

hw06 Question 6

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```
library(bio3d)
```

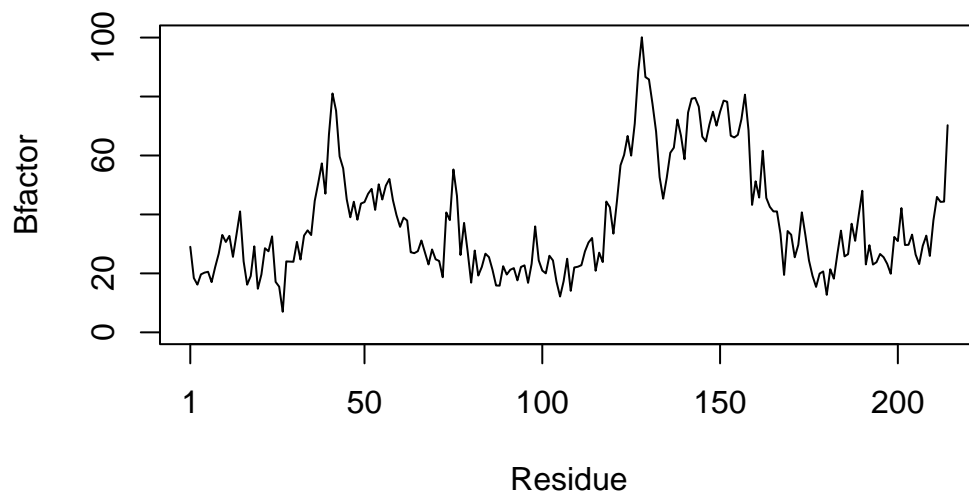
protein_plot function takes in protein drug interactions code and outputs a plot for the specified protein.

```
# Input are protein drug interactions code
protein_plot <- function(protein) {
  read_protein <- read.pdb(protein)
  read_protein.chainA <- trim.pdb(read_protein, chain="A", eley="CA")
  read_protein.b <- read_protein.chainA$atom$b

  #outputs a plot for the specified protein.
  plotb3(read_protein.b, read_protein.chainA, typ="l", ylab="Bfactor")
}
```

```
protein_plot("4AKE")
```

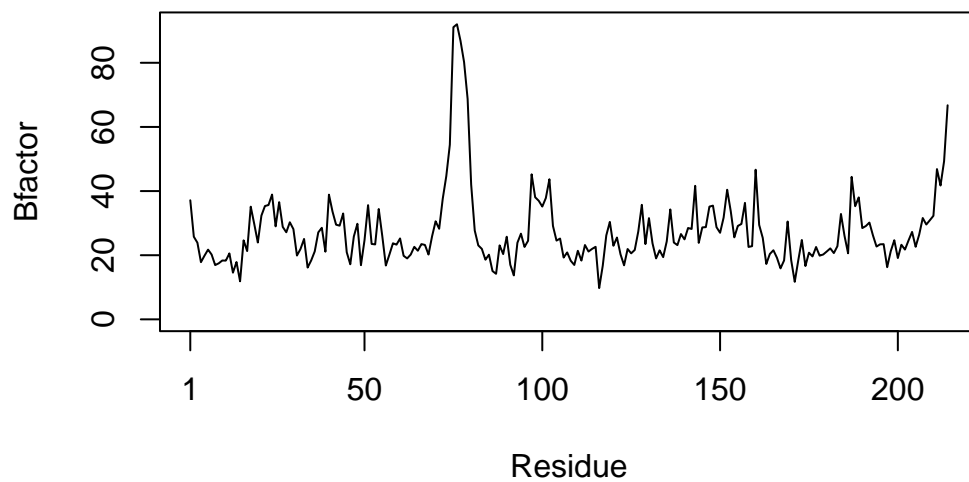
Note: Accessing on-line PDB file



```
protein_plot("1AKE")
```

Note: Accessing on-line PDB file

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



```
protein_plot("1E4Y")
```

Note: Accessing on-line PDB file

