PREDICTION OF LOOP CONFORMATION OF THE HSV-2, HCMV AND HHV8 SERINE PROTEASE

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Accurate conformation predictions of structurally variable regions (SVRs) or loops are still a bottleneck of comparative protein structure modeling. Because of its flexibility, in the experimental determination of the three-dimensional structure of a polypeptide, the loop is the hardest to be defined. The protein loops can vary in size and sequence among homologous proteins and they may play a key role in the function and specificity of proteins. Commercial databases and ab initio approaches are available for loop prediction. In this work we utilize an already validated procedure, that is, the PRODAT database of the SYBYL package as the search approach and the ab initio method RAPPER to predict the three dimensional structure of the missing residues and therefore to propose a complete three dimensional conformation of the serine proteases of the herpes Simplex virus type 2 (HSV-2), Cytomegalovirus (HCMV), and the human herpesvirus 8 (HHV-8). The herpesvirus proteases are considered to be targets to the development of new antiviral drugs and therefore the elucidation of theirs three dimensional structures emerge as a significant contribution to future study of drug design.