ProteinAnalysisFunction

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This is the original code

```
library(bio3d)
s1 <- read.pdb("4AKE") # kinase with drug
```

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

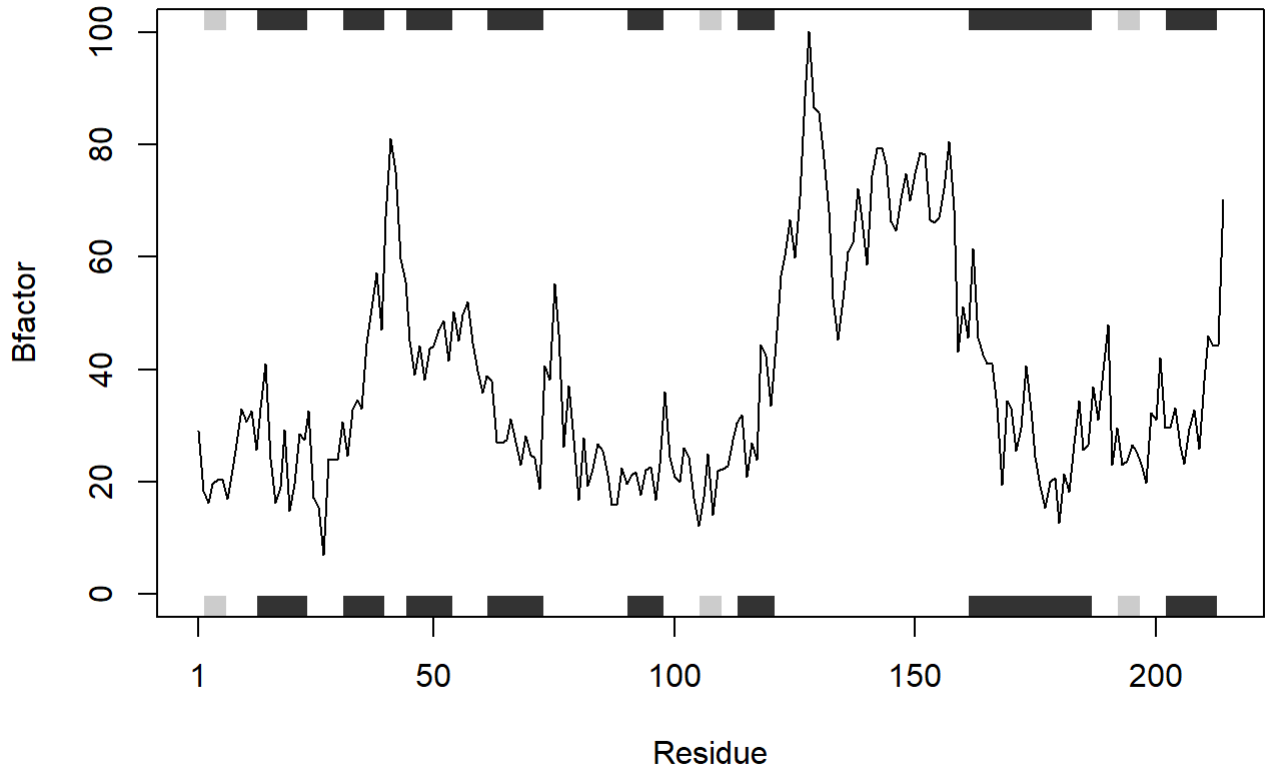
```
s2 <- read.pdb("1AKE") # kinase no drug
```

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

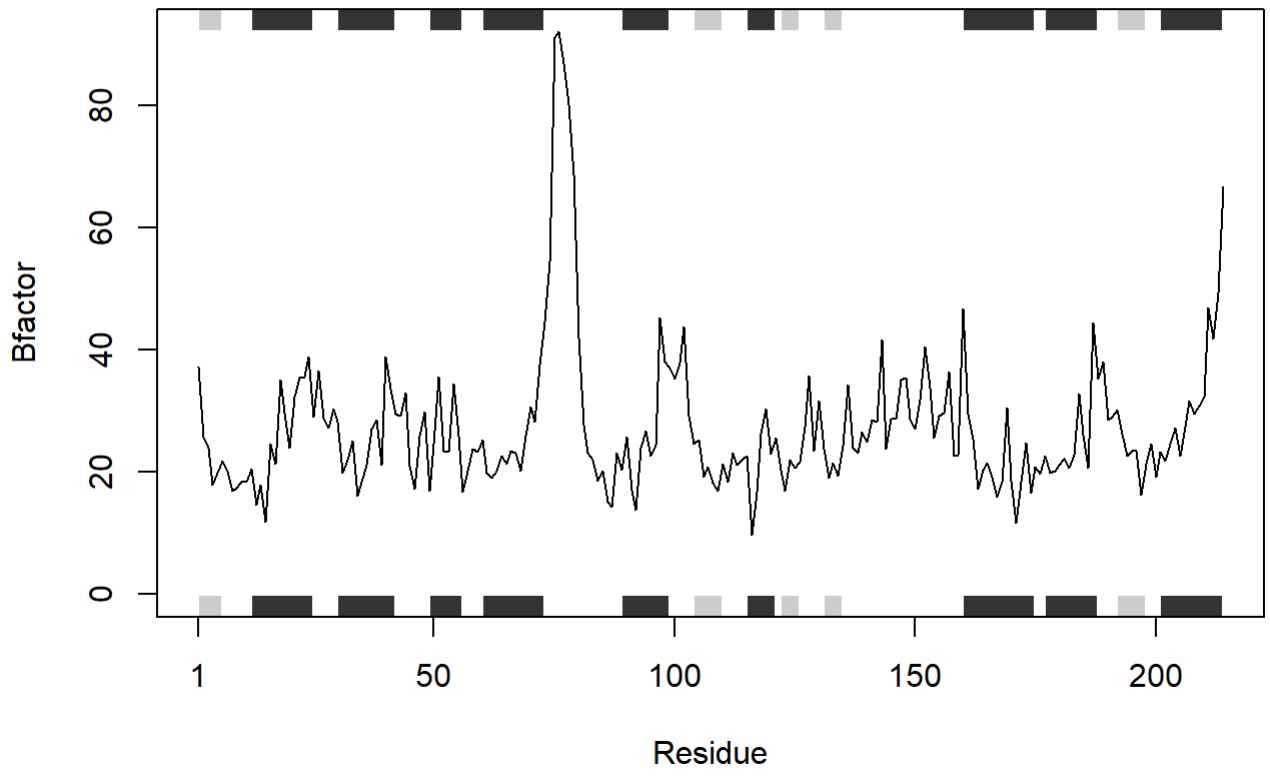
```
s3 <- read.pdb("1E4Y") # kinase with drug
```

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

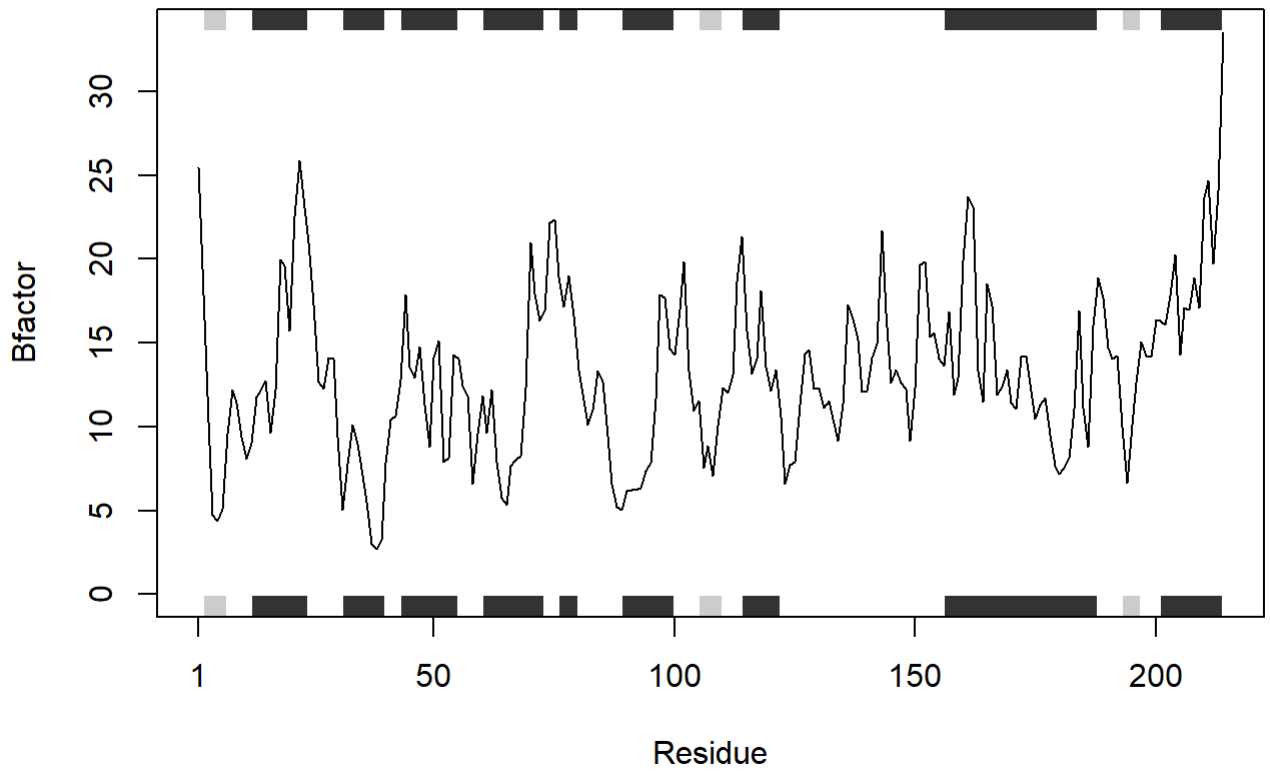
```
s1.chainA <- trim.pdb(s1, chain="A", elety="CA")
s2.chainA <- trim.pdb(s2, chain="A", elety="CA")
s3.chainA <- trim.pdb(s3, chain="A", elety="CA")
s1.b <- s1.chainA$atom$b
s2.b <- s2.chainA$atom$b
s3.b <- s3.chainA$atom$b
plotb3(s1.b, sse=s1.chainA, typ="l", ylab="Bfactor")
```




```
plotb3(s2.b, sse=s2.chainA, typ="l", ylab="Bfactor")
```




```
plotb3(s3.b, sse=s3.chainA, typ="l", ylab="Bfactor")
```



The assignment is to make a function that can be used to analyze any protein.

The input of this function is x, which is the protein name (“4AKE”, etc).

When you use the function anaylzeprotein(), it will make a plot that maps the Bfactor of the protein in relation to its residue. You use it by typing anaylzeprotein(“x”), where x is the code name for the protein you want to analzye.

The output of the function is analyzeprotein, which will make a plot of the protein you inputted.

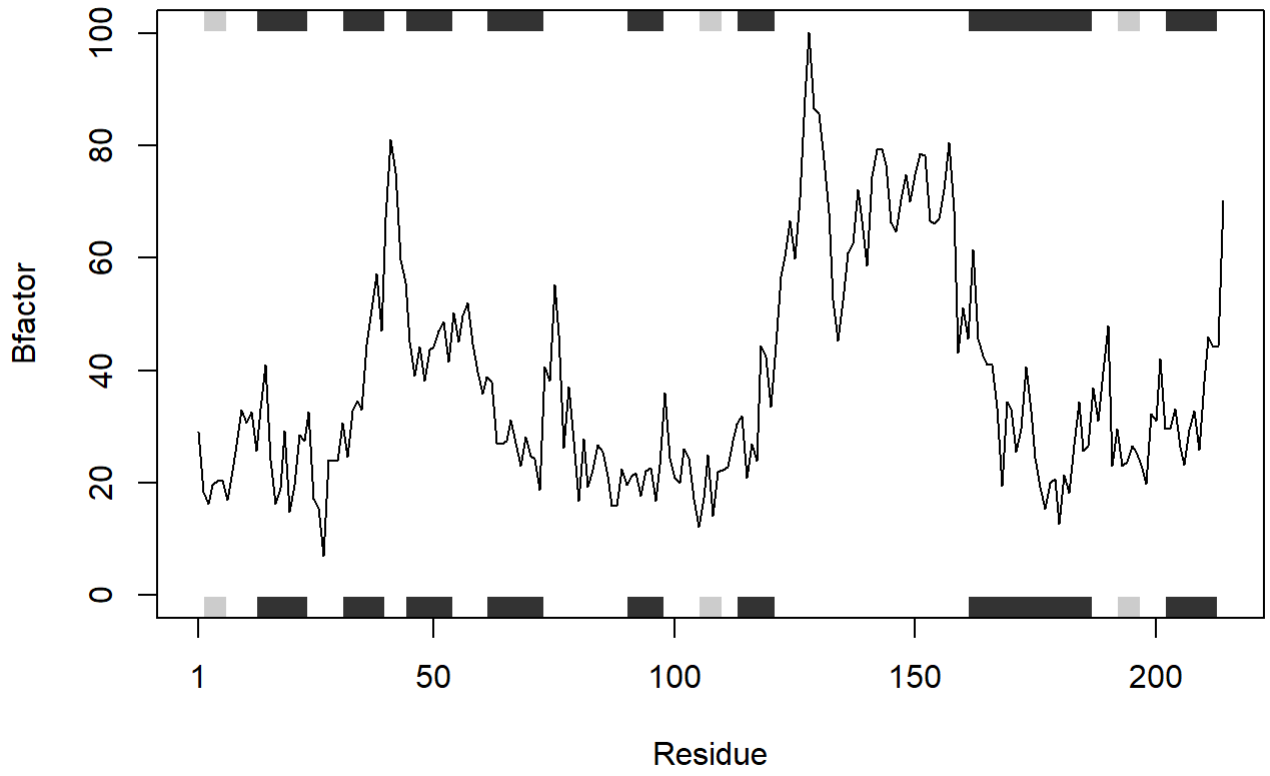
```
library(bio3d)
analyzeprotein <- function(x) {
  s1 <- read.pdb(x)
  s1.chainA <- trim.pdb(s1, chain = "A", elety= "CA")
  s1.b <- s1.chainA$atom$b
  plotb3(s1.b, sse=s1.chainA, typ= "l", ylab= "Bfactor")
}
```

Testing out to see if we get the same results.

```
analyzeprotein("4AKE")
```

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

```
## Warning in get.pdb(file, path = tempdir(), verbose = FALSE): C:
## \Users\pvara\AppData\Local\Temp\RtmpeEtphR/4AKE.pdb exists. Skipping
## download
```

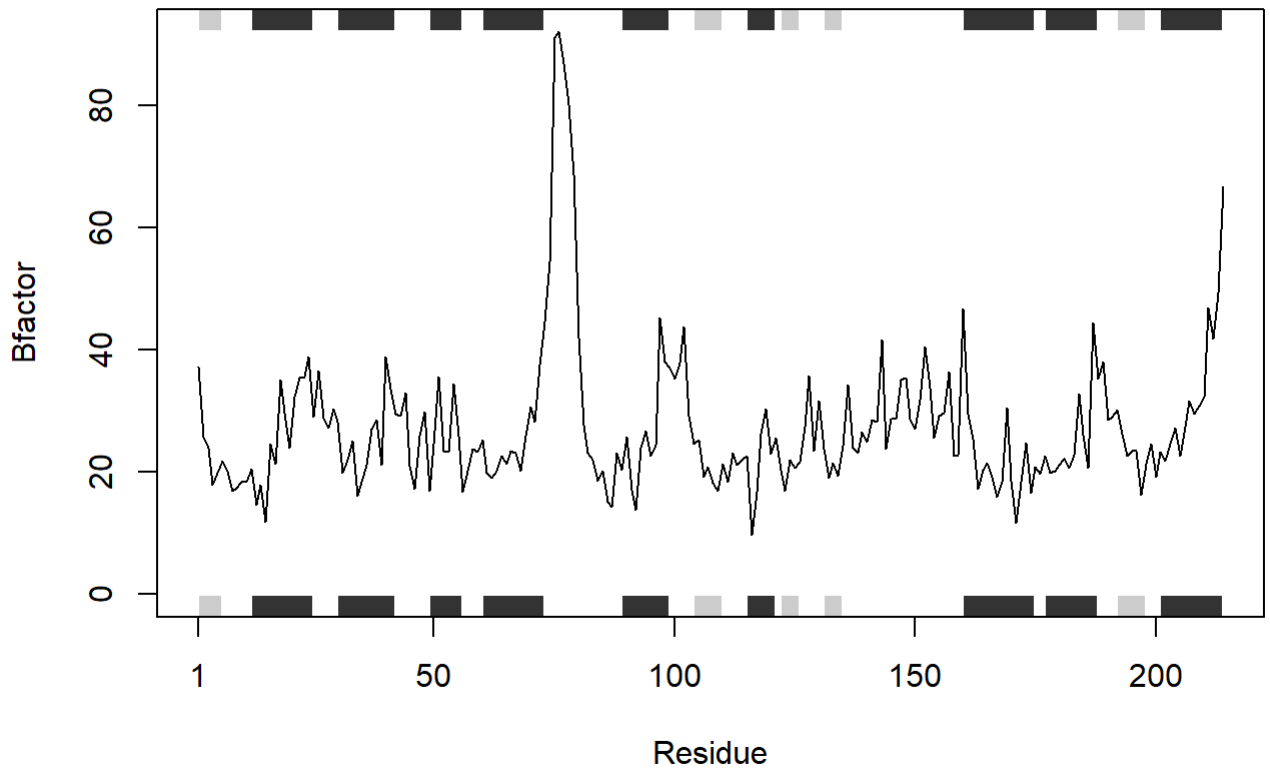



```
analyzeprotein("1AKE")
```

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

```
## Warning in get.pdb(file, path = tempdir(), verbose = FALSE): C:
## \Users\pvara\AppData\Local\Temp\RtmpeEtphR/1AKE.pdb exists. Skipping
## download
```

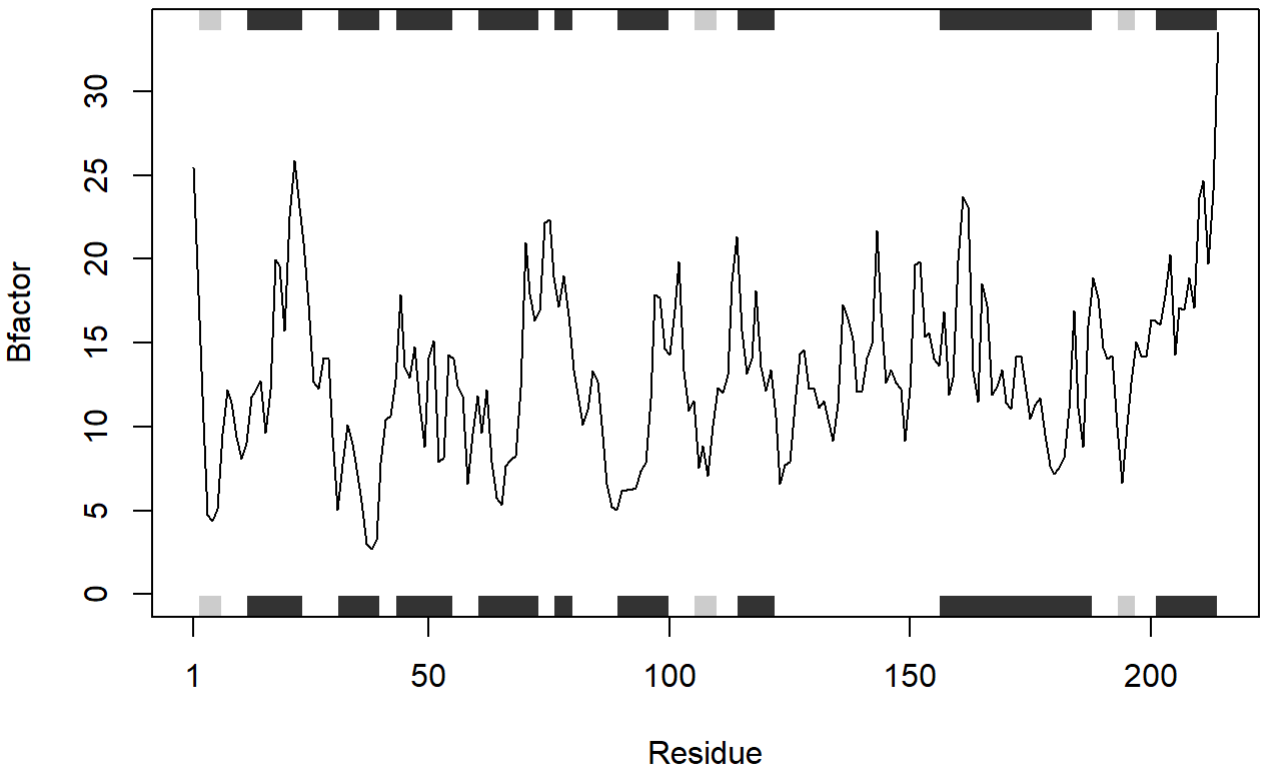
```
##    PDB has ALT records, taking A only, rm.alt=TRUE
```




```
analyzeprotein("1E4Y")
```

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

```
## Warning in get.pdb(file, path = tempdir(), verbose = FALSE): C:
## \Users\pvara\AppData\Local\Temp\RtmpeEtphR/1E4Y.pdb exists. Skipping
## download
```


Bfactor
0
5
10
15
20
25
30
1
50
100
150
200
Residue