinagar

BE623 Biocomputing
Sem1 2025-2026
Lab Assignment –3

Text processing (sed and awk)

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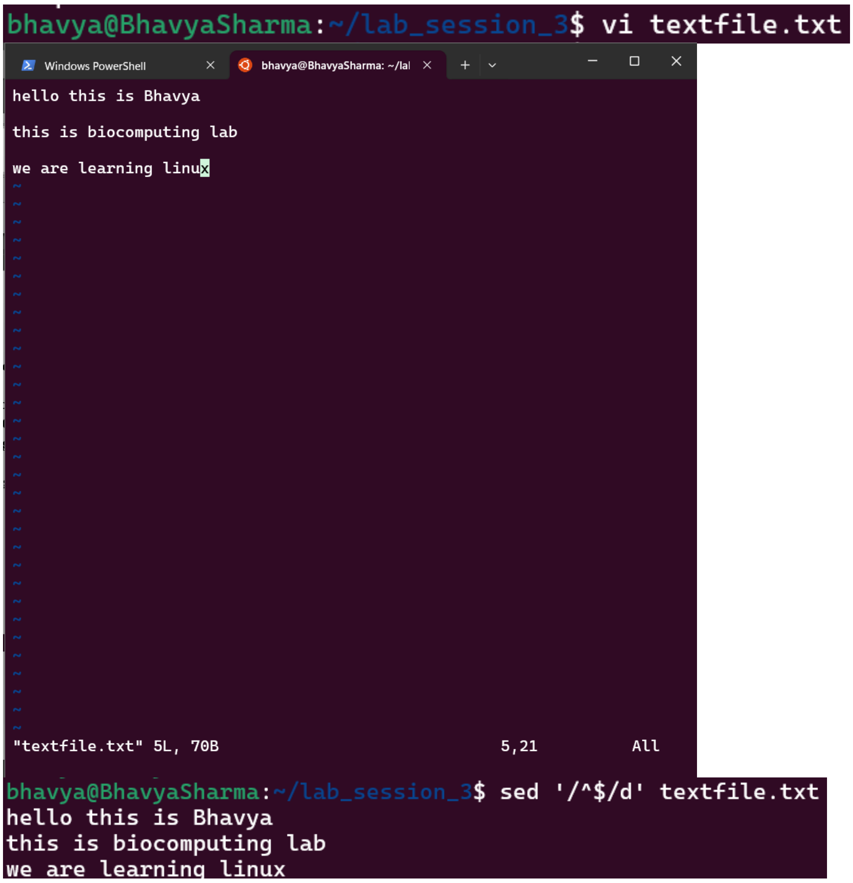
Q1)
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ vi textfile.txt
```

```
hello this is Bhavya

this is biocomputing lab

we are learning linux
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~
"textfile.txt" 5L, 70B                                    5,21          All
```
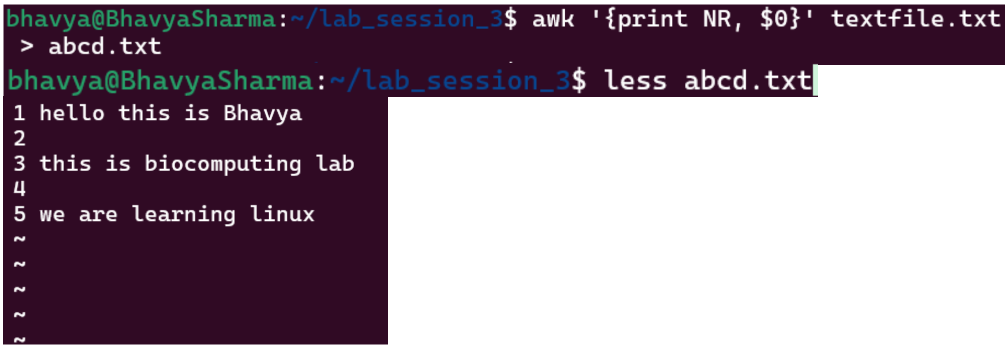

```
bhavya@BhavyaSharma:~/lab_session_3$ sed '/^$/d' textfile.txt
hello this is Bhavya
this is biocomputing lab
we are learning linux
```

Q2)

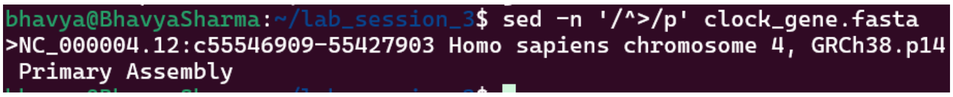
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '{print NR, $0}' textfile.txt
 > abcd.txt
bhavya@BhavyaSharma:~/lab_session_3$ less abcd.txt
1 hello this is Bhavya
2
3 this is biocomputing lab
4
5 we are learning linux
~
~
~
~
~
```

Q3)

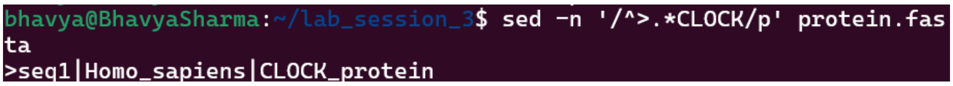
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ sed -n '/^>/p' clock_gene.fasta
>NC_000004.12:c55546909-55427903 Homo sapiens chromosome 4, GRCh38.p14
 Primary Assembly
```

Q4)

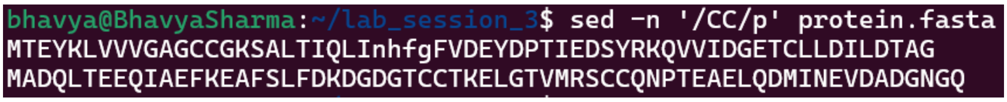
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ sed -n '/^>.*CLOCK/p' protein.fas
ta
>seq1|Homo_sapiens|CLOCK_protein
```

Q5)

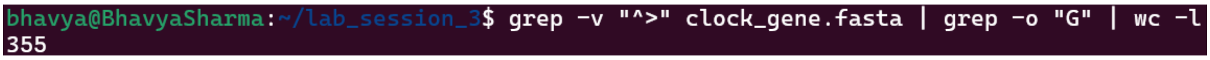
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ sed -n '/CC/p' protein.fasta
MTEYKLVVVGAGCCGKSALTIQLInhfgFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAG
MADQLTEEQIAEFKEAFSLFDKDGDGTCCTKELGTVMRSCCQNPTEAELQDMINEVDADGNGQ
```

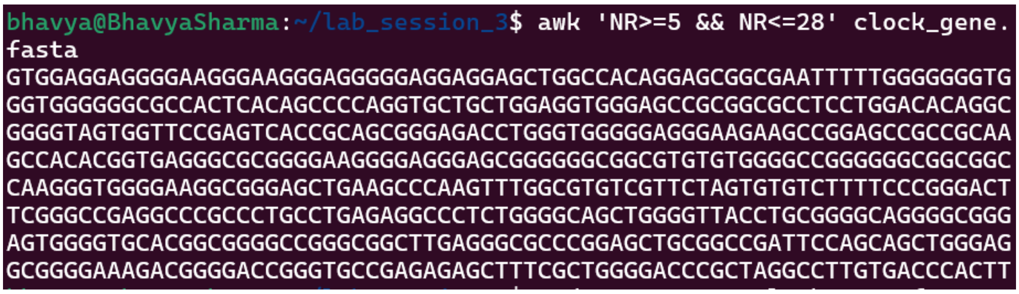
Q6)

Output-



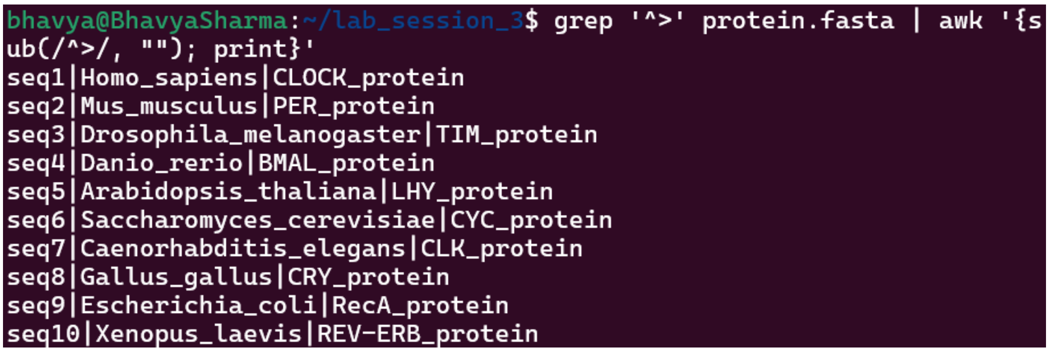
```
bhavya@BhavyaSharma:~/lab_session_3$ grep -v "^>" clock_gene.fasta | grep -o "G" | wc -l
355
```

Q7)
Output-



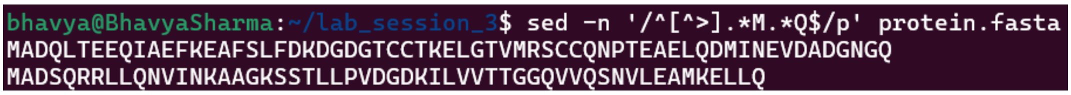
```
bhavya@BhavyaSharma:~/lab_session_3$ awk 'NR>=5 && NR<=28' clock_gene.
fasta
GTGGAGGAGGGGAAGGGAAGGGAGGGGGAGGAGGAGCTGGCCACAGGAGCGGCGAATTTTTGGGGGGGTG
GGTGGGGGGCGCCACTCACAGCCCCAGGTGCTGCTGGAGGTGGGAGCCGCGGCGCCTCCTGGACACAGGC
GGGGTAGTGGTTCCGAGTCACCGCAGCGGGAGACCTGGGTGGGGGAGGGAAGAAGCCGGAGCCGCCGCAA
GCCACACGGTGAGGGCGCGGGGAAGGGGAGGGAGCGGGGGGCGGCGTGTGTGGGGCCGGGGGGCGGCGGC
CAAGGGTGGGGAAGGCGGGAGCTGAAGCCCAAGTTTGGCGTGTCGTTCTAGTGTGTCTTTTCCCGGGACT
TCGGGCCGAGGCCCGCCCTGCCTGAGAGGCCCTCTGGGGCAGCTGGGGTTACCTGCGGGGCAGGGGCGGG
AGTGGGGTGCACGGCGGGGCCGGGCGGCTTGAGGGCGCCCGGAGCTGCGGCCGATTCCAGCAGCTGGGAG
GCGGGGAAAGACGGGGACCGGGTGCCGAGAGAGCTTTCGCTGGGGACCCGCTAGGCCTTGTGACCCACTT
```

Q8)
Output-

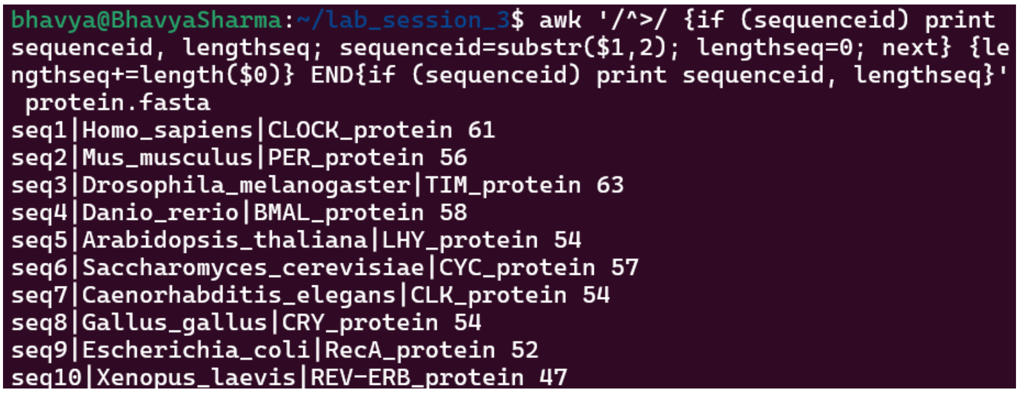


```
bhavya@BhavyaSharma:~/lab_session_3$ grep '^>' protein.fasta | awk '{s
ub(/^>/, ""); print}'
seq1|Homo_sapiens|CLOCK_protein
seq2|Mus_musculus|PER_protein
seq3|Drosophila_melanogaster|TIM_protein
seq4|Danio_rerio|BMAL_protein
seq5|Arabidopsis_thaliana|LHY_protein
seq6|Saccharomyces_cerevisiae|CYC_protein
seq7|Caenorhabditis_elegans|CLK_protein
seq8|Gallus_gallus|CRY_protein
seq9|Escherichia_coli|RecA_protein
seq10|Xenopus_laevis|REV-ERB_protein
```

Q9)
Output-



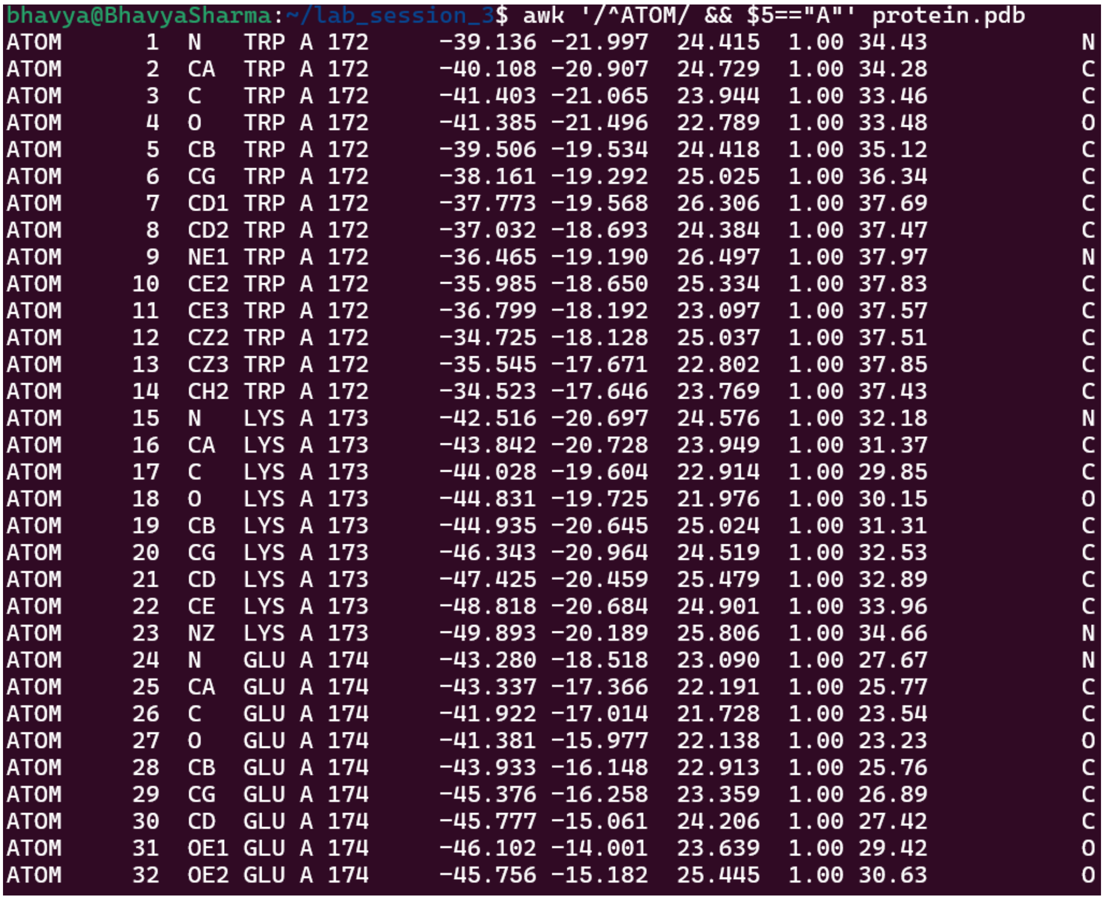
```
bhavya@BhavyaSharma:~/lab_session_3$ sed -n '/^[^>].*M.*Q$/p' protein.fasta
MADQLTEEQIAEFKEAFSLFDKDGDGTCCTKELGTVMRSCCQNPTEAELQDMINEVDADGNGQ
MADSQRRLLQNVINKAAGKSSTLLPVDGDKILVVTTGGQVVQSNVLEAMKELLQ
```



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^>/ {if (sequenceid) print
sequenceid, lengthseq; sequenceid=substr($1,2); lengthseq=0; next} {le
ngthseq+=length($0)} END{if (sequenceid) print sequenceid, lengthseq}'
 protein.fasta
seq1|Homo_sapiens|CLOCK_protein 61
seq2|Mus_musculus|PER_protein 56
seq3|Drosophila_melanogaster|TIM_protein 63
seq4|Danio_rerio|BMAL_protein 58
seq5|Arabidopsis_thaliana|LHY_protein 54
seq6|Saccharomyces_cerevisiae|CYC_protein 57
seq7|Caenorhabditis_elegans|CLK_protein 54
seq8|Gallus_gallus|CRY_protein 54
seq9|Escherichia_coli|RecA_protein 52
seq10|Xenopus_laevis|REV-ERB_protein 47
```

Q10)

Output-

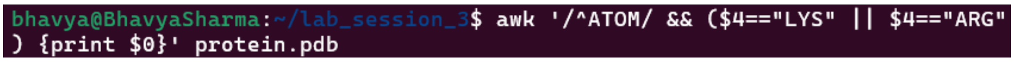


```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^ATOM/ && $5=="A"' protein.pdb
ATOM      1  N   TRP A 172     -39.136 -21.997  24.415  1.00 34.43           N
ATOM      2  CA  TRP A 172     -40.108 -20.907  24.729  1.00 34.28           C
ATOM      3  C   TRP A 172     -41.403 -21.065  23.944  1.00 33.46           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
```

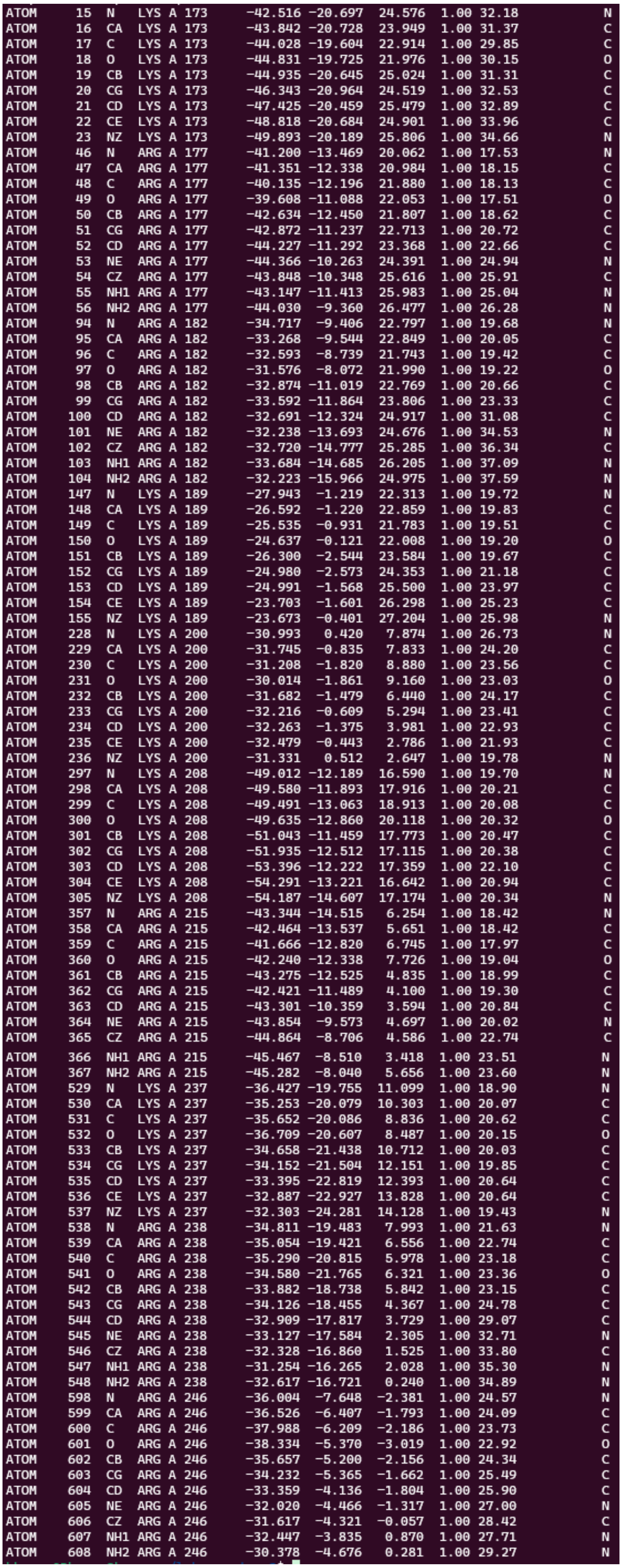
(Printed all the ATOM lines with Chain A- The output was quite large so pasting this snippet here to avoid taking up too much space.)

Q11)

Output-



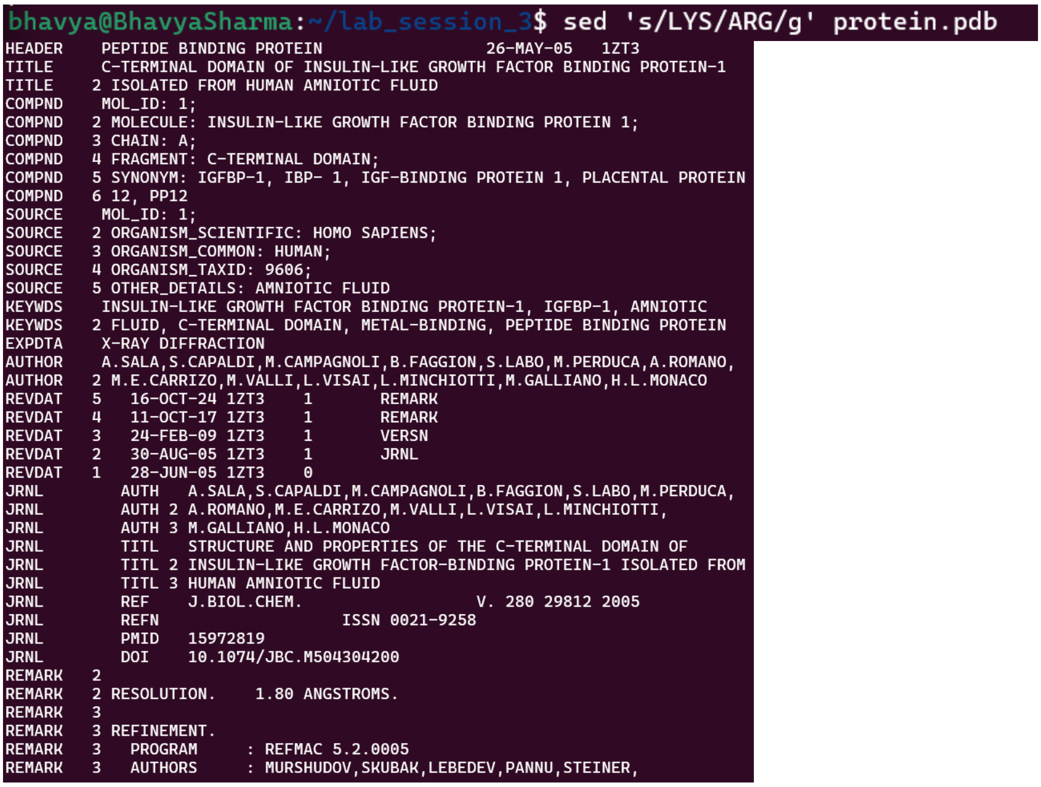
```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^ATOM/ && ($4=="LYS" || $4=="ARG"
) {print $0}' protein.pdb
```



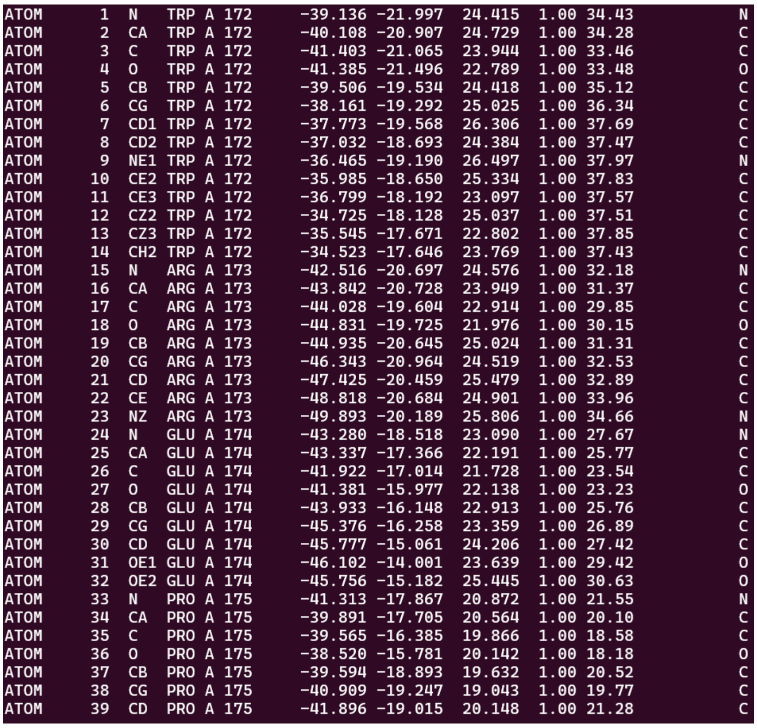
```
ATOM     15  N   LYS A 173     -42.516 -20.697  24.576  1.00 32.18           N
ATOM     16  CA  LYS A 173     -43.842 -20.728  23.949  1.00 31.37           C
ATOM     17  C   LYS A 173     -44.028 -19.604  22.914  1.00 29.85           C
ATOM     18  O   LYS A 173     -44.831 -19.725  21.976  1.00 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
ATOM    151  CB  LYS A 189     -26.300  -2.544  23.584  1.00 19.67           C
ATOM    152  CG  LYS A 189     -24.980  -2.573  24.353  1.00 21.18           C
ATOM    153  CD  LYS A 189     -24.991  -1.568  25.500  1.00 23.97           C
ATOM    154  CE  LYS A 189     -23.703  -1.601  26.298  1.00 25.23           C
ATOM    155  NZ  LYS A 189     -23.673  -0.401  27.204  1.00 25.98           N
ATOM    228  N   LYS A 200     -30.993   0.420   7.874  1.00 26.73           N
ATOM    229  CA  LYS A 200     -31.745  -0.835   7.833  1.00 24.20           C
ATOM    230  C   LYS A 200     -31.208  -1.820   8.880  1.00 23.56           C
ATOM    231  O   LYS A 200     -30.014  -1.861   9.160  1.00 23.03           O
ATOM    232  CB  LYS A 200     -31.682  -1.479   6.440  1.00 24.17           C
ATOM    233  CG  LYS A 200     -32.216  -0.609   5.294  1.00 23.41           C
ATOM    234  CD  LYS A 200     -32.263  -1.375   3.981  1.00 22.93           C
ATOM    235  CE  LYS A 200     -32.479  -0.443   2.786  1.00 21.93           C
ATOM    236  NZ  LYS A 200     -31.331   0.512   2.647  1.00 19.78           N
ATOM    297  N   LYS A 208     -49.012 -12.189  16.590  1.00 19.70           N
ATOM    298  CA  LYS A 208     -49.580 -11.893  17.916  1.00 20.21           C
ATOM    299  C   LYS A 208     -49.491 -13.063  18.913  1.00 20.08           C
ATOM    300  O   LYS A 208     -49.635 -12.860  20.118  1.00 20.32           O
ATOM    301  CB  LYS A 208     -51.043 -11.459  17.773  1.00 20.47           C
ATOM    302  CG  LYS A 208     -51.935 -12.512  17.115  1.00 20.38           C
ATOM    303  CD  LYS A 208     -53.396 -12.222  17.359  1.00 22.10           C
ATOM    304  CE  LYS A 208     -54.291 -13.221  16.642  1.00 20.94           C
ATOM    305  NZ  LYS A 208     -54.187 -14.607  17.174  1.00 20.34           N
ATOM    357  N   ARG A 215     -43.344 -14.515   6.254  1.00 18.42           N
ATOM    358  CA  ARG A 215     -42.464 -13.537   5.651  1.00 18.42           C
ATOM    359  C   ARG A 215     -41.666 -12.820   6.745  1.00 17.97           C
ATOM    360  O   ARG A 215     -42.240 -12.338   7.726  1.00 19.04           O
ATOM    361  CB  ARG A 215     -43.275 -12.525   4.835  1.00 18.99           C
ATOM    362  CG  ARG A 215     -42.421 -11.489   4.100  1.00 19.30           C
ATOM    363  CD  ARG A 215     -43.301 -10.359   3.594  1.00 20.84           C
ATOM    364  NE  ARG A 215     -43.854  -9.573   4.697  1.00 20.02           N
ATOM    365  CZ  ARG A 215     -44.864  -8.706   4.586  1.00 22.74           C
ATOM    366  NH1 ARG A 215     -45.467  -8.510   3.418  1.00 23.51           N
ATOM    367  NH2 ARG A 215     -45.282  -8.040   5.656  1.00 23.60           N
ATOM    529  N   LYS A 237     -36.427 -19.755  11.099  1.00 18.90           N
ATOM    530  CA  LYS A 237     -35.253 -20.079  10.303  1.00 20.07           C
ATOM    531  C   LYS A 237     -35.652 -20.086   8.836  1.00 20.62           C
ATOM    532  O   LYS A 237     -36.709 -20.607   8.487  1.00 20.15           O
ATOM    533  CB  LYS A 237     -34.658 -21.438  10.712  1.00 20.03           C
ATOM    534  CG  LYS A 237     -34.152 -21.504  12.151  1.00 19.85           C
ATOM    535  CD  LYS A 237     -33.395 -22.819  12.393  1.00 20.64           C
ATOM    536  CE  LYS A 237     -32.887 -22.927  13.828  1.00 20.64           C
ATOM    537  NZ  LYS A 237     -32.303 -24.281  14.128  1.00 19.43           N
ATOM    538  N   ARG A 238     -34.811 -19.483   7.993  1.00 21.63           N
ATOM    539  CA  ARG A 238     -35.054 -19.421   6.556  1.00 22.74           C
ATOM    540  C   ARG A 238     -35.290 -20.815   5.978  1.00 23.18           C
ATOM    541  O   ARG A 238     -34.580 -21.765   6.321  1.00 23.36           O
ATOM    542  CB  ARG A 238     -33.882 -18.738   5.842  1.00 23.15           C
ATOM    543  CG  ARG A 238     -34.126 -18.455   4.367  1.00 24.78           C
ATOM    544  CD  ARG A 238     -32.909 -17.817   3.729  1.00 29.07           C
ATOM    545  NE  ARG A 238     -33.127 -17.584   2.305  1.00 32.71           N
ATOM    546  CZ  ARG A 238     -32.328 -16.860   1.525  1.00 33.80           C
ATOM    547  NH1 ARG A 238     -31.254 -16.265   2.028  1.00 35.30           N
ATOM    548  NH2 ARG A 238     -32.617 -16.721   0.240  1.00 34.89           N
ATOM    598  N   ARG A 246     -36.004  -7.648  -2.381  1.00 24.57           N
ATOM    599  CA  ARG A 246     -36.526  -6.407  -1.793  1.00 24.09           C
ATOM    600  C   ARG A 246     -37.988  -6.209  -2.186  1.00 23.73           C
ATOM    601  O   ARG A 246     -38.334  -5.370  -3.019  1.00 22.92           O
ATOM    602  CB  ARG A 246     -35.657  -5.200  -2.156  1.00 24.34           C
ATOM    603  CG  ARG A 246     -34.232  -5.365  -1.662  1.00 25.49           C
ATOM    604  CD  ARG A 246     -33.359  -4.136  -1.804  1.00 25.90           C
ATOM    605  NE  ARG A 246     -32.020  -4.466  -1.317  1.00 27.00           N
ATOM    606  CZ  ARG A 246     -31.617  -4.321  -0.057  1.00 28.42           C
ATOM    607  NH1 ARG A 246     -32.447  -3.835   0.870  1.00 27.71           N
ATOM    608  NH2 ARG A 246     -30.378  -4.676   0.281  1.00 29.27           N
```

Q12)

Output-



```
bhavya@BhavyaSharma:~/lab_session_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
JRNL        REF    J.BIOL.CHEM.                  V. 280 29812 2005
JRNL        REFN                   ISSN 0021-9258
JRNL        PMID   15972819
JRNL        DOI    10.1074/JBC.M504304200
REMARK   2
REMARK   2 RESOLUTION.    1.80 ANGSTROMS.
REMARK   3
REMARK   3 REFINEMENT.
REMARK   3   PROGRAM     : REFMAC 5.2.0005
REMARK   3   AUTHORS     : MURSHUDOV,SKUBAK,LEBEDEV,PANNU,STEINER,
```

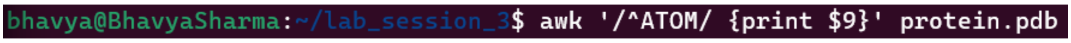


```
ATOM      1  N   TRP A 172     -39.136 -21.997  24.415  1.00 34.43           N
ATOM      2  CA  TRP A 172     -40.108 -20.907  24.729  1.00 34.28           C
ATOM      3  C   TRP A 172     -41.403 -21.065  23.944  1.00 33.46           C
ATOM      4  O   TRP A 172     -41.385 -21.496  22.789  1.00 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   ARG A 173     -42.516 -20.697  24.576  1.00 32.18           N
ATOM     16  CA  ARG A 173     -43.842 -20.728  23.949  1.00 31.37           C
ATOM     17  C   ARG A 173     -44.028 -19.604  22.914  1.00 29.85           C
ATOM     18  O   ARG A 173     -44.831 -19.725  21.976  1.00 30.15           O
ATOM     19  CB  ARG A 173     -44.935 -20.645  25.024  1.00 31.31           C
ATOM     20  CG  ARG A 173     -46.343 -20.964  24.519  1.00 32.53           C
ATOM     21  CD  ARG A 173     -47.425 -20.459  25.479  1.00 32.89           C
ATOM     22  CE  ARG A 173     -48.818 -20.684  24.901  1.00 33.96           C
ATOM     23  NZ  ARG 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
ATOM     39  CD  PRO A 175     -41.896 -19.015  20.148  1.00 21.28           C
```

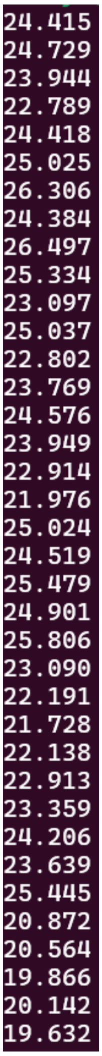
(Replaced every occurrence of LYS with ARG in protein.pdb. The output was quite large, so I'm pasting this snippet here to avoid taking up too much space.)

Q13)

Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^ATOM/ {print $9}' protein.pdb
```

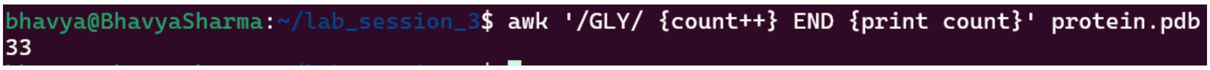


```
24.415
24.729
23.944
22.789
24.418
25.025
26.306
24.384
26.497
25.334
23.097
25.037
22.802
23.769
24.576
23.949
22.914
21.976
25.024
24.519
25.479
24.901
25.806
23.090
22.191
21.728
22.138
22.913
23.359
24.206
23.639
25.445
20.872
20.564
19.866
20.142
19.632
```

(Printed only the z-coordinate (third number in coordinates) for each atom from protein.pdb. The output was quite large, so I'm pasting this snippet here to avoid taking up too much space.)

Q14)

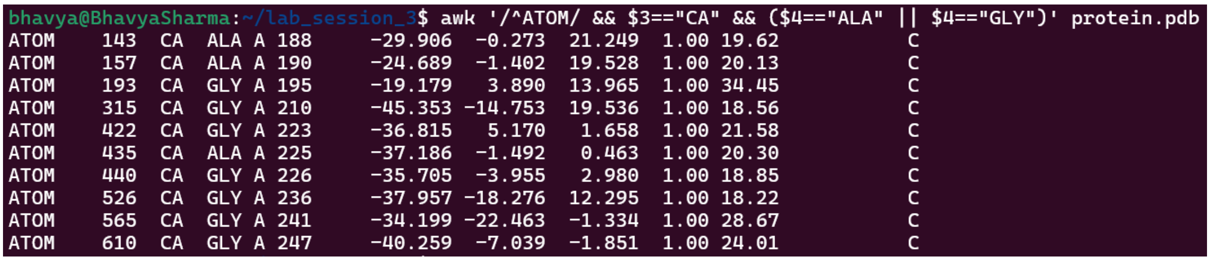
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/GLY/ {count++} END {print count}' protein.pdb
33
```

Q15)

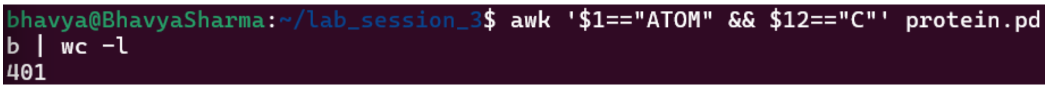
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^ATOM/ && $3=="CA" && ($4=="ALA" || $4=="GLY")' 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
```

Q16)

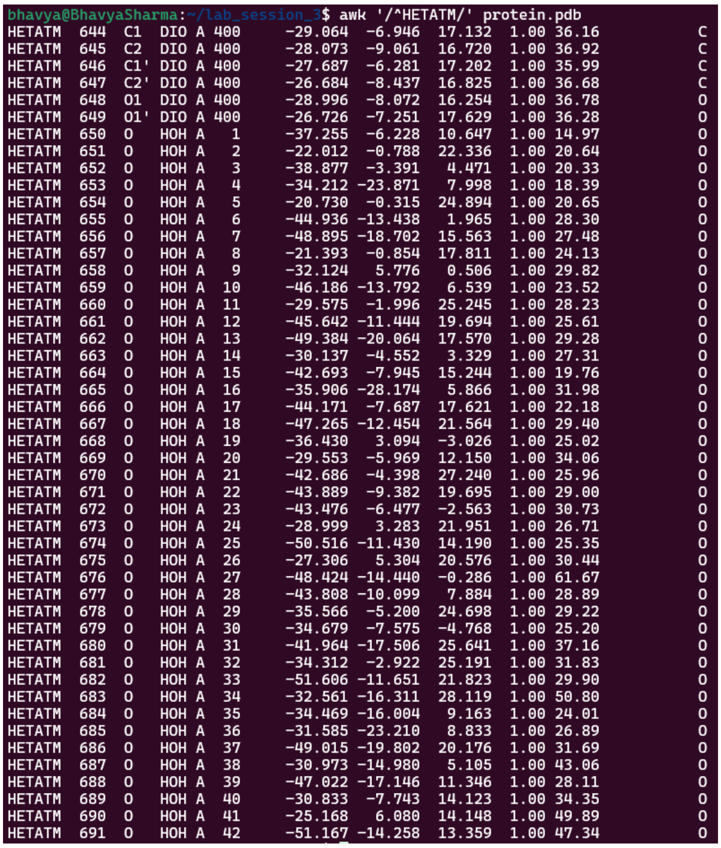
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '$1=="ATOM" && $12=="C"' protein.pd
b | wc -l
401
```

Q17)

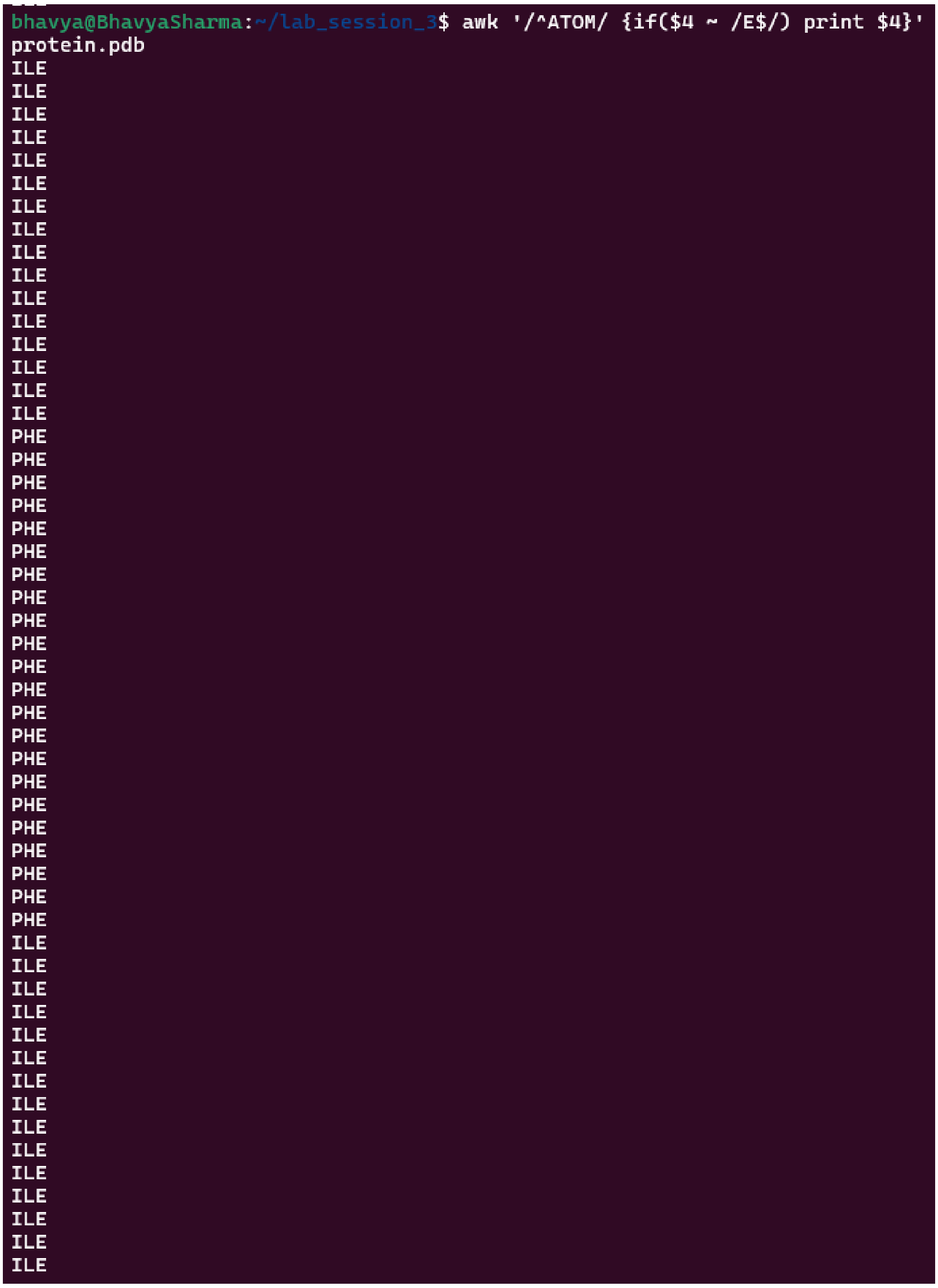
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^HETATM/' 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
HETATM  673  O   HOH A  24     -28.999   3.283  21.951  1.00 26.71           O
HETATM  674  O   HOH A  25     -50.516 -11.430  14.190  1.00 25.35           O
HETATM  675  O   HOH A  26     -27.306   5.304  20.576  1.00 30.44           O
HETATM  676  O   HOH A  27     -48.424 -14.440  -0.286  1.00 61.67           O
HETATM  677  O   HOH A  28     -43.808 -10.099   7.884  1.00 28.89           O
HETATM  678  O   HOH A  29     -35.566  -5.200  24.698  1.00 29.22           O
HETATM  679  O   HOH A  30     -34.679  -7.575  -4.768  1.00 25.20           O
HETATM  680  O   HOH A  31     -41.964 -17.506  25.641  1.00 37.16           O
HETATM  681  O   HOH A  32     -34.312  -2.922  25.191  1.00 31.83           O
HETATM  682  O   HOH A  33     -51.606 -11.651  21.823  1.00 29.90           O
HETATM  683  O   HOH A  34     -32.561 -16.311  28.119  1.00 50.80           O
HETATM  684  O   HOH A  35     -34.469 -16.004   9.163  1.00 24.01           O
HETATM  685  O   HOH A  36     -31.585 -23.210   8.833  1.00 26.89           O
HETATM  686  O   HOH A  37     -49.015 -19.802  20.176  1.00 31.69           O
HETATM  687  O   HOH A  38     -30.973 -14.980   5.105  1.00 43.06           O
HETATM  688  O   HOH A  39     -47.022 -17.146  11.346  1.00 28.11           O
HETATM  689  O   HOH A  40     -30.833  -7.743  14.123  1.00 34.35           O
HETATM  690  O   HOH A  41     -25.168   6.080  14.148  1.00 49.89           O
HETATM  691  O   HOH A  42     -51.167 -14.258  13.359  1.00 47.34           O
```

Q18)

Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^ATOM/ {if($4 ~ /E$/) print $4}'
protein.pdb
ILE
ILE
ILE
ILE
ILE
ILE
ILE
ILE
ILE
ILE
ILE
ILE
ILE
ILE
ILE
ILE
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```
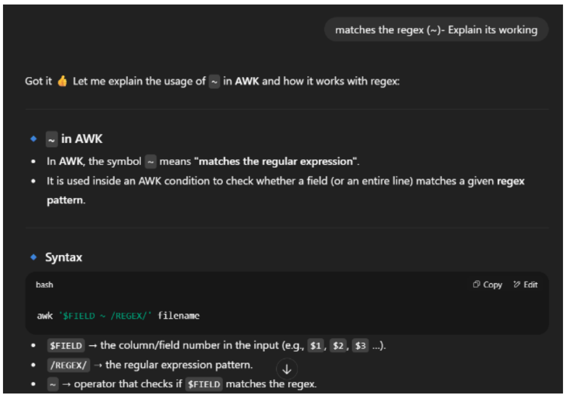

Used ChatGPT-



matches the regex (~)- Explain its working

Got it 👍 Let me explain the usage of `~` in **AWK** and how it works with regex:

◆ `~` **in AWK**

- In **AWK**, the symbol `~` means **"matches the regular expression"**.
- It is used inside an AWK condition to check whether a field (or an entire line) matches a given **regex pattern**.

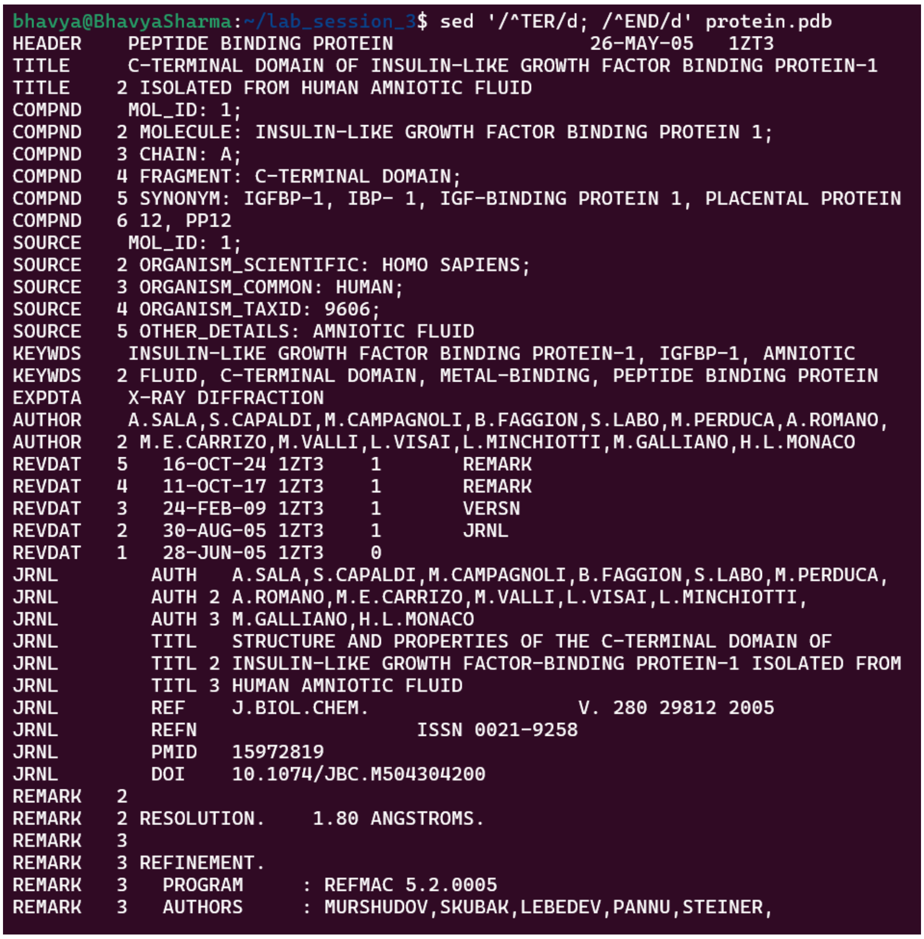
◆ **Syntax**

```bash
awk '$FIELD ~ /REGEX/' filename
```

- `$FIELD` → the column/field number in the input (e.g., `$1`, `$2`, `$3` ...).
- `/REGEX/` → the regular expression pattern.
- `~` → operator that checks if `$FIELD` matches the regex.

Q19)

Output-

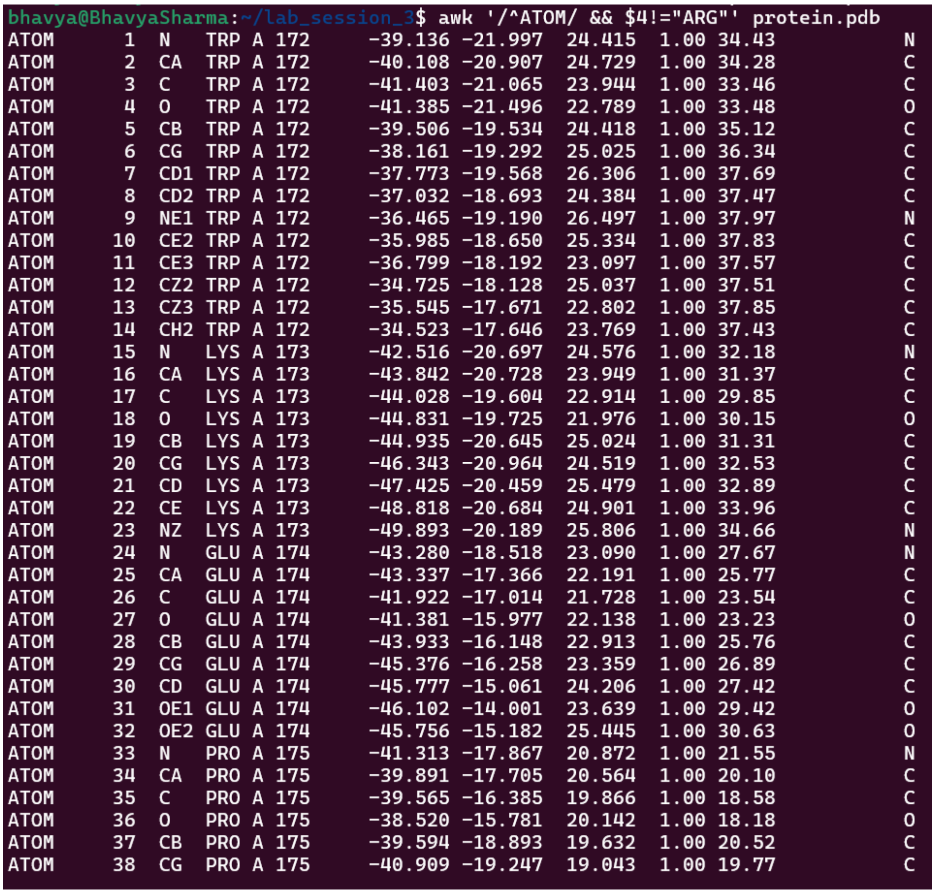


```
bhavya@BhavyaSharma:~/lab_session_3$ sed '/^TER/d; /^END/d' protein.pdb
HEADER    PEPTIDE BINDING PROTEIN                 26-MAY-05   1ZT3
TITLE     C-TERMINAL DOMAIN OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-1
TITLE    2 ISOLATED FROM HUMAN AMNIOTIC FLUID
COMPND    MOL_ID: 1;
COMPND   2 MOLECULE: 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
JRNL        REF    J.BIOL.CHEM.                  V. 280 29812 2005
JRNL        REFN                   ISSN 0021-9258
JRNL        PMID   15972819
JRNL        DOI    10.1074/JBC.M504304200
REMARK   2
REMARK   2 RESOLUTION.    1.80 ANGSTROMS.
REMARK   3
REMARK   3 REFINEMENT.
REMARK   3   PROGRAM     : REFMAC 5.2.0005
REMARK   3   AUTHORS     : MURSHUDOV,SKUBAK,LEBEDEV,PANNU,STEINER,
```

(Deleted all the lines that contain TER or END from protein.pdb. The output was quite large so pasting this snippet here to avoid taking up too much space.)

Q20)

Output-

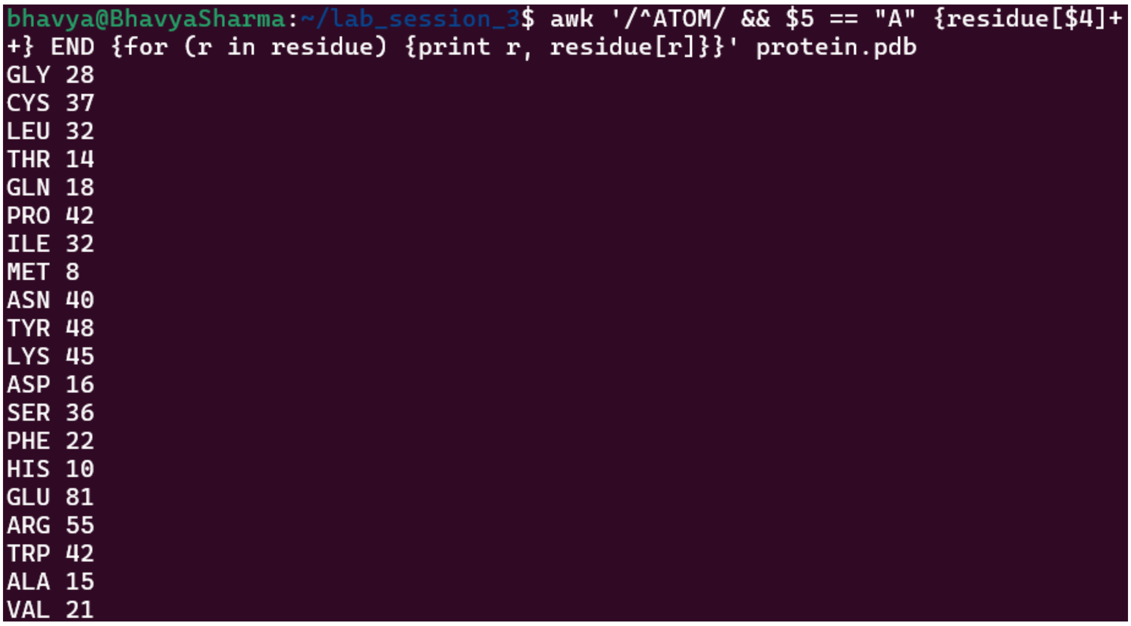


```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^ATOM/ && $4!="ARG"' protein.pdb
ATOM      1  N   TRP A 172     -39.136 -21.997  24.415  1.00 34.43           N
ATOM      2  CA  TRP A 172     -40.108 -20.907  24.729  1.00 34.28           C
ATOM      3  C   TRP A 172     -41.403 -21.065  23.944  1.00 33.46           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
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
```

(From protein.pdb, printed only the ATOM lines that do not belong to residue ARG. The output was quite large, so I'm pasting this snippet here to avoid taking up too much space.)

Q21)

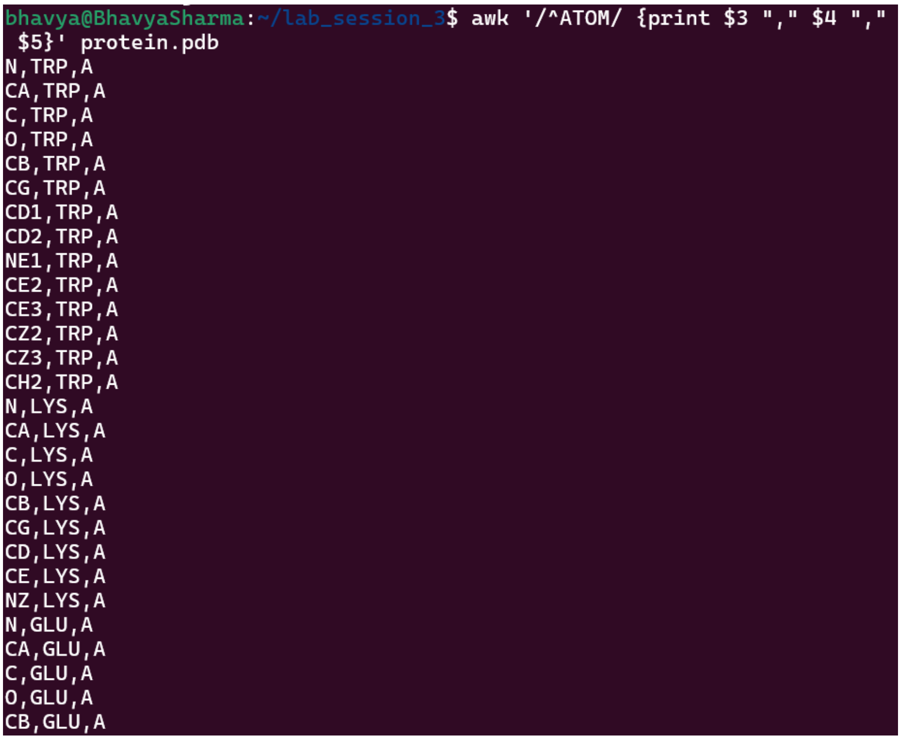
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^ATOM/ && $5 == "A" {residue[$4]+
+} END {for (r in residue) {print r, residue[r]}}' protein.pdb
GLY 28
CYS 37
LEU 32
THR 14
GLN 18
PRO 42
ILE 32
MET 8
ASN 40
TYR 48
LYS 45
ASP 16
SER 36
PHE 22
HIS 10
GLU 81
ARG 55
TRP 42
ALA 15
VAL 21
```

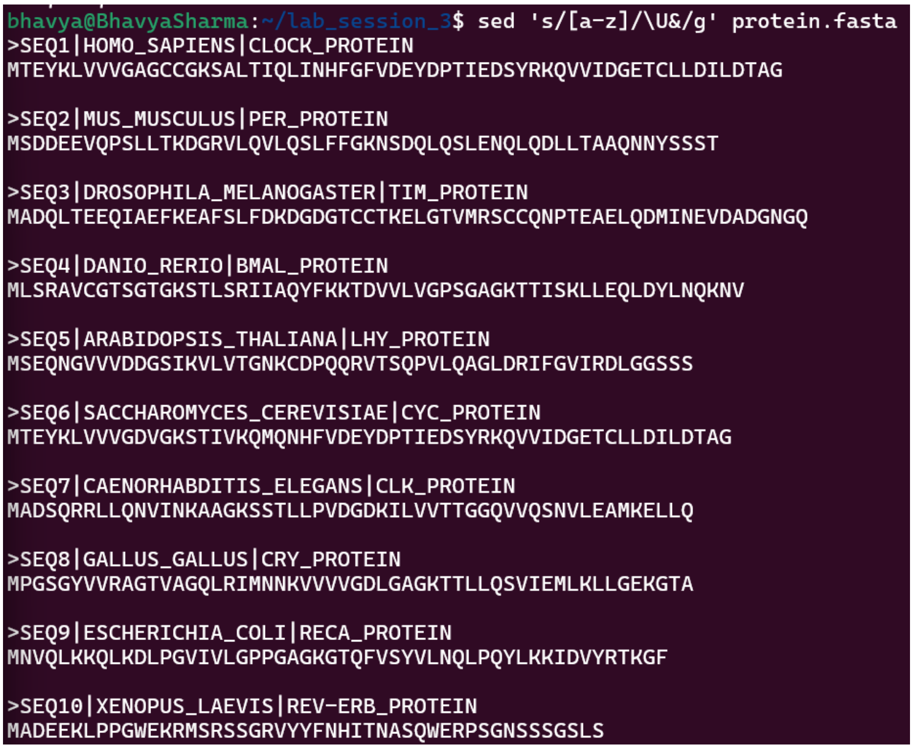
Q22)

Output-



```
bhavya@BhavyaSharma:~/lab_session_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
CG,LYS,A
CD,LYS,A
CE,LYS,A
NZ,LYS,A
N,GLU,A
CA,GLU,A
C,GLU,A
O,GLU,A
CB,GLU,A
```

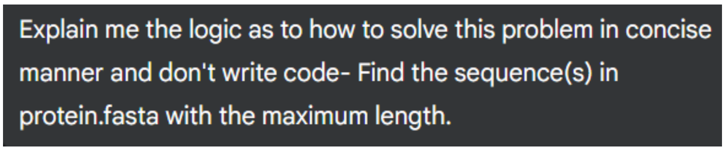
From protein.pdb, printed only the atom name, residue name, and chain ID, separated by commas. The output was quite large, so I pasted this snippet here to avoid taking up too much space.)



```
bhavya@BhavyaSharma:~/lab_session_3$ sed 's/[a-z]/\U&/g' 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
```

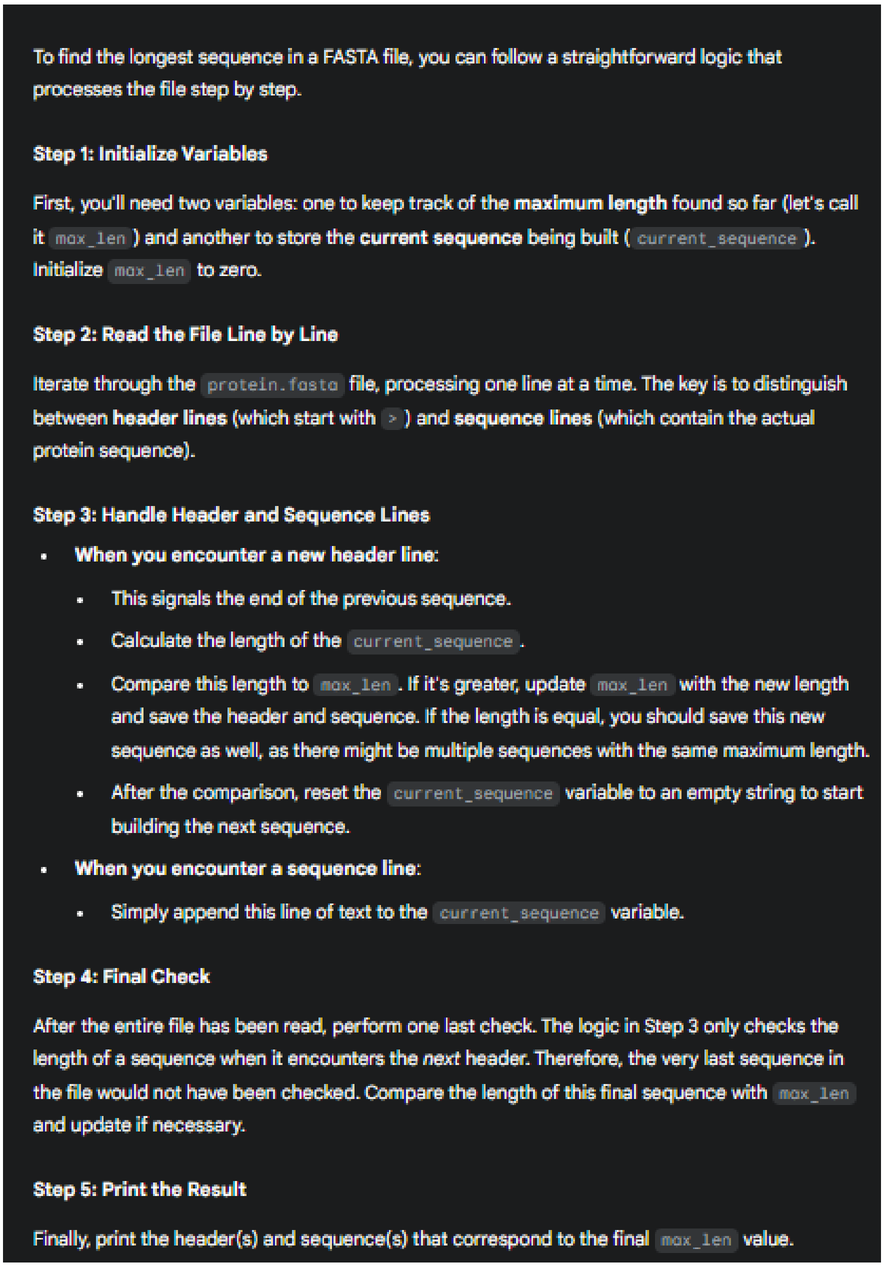
Q23)
Output-

For this question, I took the help of Gemini AI to understand the logic behind this problem-
Prompt given-



Explain me the logic as to how to solve this problem in concise manner and don't write code- Find the sequence(s) in protein.fasta with the maximum length.

Output-



To find the longest sequence in a FASTA file, you can follow a straightforward logic that processes the file step by step.

Step 1: Initialize Variables

First, you'll need two variables: one to keep track of the **maximum length** found so far (let's call it `max_len`) and another to store the **current sequence** being built (`current_sequence`). Initialize `max_len` to zero.

Step 2: Read the File Line by Line

Iterate through the `protein.fasta` file, processing one line at a time. The key is to distinguish between **header lines** (which start with `>`) and **sequence lines** (which contain the actual protein sequence).

Step 3: Handle Header and Sequence Lines

- **When you encounter a new header line:**
  - This signals the end of the previous sequence.
  - Calculate the length of the `current_sequence`.
  - Compare this length to `max_len`. If it's greater, update `max_len` with the new length and save the header and sequence. If the length is equal, you should save this new sequence as well, as there might be multiple sequences with the same maximum length.
  - After the comparison, reset the `current_sequence` variable to an empty string to start building the next sequence.
- **When you encounter a sequence line:**
  - Simply append this line of text to the `current_sequence` variable.

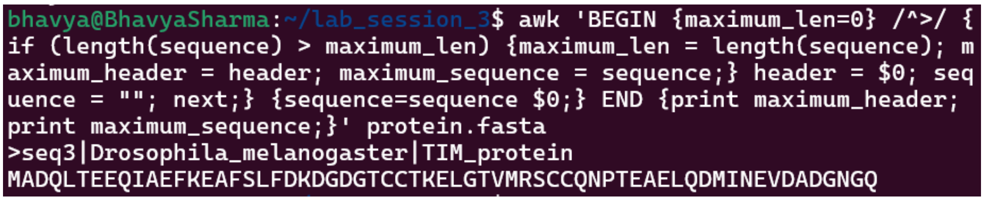
Step 4: Final Check

After the entire file has been read, perform one last check. The logic in Step 3 only checks the length of a sequence when it encounters the *next* header. Therefore, the very last sequence in the file would not have been checked. Compare the length of this final sequence with `max_len` and update if necessary.

Step 5: Print the Result

Finally, print the header(s) and sequence(s) that correspond to the final `max_len` value.

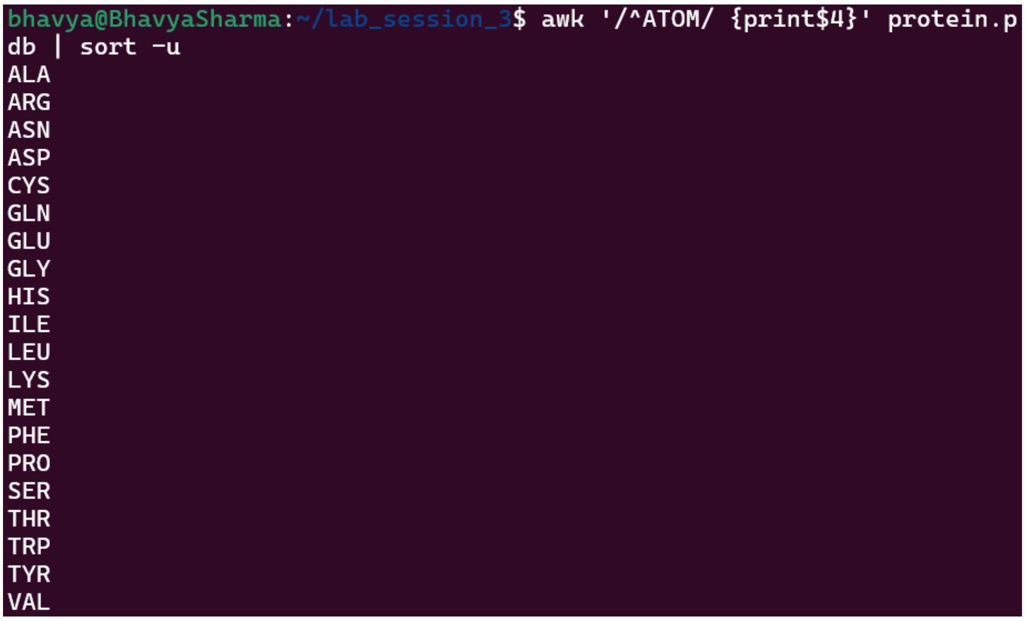
The code that I wrote and got the output is as follows-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk 'BEGIN {maximum_len=0} /^>/ {
if (length(sequence) > maximum_len) {maximum_len = length(sequence); m
aximum_header = header; maximum_sequence = sequence;} header = $0; seq
uence = ""; next;} {sequence=sequence $0;} END {print maximum_header;
print maximum_sequence;}' protein.fasta
>seq3|Drosophila_melanogaster|TIM_protein
MADQLTEEQIAEFKEAFSLFDKDGDGTCCTKELGTVMRSCCQNPTEAELQDMINEVDADGNGQ
```

Q24)

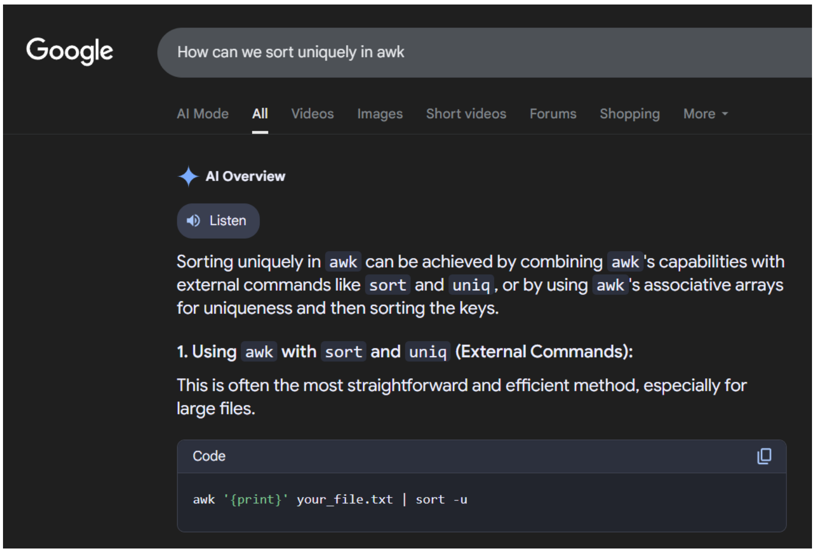
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^ATOM/ {print$4}' protein.p
db | sort -u
ALA
ARG
ASN
ASP
CYS
GLN
GLU
GLY
HIS
ILE
LEU
LYS
MET
PHE
PRO
SER
THR
TRP
TYR
VAL
```

In this question, I used a Google search to understand how to sort uniquely in awk.

This is the output I got-



How can we sort uniquely in awk

Sorting uniquely in `awk` can be achieved by combining `awk`'s capabilities with external commands like `sort` and `uniq`, or by using `awk`'s associative arrays for uniqueness and then sorting the keys.

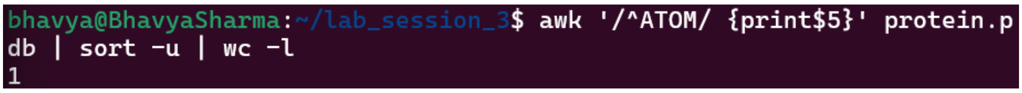
1. Using `awk` with `sort` and `uniq` (External Commands):

This is often the most straightforward and efficient method, especially for large files.

```
awk '{print}' your_file.txt | sort -u
```

Q25)

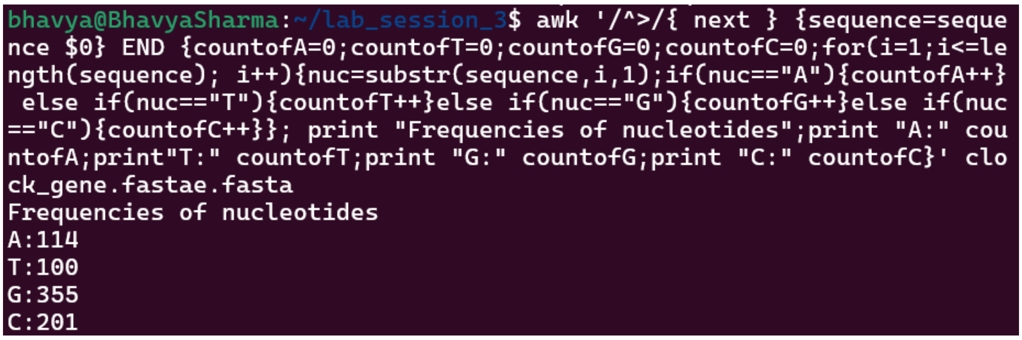
Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^ATOM/ {print$5}' protein.p
db | sort -u | wc -l
1
```

Q26)

Output-



```
bhavya@BhavyaSharma:~/lab_session_3$ awk '/^>/{ next } {sequence=seque
nce $0} END {countofA=0;countofT=0;countofG=0;countofC=0;for(i=1;i<=le
ngth(sequence); i++){nuc=substr(sequence,i,1);if(nuc=="A"){countofA++}
 else if(nuc=="T"){countofT++}else if(nuc=="G"){countofG++}else if(nuc
=="C"){countofC++}}; print "Frequencies of nucleotides";print "A:" cou
ntofA;print"T:" countofT;print "G:" countofG;print "C:" countofC}' clo
ck_gene.fastae.fasta
Frequencies of nucleotides
A:114
T:100
G:355
C:201
```