

Class06 HW

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Load library

```
library(bio3d)
```

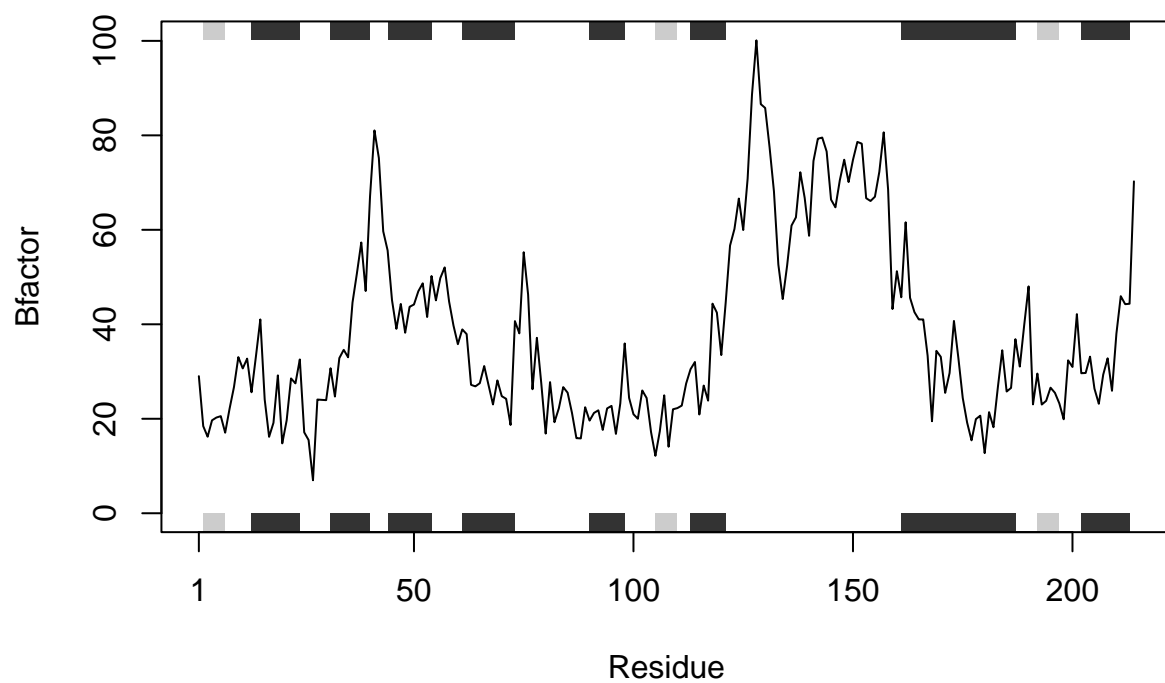
Function to read and process PDB structure

```
process_pdb <- function(pdb_id) {  
  pdb <- read.pdb(pdb_id)  
  # Trim PDB to chain A and CA atoms only  
  chainA <- trim.pdb(pdb, chain = "A", eley = "CA")  
  # Extract B-factors for CA atoms  
  b_factors <- chainA$atom$b  
  # Return plot  
  plotb3(b_factors, sse=chainA, typ="l", ylab="Bfactor")  
}
```

Plots Generation with input to test function process_pdb

```
process_pdb("4AKE")
```

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



```
process_pdb("1AKE")
```

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



```
process_pdb("1E4Y")
```

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

