homework-class6

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```r
# Can you improve this analysis code?


library(bio3d)
prostructure<-function(id){
  s1<-read.pdb(id)
  s1.chainA<-trim.pdb(s1, chain = "A", elety="CA")
  s1.b<-s1.chainA$atom$b
  plotb3(s1.b,sse=s1.chainA, typ="l", ylab="Bfactor")

}


prostructure("4AKE")
```
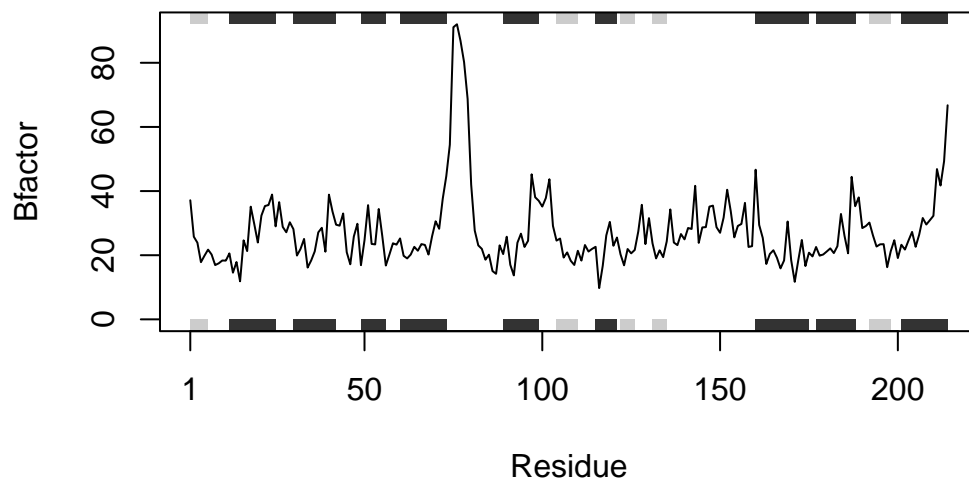
Note: Accessing on-line PDB file

```
prostructure("1AKE")
```

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

```
prostructure("1E4Y")
```

    Note: Accessing on-line PDB file