

# hw06

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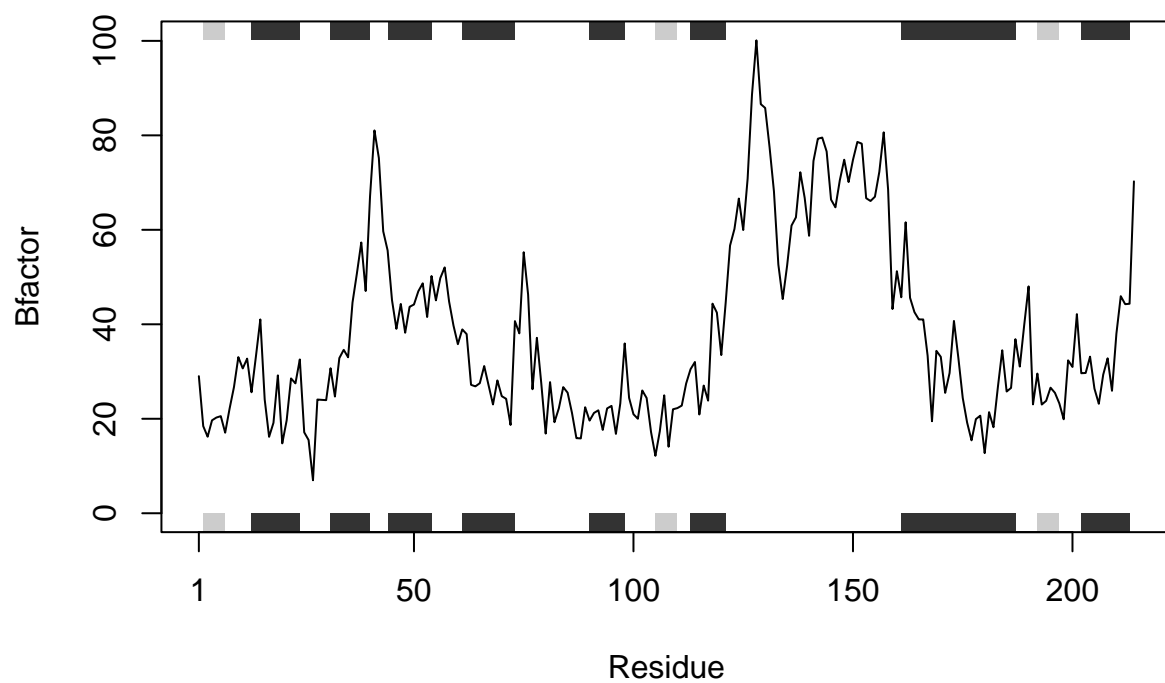
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```
# install.packages("bio3d")  
library("bio3d")
```

```
#' This function takes in the name and chain of a specific protein and plot the Bfactor across the resi  
#'  
#' @param prot a string representative of the name of the protein  
#' @param chain a string representative of the protein chain  
#'  
#' @return # a graph that shows the Bfactor across the residue of the protein  
#' @export  
#'  
#' @examples  
#' prot <- "4AKE"  
#' chain <- "A"  
#'  
#' prot_func(prot, chain)  
#'  
prot_func <- function(prot, chain) {  
  # get the data of specified protein  
  kinase <- read.pdb(prot)  
  # trim the data based on specific chain  
  kinase.chain <- trim.pdb(kinase, chain=chain, eley="CA")  
  # plot Bfactor across residue of the protein.  
  kinase.b <- kinase.chain$atom$b  
  plotb3(kinase.b, sse=kinase.chain, typ="l", ylab="Bfactor")  
}
```

```
prot_func("4AKE", "A")
```

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



```
prot_func("1AKE", "B")
```

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

