Class 6 HW

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I simplified the code because I noticed that a lot of the steps being done were redundant and could be simplified using a function! Below I made a plot kinase function that takes an input and outputs a plot.

```r
library(bio3d)

plot_kinase <- function(input){
  output <- read.pdb(input)
  output.chainA <- trim.pdb(output, chain="A", elety="CA")
  output.B <- output.chainA$atom$b
  plotb3(output.B, sse = output.chainA, typ = "l", ylab = "Bfactor")
}
```
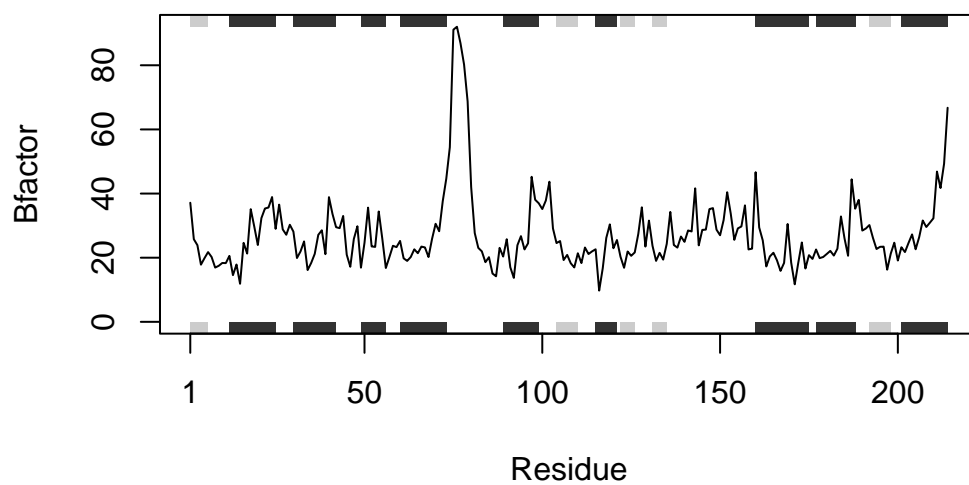
I used the `sapply()` function over the 3 genes of interest in order to apply the `plot_kinase()` function for these 3 genes.

```r
sapply(c("4AKE","1AKE", "1E4Y"), FUN = plot_kinase)
```
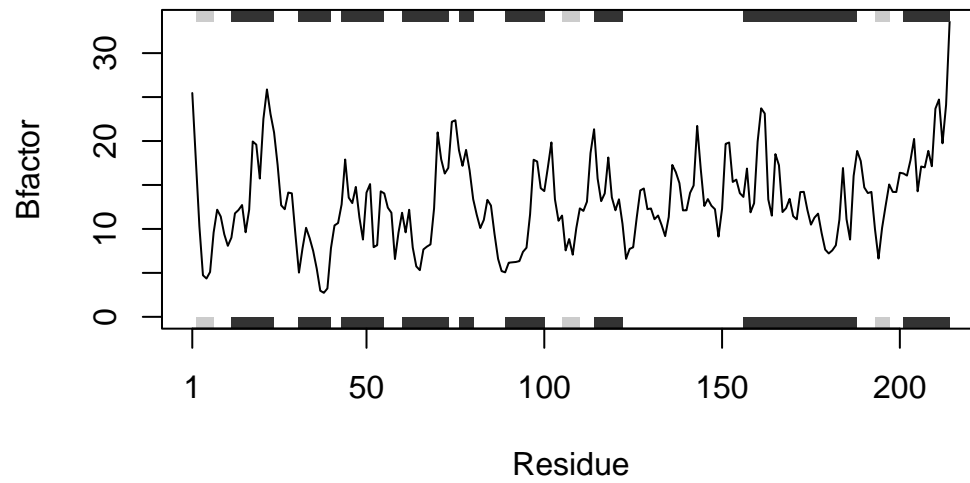
```
  Note: Accessing on-line PDB file
```

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

Note: Accessing on-line PDB file

$`4AKE`
NULL

$`1AKE`
NULL

$`1E4Y`
NULL