

Hw

A17576411

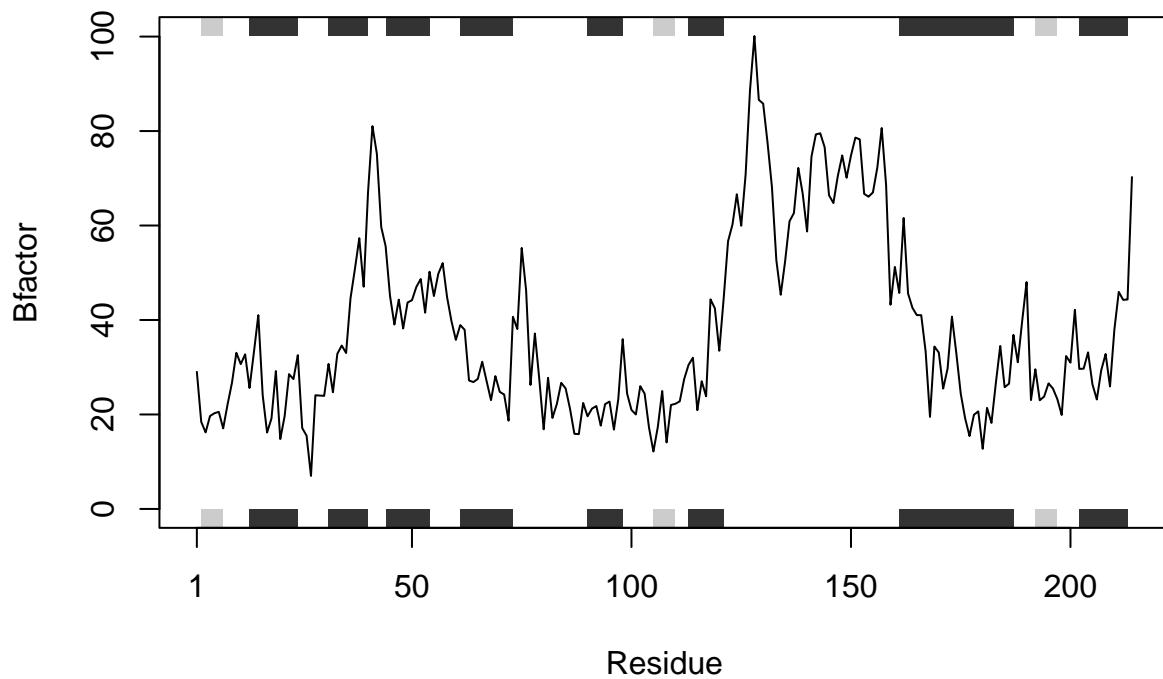
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```
library(bio3d)

find_protein <- function(pdb_id) {
  prot <- read.pdb(pdb_id)
  xchain <- trim.pdb(prot, chain = "A", eley = "CA")
  s3.b <- xchain$atom$b
  plotb3(s3.b, sse=xchain, ylab = "Bfactor", type = "l")
}

find_protein("4AKE")
```

Note: Accessing on-line PDB file



```
#The input is `find_protein("the protein you want")`
#The function constructs a plot for whichever protein you enter in
```

#The output of the function is a line plot