HW6

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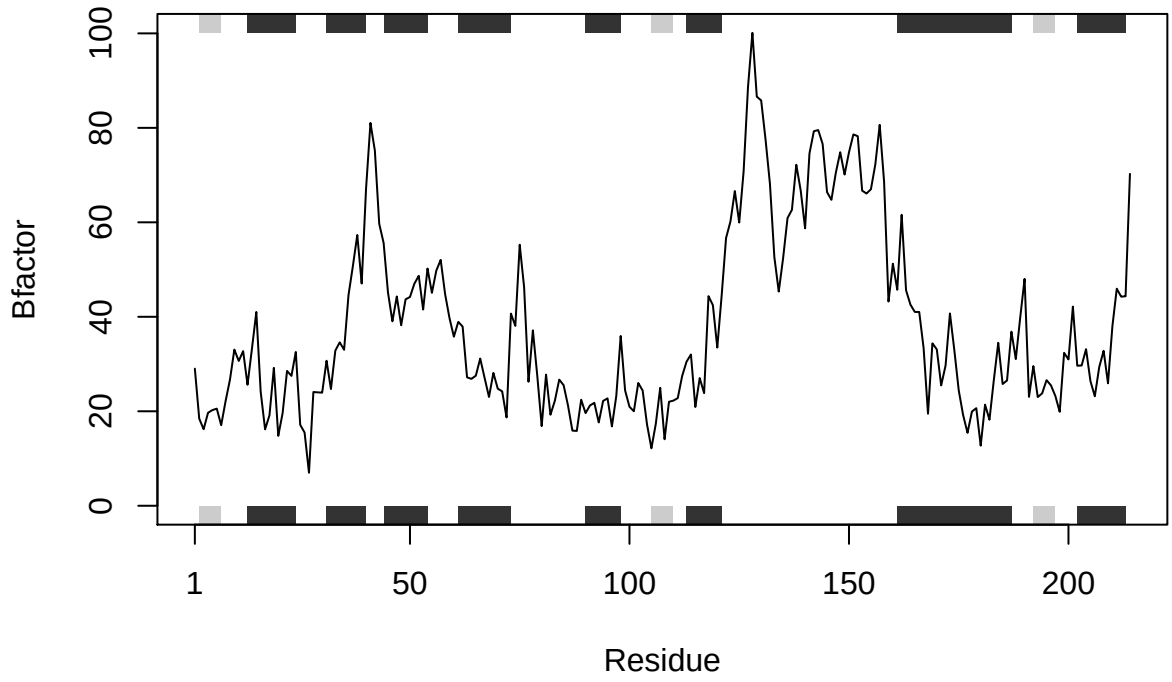
```
library(bio3d)
prostr <- function(x, chain_name = "A", elety_name = "CA", yl = "Bfactor", atom_col = "b"){
  s <- read.pdb(x)
  s.chain <- trim.pdb(s, chain = chain_name, elety = elety_name)
  s.atom <- s.chain$atom[,atom_col]
  plotb3(s.atom, sse=s.chain, typ="l", ylab = yl)
}
prostr("4AKE")
```

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




```
#Inputs: PDB ID (e.g., "4AKE")
#Optional Inputs: we can also specify which chain or atom
#or ylabel or elemet within dataframe atom we want.

#Process: the function first reads the pdb file and choose
#chainA, atom CA, and b, then makes a plot

#Output: the plot for the specified protein with x axis
#representing residues and y axis representing B factor
```