Proteins, as the main functional molecules of the cell, play a critical role in shaping phenotypic traits. This thesis investigates the application of proteomics data, obtained via LC-MS/MS, to understand the link between protein expression and resulting phenotypes. Various bioinformatic approaches are discussed, including data preprocessing, normalization techniques, and missing value imputation methods, to ensure the reliability and accuracy of downstream analyses. Furthermore, this work describes how one can gain insights into phenotypic traits across species or medical conditions by employing differential expression analysis, evolutionary modeling using the Ornstein-Uhlenbeck process, and machine learning algorithms.