HW06.

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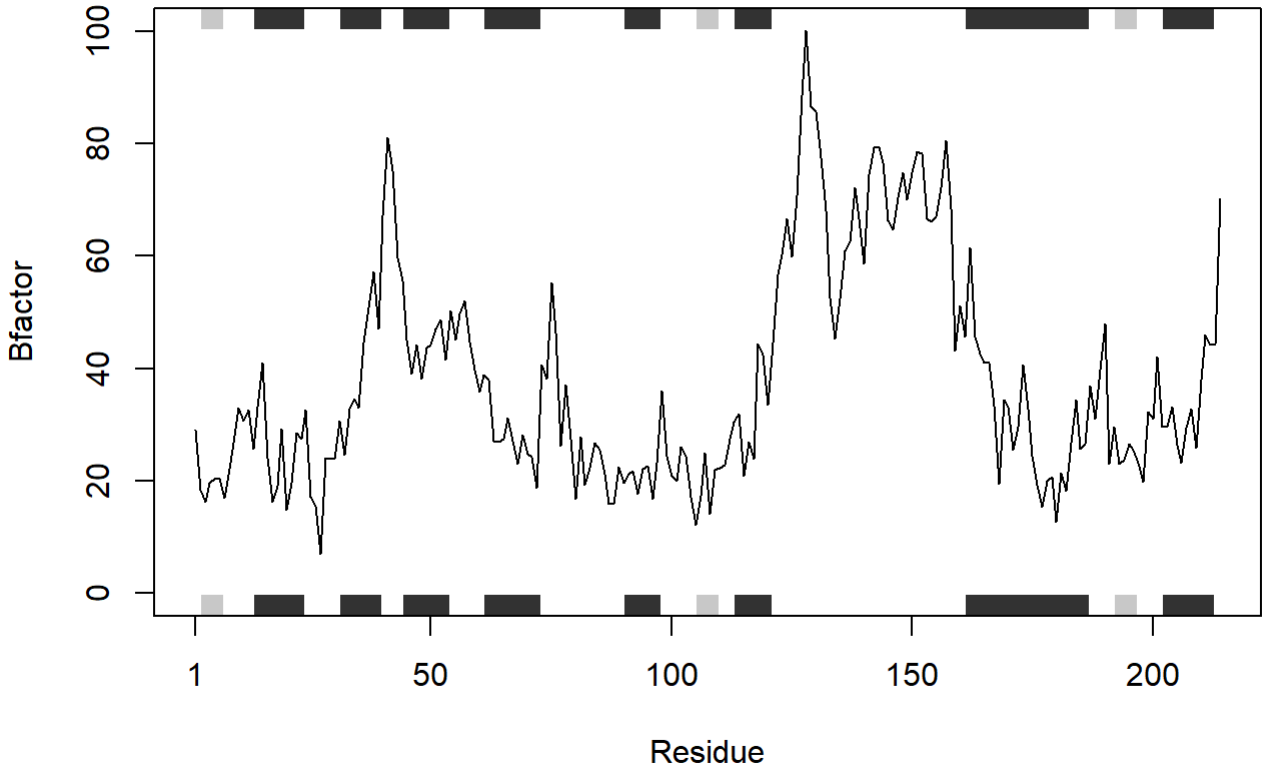
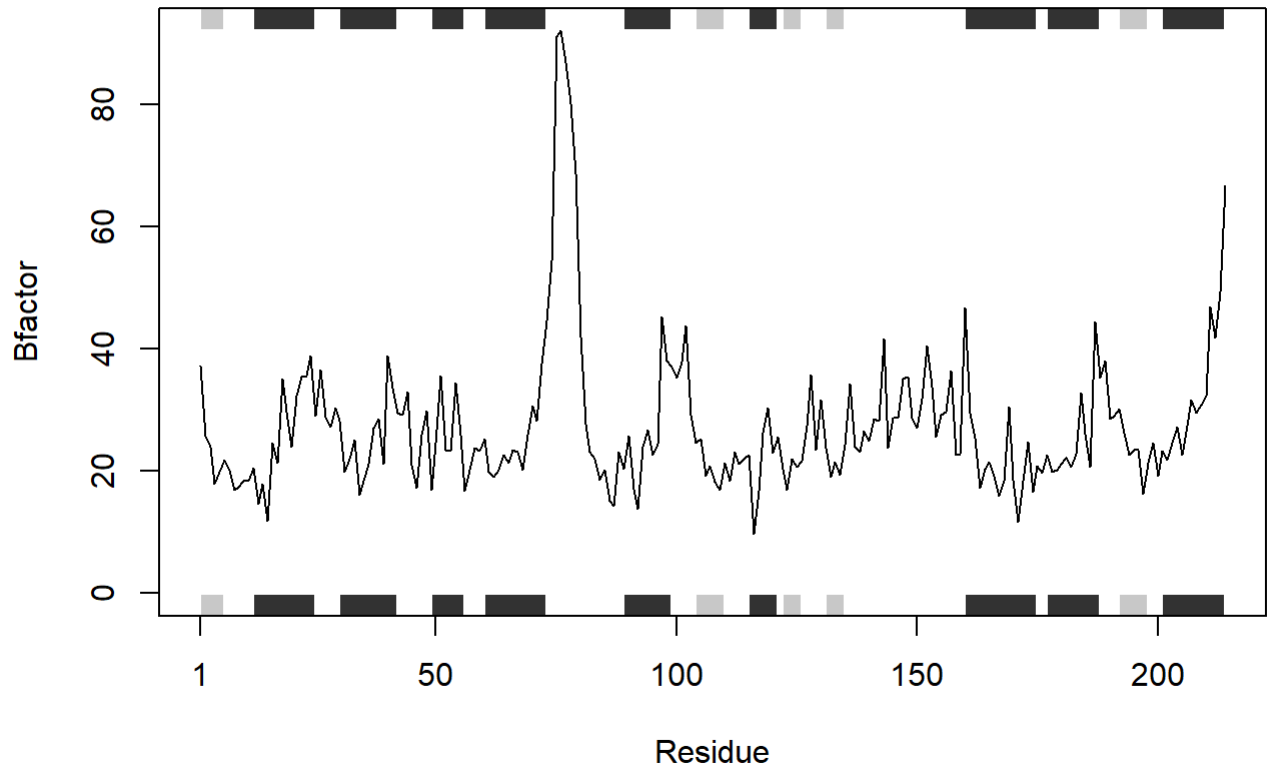
```
# Load bio3d package
library(bio3d)

# Define a function to analyze protein drug interactions
analyze_protein_drug_interactions <- function(pdb_file, chain="A") {
  pdb <- read.pdb(pdb_file)
  pdb.chainA <- trim.pdb(pdb, chain=chain, elety="CA")
  b_factors <- pdb.chainA$atom$b
  plotb3(b_factors, sse=pdb.chainA, typ="l", ylab="Bfactor")
}

# List of PDB files to analyze
pdb_files <- c("4AKE", "1AKE", "1E4Y")

# Analyze each PDB file using lapply
lapply(pdb_files, analyze_protein_drug_interactions)
```

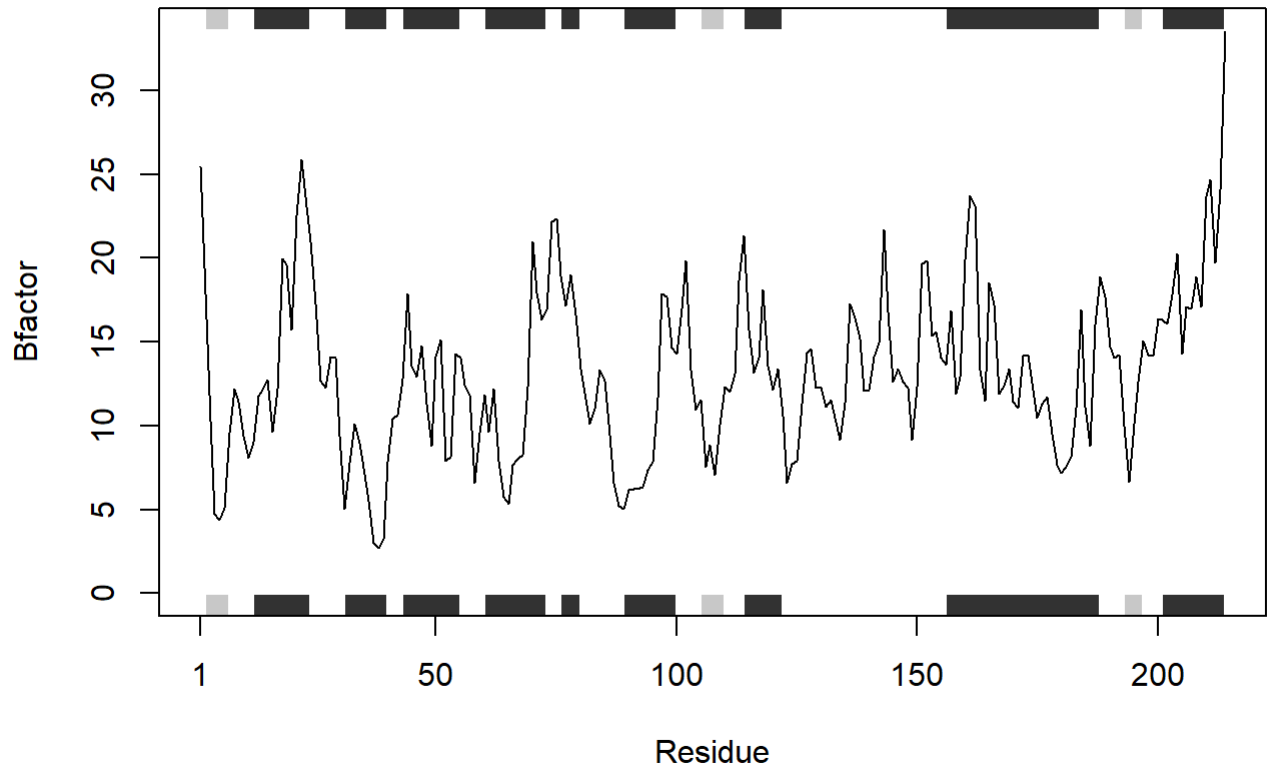
```
##   Note: Accessing on-line PDB file
```




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




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




```
## [[1]]
## NULL
##
## [[2]]
## NULL
##
## [[3]]
## NULL
```