

Class 6 Lab

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#Code takes PDB IDs and plots the B factor of the protein structures after removing polyA tail
# Input is PBD ID
# Output is B factor vs. residue plot

#install.packages("bio3d") if not previously installed
library(bio3d)
bfactor_plot <- function(pdb_input) {
  #Read pdb file
  pdb <- read.pdb(pdb_input)
  #Trim amino acid polyA tail
  pdb.chainA <- trim.pdb(pdb, chain = "A", elety = "CA")
  #Get B factor
  pdb.b <- pdb.chainA$atom$b
  #Plot B factor
  plotb3(pdb.b, sse = pdb.chainA, typ = "l", ylab = "Bfactor")
}

#PDB 4AKE used as example of functional code
bfactor_plot("4AKE")

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

