# Homework 6 - (R Functions

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Drug_analysis function takes a set of proteins from a database and runs analysis on drug interactions and displays results graphically.

To use this function, call the `drug_analysis()` function with a single or multiple 4 character protein tag from the protein database to run analysis.

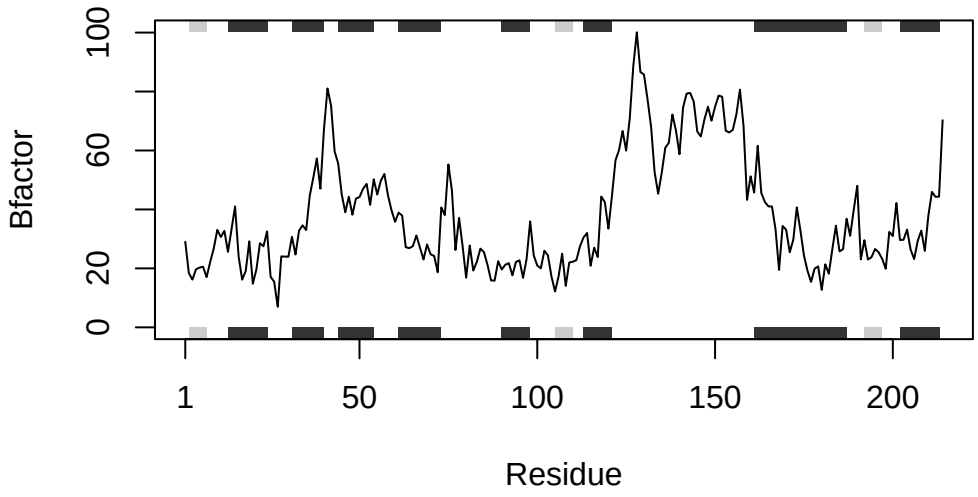
```
drug_analysis <- function(pdb_id){
  # pdb_id input is a set of ID inputs from the pdb database
  library(bio3d)

  for(i in 1:length(pdb_id)){
    s <- read.pdb(pdb_id[i])
    s.chainA <- trim.pdb(s, chain="A", elety = "CA")
    s.b <- s.chainA$atom$b
    plotb3(s.b, sse=s.chainA, typ="l", ylab="Bfactor")
  }
}
```

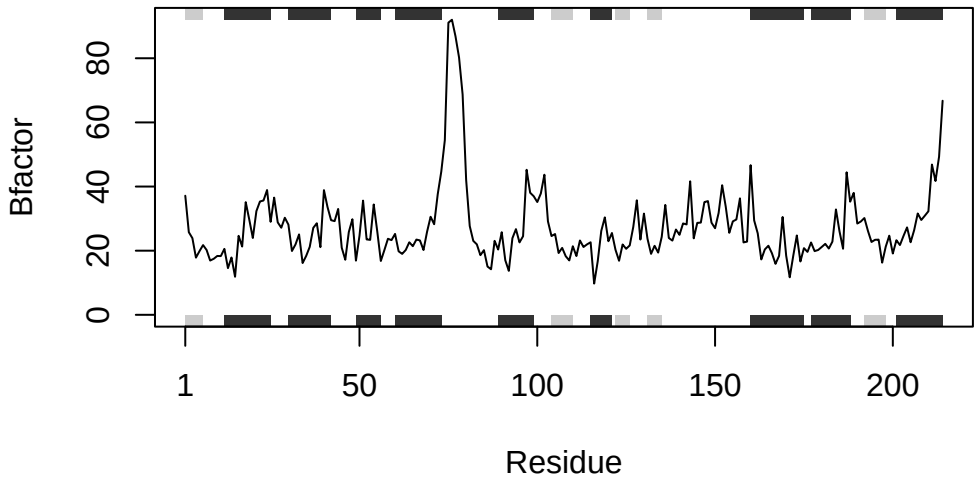
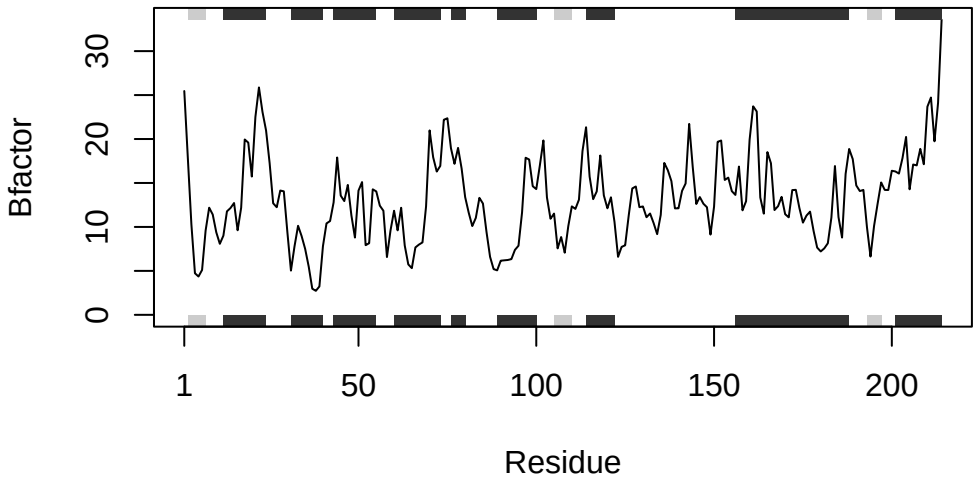
Test code that displays the results of the function, `drug_analysis()` of 3 different proteins.

```
drug_analysis(c("4AKE", "1AKE", "1E4Y"))
```

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




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



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