hw6

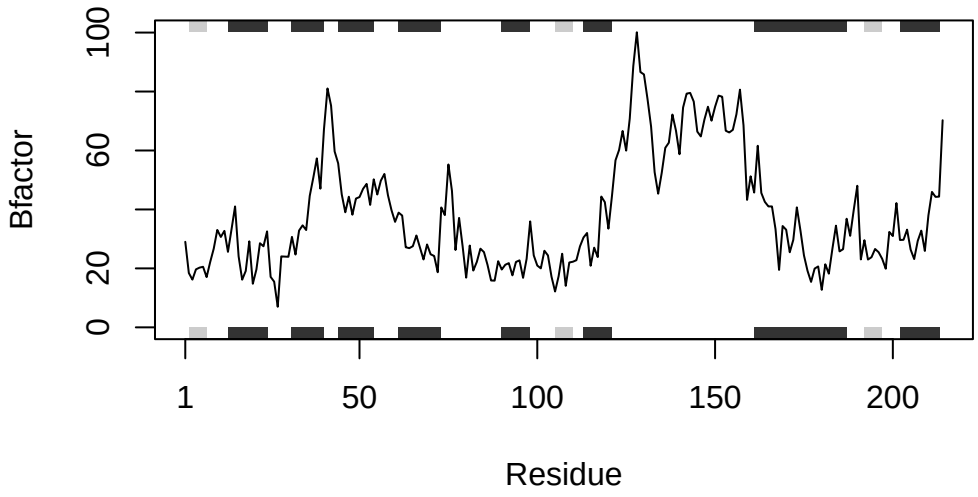
Angelica Rock (PID: A15781397)

My attempt at improved code

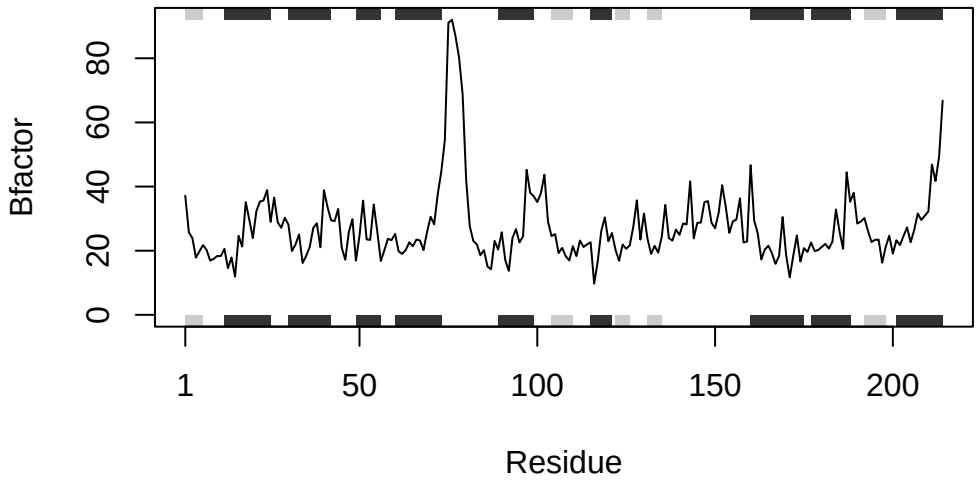
```
Run_PDB <- function(x) {
  library(bio3d) ## call bio3d after downloading package.
## If not downloaded, install.packages("bio3d")
## The input x is a variable which specifies what you are calling from the database

## Read a PDB file from the bio3d package
  read <- read.pdb(x)
## Specifies to retrieve the data from chain A and Calpha atoms
  trim <- trim.pdb(read, chain="A", elety="CA")
## Returns the Bfactor for each residue
  readb <- trim$atom$b
## Creates a standard lined scatter plot
  ## with a secondary structure (sse) returned from the specified data in trim object
  plotb3(readb, sse=trim, typ="l", ylab="Bfactor")
## Returns the results from the body of the function
    return(x)
}
## To call the function to run it and generate all graphs together as the output
  sapply(c("4AKE", "1AKE", "1E4Y"), Run_PDB)
```

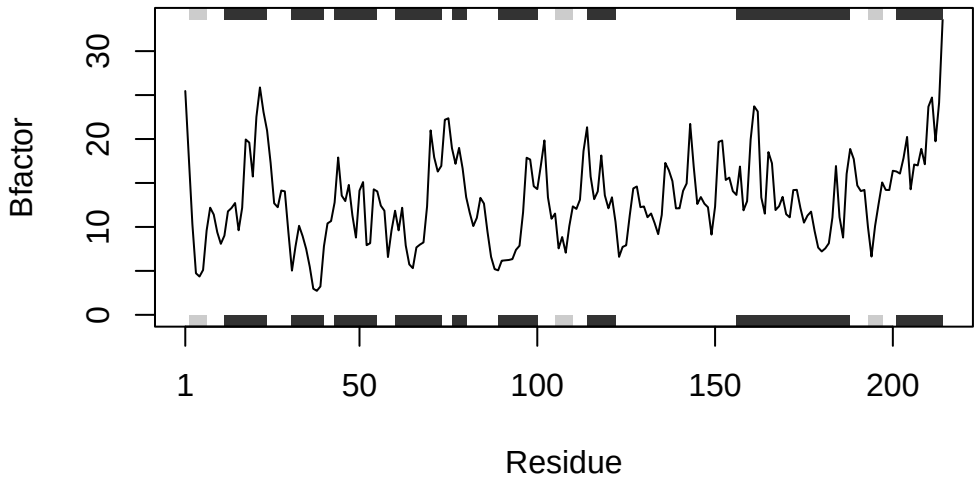
```
  Note: Accessing on-line PDB file
```




```
Note: Accessing on-line PDB file
 PDB has ALT records, taking A only, rm.alt=TRUE
```



```
Note: Accessing on-line PDB file
```




```
  4AKE   1AKE   1E4Y
"4AKE" "1AKE" "1E4Y"
```