Backbone building is the preliminary step to designing a protein from scratch. The scientific community has adopted various methods to solve this problem. For symmetrical proteins, the method is necessary to ideally assemble secondary structural elements such as α-helices, β-chains, etc. that fall into the allowable area of the Ramachandran diagram, and then connect them with appropriate loops. If the target protein contains many structural elements, the spacing between these elements and the loop connecting them needs to be optimized. For symmetric proteins, backbone building can be optimized using a set of defined parameters. For proteins with irregular structures, backbone building follows a separate trend as the loops have to be designed separately with the assistance of PDB database. In this modern age of computer programming and algorithms, structure prediction programs can also be used to build the backbone structure.