Hepatitis C virus (HCV) is a major global health concern, and though therapeutic options have improved, no vaccine is available. Effective vaccine development is hindered by the lack of understanding the mechanisms of viral recognition and entry. Computational modeling of HCV envelope glycoprotein structure can provide insights into the virus-host interactions and facilitate vaccine development. This review highlights recent advances in computational modeling of HCV envelope glycoprotein structure and recognition and discusses the potential of these models to provide lessons and insights relevant to modeling and characterizing other viruses.