

# Homework 6

Joshua Khalil

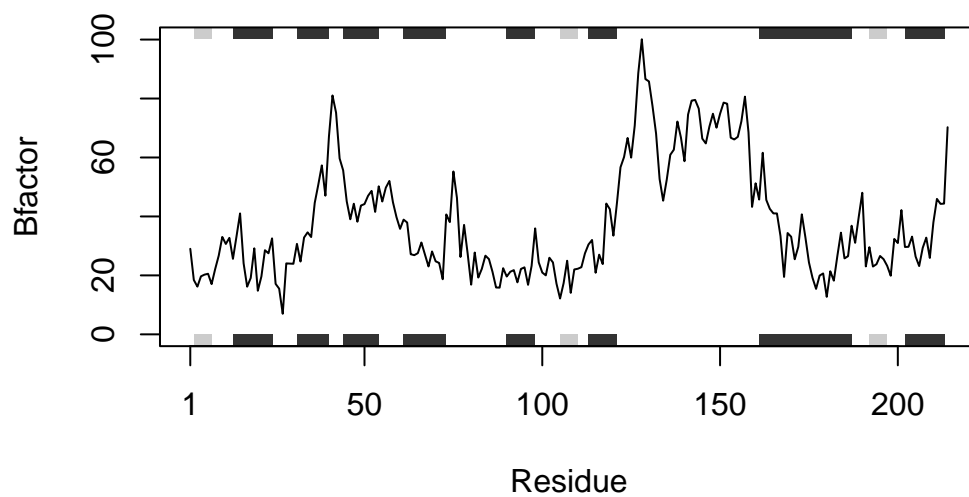
```
library(bio3d)

analyze_bfactors <- function(pdb_ids, chain="A", elety="CA") {
  for (id in pdb_ids) {
    s <- read.pdb(id)
    s.chainA <- trim.pdb(s, chain=chain, elety=elety)
    s.b <- s.chainA$atom$b
    plotb3(s.b, sse=s.chainA, typ="l", ylab="Bfactor")
    title(main=id)
  }
}

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

Note: Accessing on-line PDB file

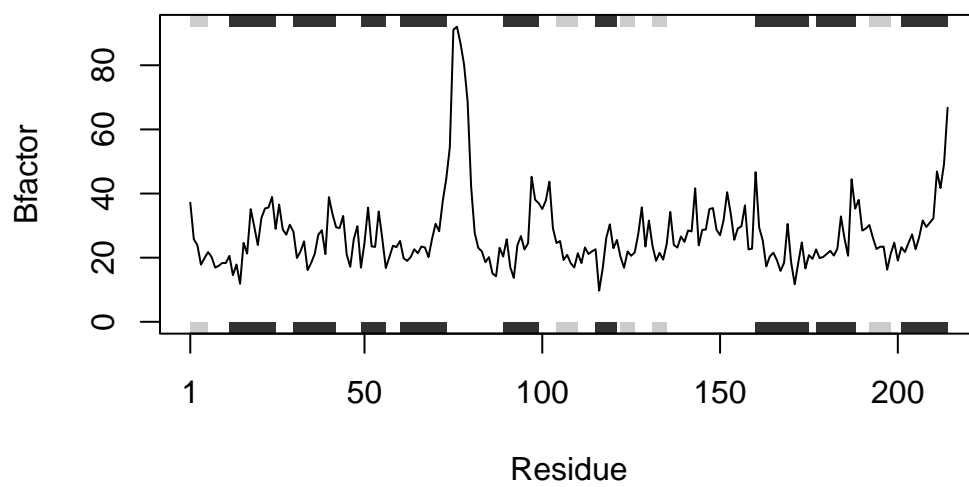
## 4AKE



Note: Accessing on-line PDB file

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

## 1AKE



Note: Accessing on-line PDB file

