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---
title: "Lecture 6 Homework"
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date: "1/23/2020"
output:
  html_document: default
  pdf_document: default
---
```

The input to the function **protein\_activity\_plot** is the four letter PDB identifier for online file access in the form of a string. The function generates a line plot from a four letter PDB identifier. To use the function, simply input the PDB code.  
Ex: improved ('A3F4').  
The output of the function is a line plot.

```
```{r}
library(bio3d)
protein_activity_plot <- function(PDB) {
  protein <- read.pdb(PDB)
  protein.chainA <- trim.pdb(protein, chain="A", elty="CA")
  protein.b <- protein.chainA$atom$b
  plotb3(protein.b, sse = protein.chainA, typ="l", ylab="Bfactor")
}
```
```

```
```{r}
protein_activity_plot('4AKE') # kinase with drug
protein_activity_plot('1AKE') # kinase no drug
protein_activity_plot('1E4Y') # kinase with drug
```
```