HWFunction

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Simplier function for similar repetitive units

```
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

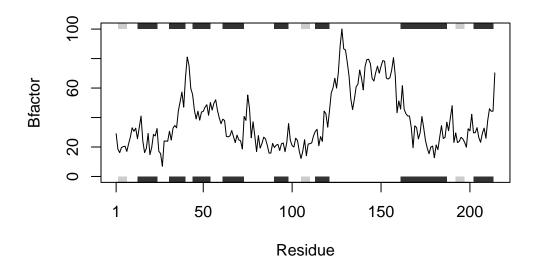
Note: Accessing on-line PDB file

s1.chainA <- trim.pdb(s1, chain="A", elety="CA")
s2.chainA <- trim.pdb(s2, chain="A", elety="CA")
s3.chainA <- trim.pdb(s1, chain="A", elety="CA")
s3.chainA <- trim.pdb(s1, 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")</pre>
```



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





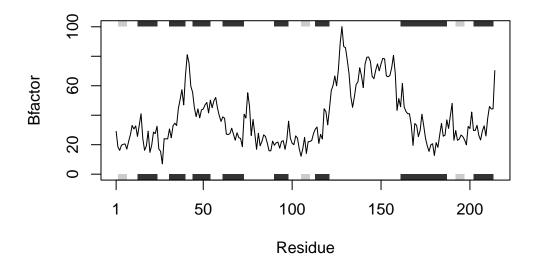
```
#Generating a general function for repetitive sequences
mypdb <- function(x) {
    spdb <- read.pdb(x)
#Generating function called mypdbchain
    mypdbchain <- trim.pdb(spdb, chain="A", elety="CA")

#Generating a function called chainatoms
    chainatoms <- mypdbchain$atom$b

plotb3(chainatoms, sse=mypdbchain, typ="l", ylab="Bfactor")
}</pre>
```

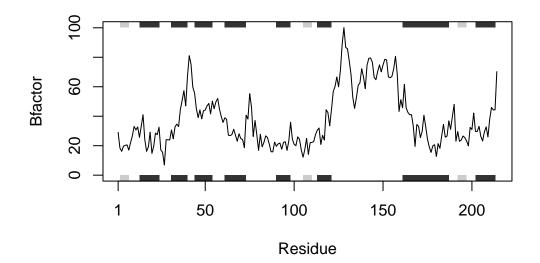
```
#Running Function
mypdb("4AKE")
```

Warning in get.pdb(file, path = tempdir(), verbose = FALSE):
/var/folders/sy/_fr9v5r51nxc7bzp4h_683nh0000gn/T//Rtmpl6T3K6/4AKE.pdb exists.
Skipping download



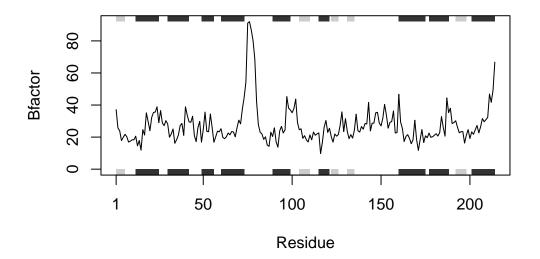
```
#Generating Multiple plots
sapply (c("4AKE", "1E4Y"), mypdb)
```

Warning in get.pdb(file, path = tempdir(), verbose = FALSE):
/var/folders/sy/_fr9v5r51nxc7bzp4h_683nh0000gn/T//Rtmpl6T3K6/4AKE.pdb exists.
Skipping download

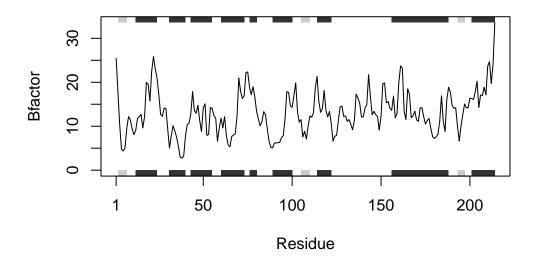


Warning in get.pdb(file, path = tempdir(), verbose = FALSE):
/var/folders/sy/_fr9v5r51nxc7bzp4h_683nh0000gn/T//Rtmpl6T3K6/1AKE.pdb exists.
Skipping download

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



Warning in get.pdb(file, path = tempdir(), verbose = FALSE):
/var/folders/sy/_fr9v5r51nxc7bzp4h_683nh0000gn/T//Rtmpl6T3K6/1E4Y.pdb exists.
Skipping download



\$`4AKE` NULL

\$`1AKE`

NULL

\$`1E4Y` NULL