Proteins are one of the fundamental types of macromolecules essential to the workings of a cell. Thus identifying proteins present in cells and their functions has garnered much interest as seen in the rise of proteomics. In order to identify proteins using various electrophoresis techniques, the proteins must be extracted. In this study we developed the superlative protein extraction protocol for protein extraction from Bean Beetles (*Callosobruchus maculatus*). To accomplish this task, various methods of protein extraction were developed and tested to determine which would produce the highest concentration of protein in the sample. The methods were tested on both male and female adult beetles. The three methods used for extraction were: simple homogenization, dry ice-acetone sublimation/heat shock, and dry ice acetone sublimation/heat shock with incision. The extracted protein samples were compared with the protein standards (2, 4, 6, 7, and 10 mg Bovine Serum Albumin (BSA)/ml) in a spot test. Using the spectrophotometer at 590 nm the absorption was determined for each of the standards and bean beetle samples. The protein standards were graphed against the absorptions and the best fit line was determined. Using the slope intercept, the protein concentration was calculated in each of the samples of bean beetle and standards. These data suggest that the best method to extract the superlative protein is using the dry ice acetone sublimation/heat shock with incision method. The calculations obtained will be used to load an equal amount of protein for the Vertical Gel SDS Page Electrophoresis for identifying the proteins.

Key Words: *Callosobruchus maculatus*, superlative protein extraction, protein concentration, Protocol.