

Class 6 Function HW

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This function takes a PDB identifier as an input. When you run it, the following functions will run:

- `read.pdb()` will read in the PDB coordinate file
- `trim.pdb()` will select a subset of the protein's atoms. My function selects atoms in chain A (using the `chain = "A"` argument) and atoms of type "CA" (using the `elety = "CA"` argument), and saves it as the `seq.chainA` variable
- Selects the values in the `b` column of the `atom` dataframe inside of the `seq.chainA` variable, and then saves the values into the `seq.b` variable
- `plotb3()` creates a plot of Residue by Bfactor for `seq.b`

Make sure you've run `install.packages("bio3d")` and `library(bio3d)` before running the function

```
library(bio3d)

plot_sequence <- function(pdb) {
  seq <- read.pdb(pdb)

  seq.chainA <- trim.pdb(seq, chain="A", elety="CA")

  seq.b <- seq.chainA$atom$b

  plotb3(seq.b, sse = seq.chainA, typ="l", ylab="Bfactor")
}
```

Running the code, using PDB identifier "4AKE" as an example:

```
plot_sequence("4AKE")
```

Note: Accessing on-line PDB file

