HW Lab 06

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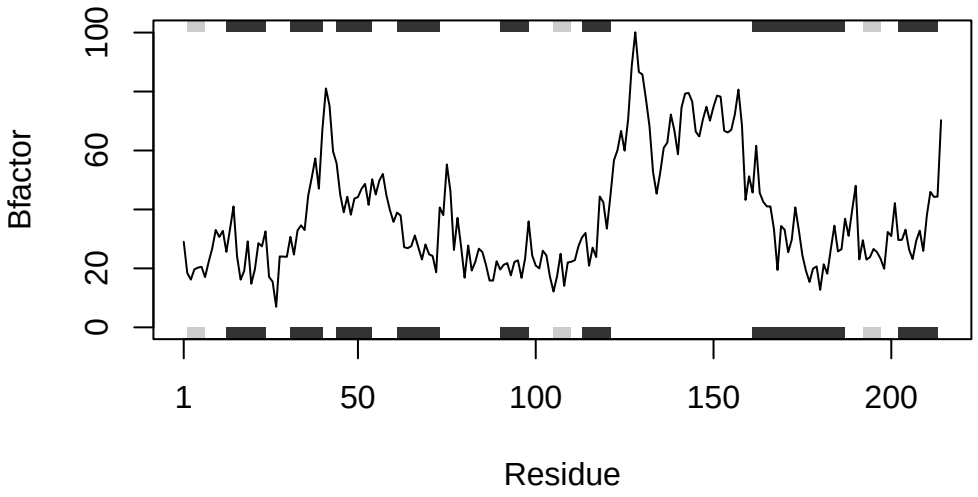
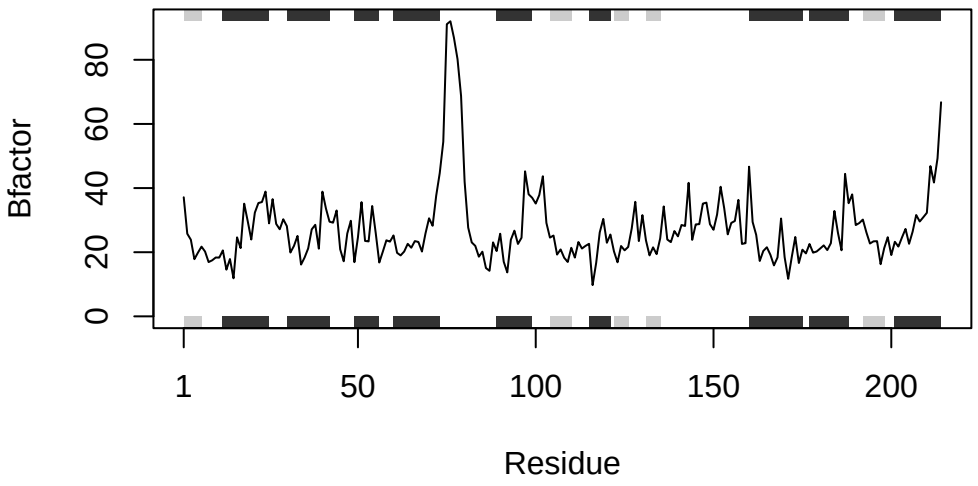
```
library(bio3d)
# Documentation
# The function analyze_protein() generates a plot for the input protein, which
# plots the protein's residues in relation to their B-factors. The input is the
# PDB ID of the protein of interest and the output is a plot. To use the
# function, just call the function with the PDB id of your protein of interest.

# Arguments (1)
#   id (string) : PDB Protein Entry ID

# Output (1)
#   Plot of the protein's residues in relation to their B-factor

analyze_protein <- function(id) {
  protein <- read.pdb(id)
  protein.chainA <- trim.pdb(protein, chain="A", elety="CA")
  plotb3(protein.chainA$atom$b, sse=protein.chainA, typ="l", ylab="Bfactor")
}


analyze_protein("4AKE") # kinase with drug
```

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



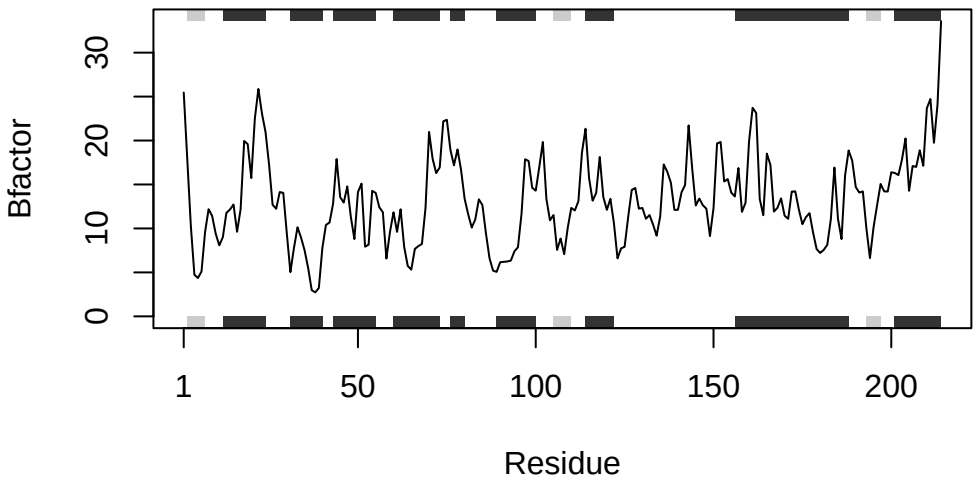

```
analyze_protein("1AKE") # kinase no drug
```

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




```
analyze_protein("1E4Y") # kinase with drug
```

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


Bfactor
0
10
20
30
1
50
100
150
200
Residue