

# Function HW Q6

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```
library("bio3d")
```

Function:

```
plot_bfactor <- function(x) {  
  #download the pdb file and trim it down to a subset: only Calpha atoms on Chain A  
  s1 <- trim.pdb( read.pdb(x), chain="A", eley="CA" )  
  
  #plot the subset against the bfactor  
  plotb3(s1$atom$b,  
    sse=s1, typ="l", ylab = "bfactor")  
}
```

The function input is a pdb file and the function output is a plot against the bfactor.

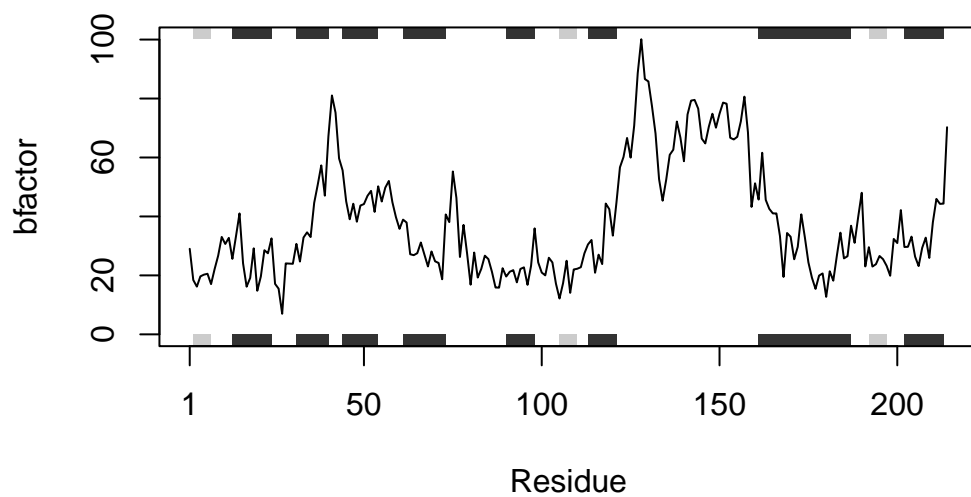
The function takes the given file, trims it down to a subset and plots the bfactor against the residues to view the atom mobility of different areas of the protein for use in analysis.

One only has to input the pdb file.

For example:

```
plot_bfactor("4AKE")
```

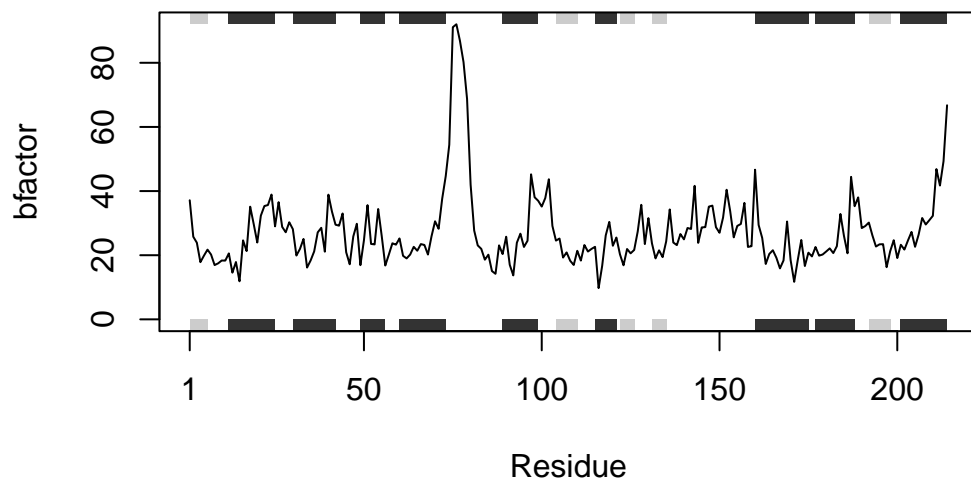
Note: Accessing on-line PDB file



```
plot_bfactor("1AKE")
```

Note: Accessing on-line PDB file

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



```
plot_bfactor("1E4Y")
```

Note: Accessing on-line PDB file

