Lab 6 supp

Vanesa Fernandez

```r
improved <- function (pdb) {
  library(bio3d)
    ##Body
 s <- read.pdb(pdb)  # kinase with drug
 s.chainA <- trim.pdb(s, chain="A", elety="CA")
 s.b <- s.chainA$atom$b

 plotb3(s.b, sse=s.chainA, typ="l", ylab="Bfactor")

}
```
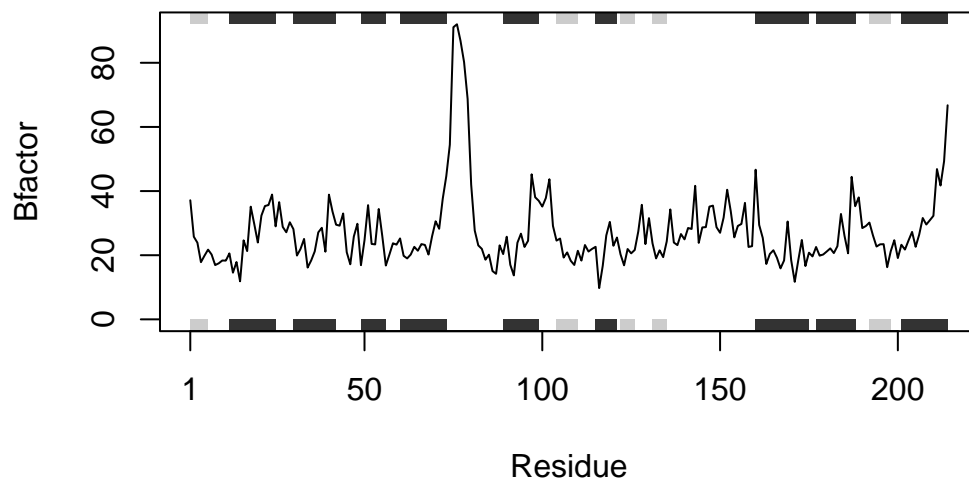
```r
improved("4AKE")
```

```
Note: Accessing on-line PDB file
```
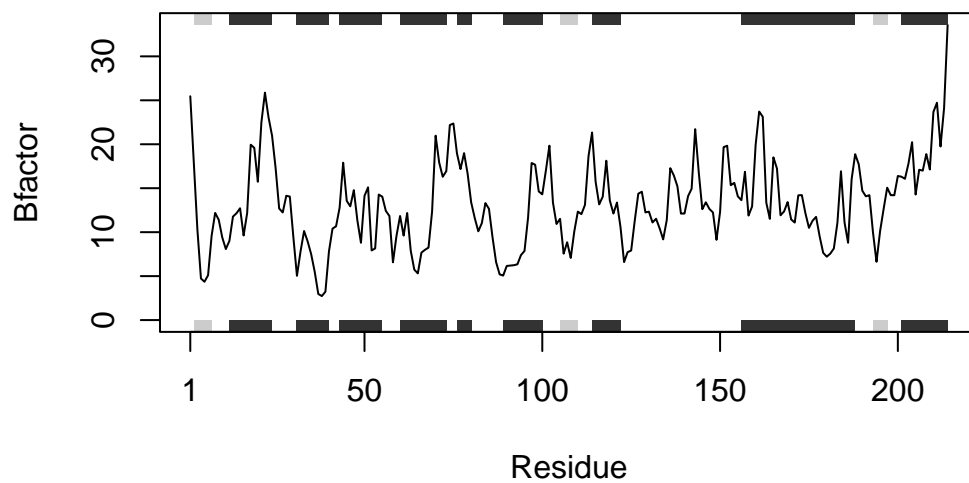
```
improved("1AKE")
```

```
  Note: Accessing on-line PDB file
   PDB has ALT records, taking A only, rm.alt=TRUE
```
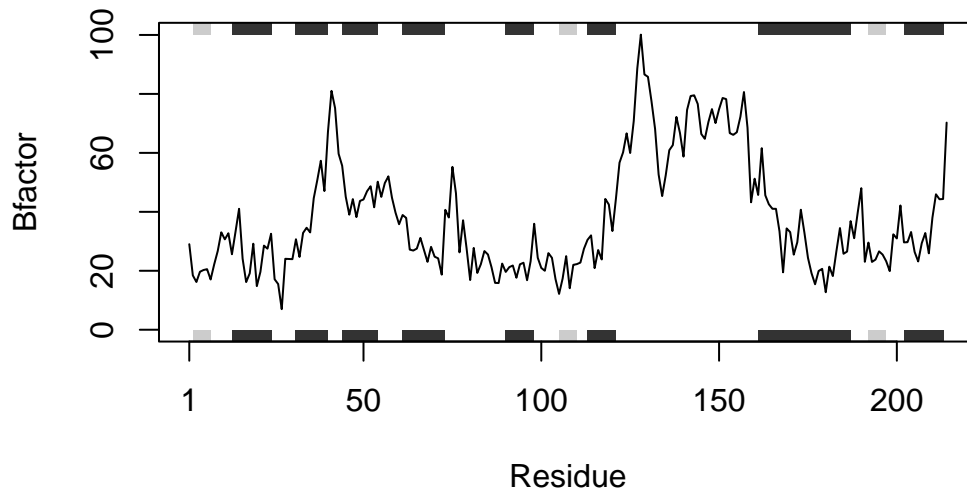
```
improved("1E4Y")
```
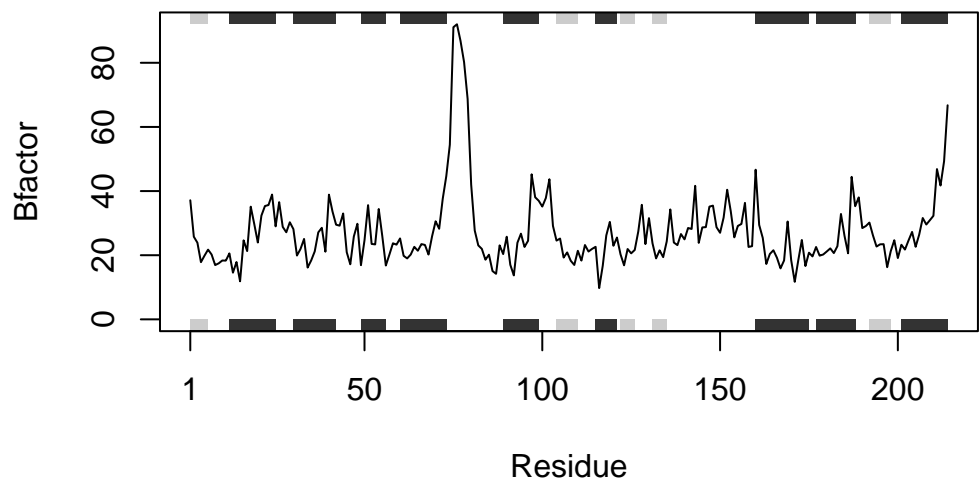
```
Note: Accessing on-line PDB file
```

```
sapply(c("4AKE", "1AKE", "1E4Y"), improved)
```
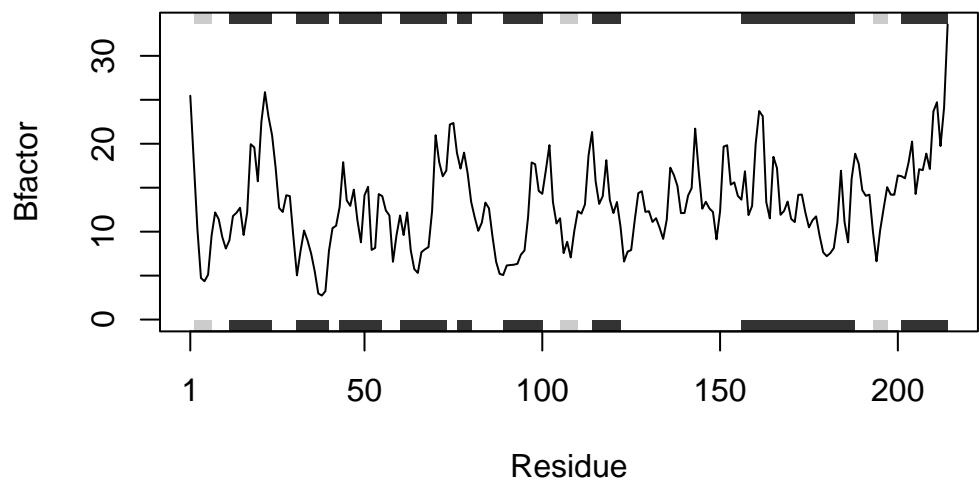
Note: Accessing on-line PDB file

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

Note: Accessing on-line PDB file

$`4AKE`

```
NULL

$`1AKE`
NULL

$`1E4Y`
NULL
```