# class06hw

James Woolley (A16440072)

```r
library(bio3d) #accessing the library

graph_the_protein <- function(str) {
  seq <- read.pdb(str)
  seq.chainA <- trim.pdb(seq, chain="A", elety="CA") #chain input "a" you could look
  #at other chains by arguing with the function i think?
  seq.b <- seq.chainA$atom$b
  plotb3(seq.b, sse=seq.chainA, typ="l", ylab="Bfactor")
}
#this function looks at protein crystallography and ouputs a graph of the bfactor
graph_the_protein("4AKE")
```

```
Note: Accessing on-line PDB file
```
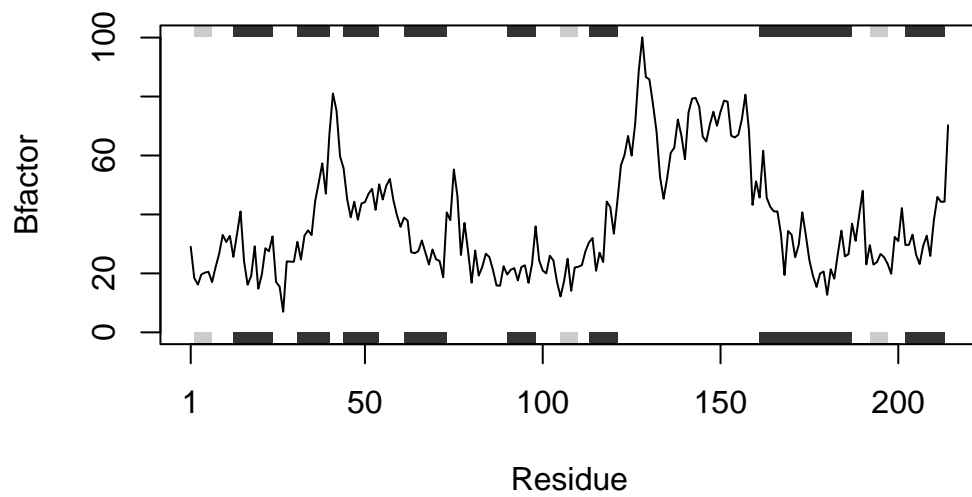
```r
graph_the_protein("1AKE")
```

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

```
graph_the_protein("1E4Y")
```

Note: Accessing on-line PDB file