A new polypeptide backbone fold for serine proteases has been identified based on the crystal structure of human cytomegalovirus protease. The structure was determined at 2.5 Å resolution by the multiple-wavelength anomalous diffraction technique using the seleno-methionyl protein and refined at 2.0 Å resolution. It reveals a seven-stranded mostly-antiparallel β-barrel, which is surrounded by seven helices. The active site residues (Ser-132 and His-63) are situated on the outside of the β-barrel and in a groove on the surface of the protease. The structure suggests that the third member of the catalytic triad is probably His-157. The protease of herpesviruses plays an essential role in the production of infectious viruses and is an attractive target for the development of antiherpes agents. The crystal structure information will help in the design and optimization of inhibitors against herpes virus protease.


**THE CRYSTAL STRUCTURE OF HUMAN CYTOMEGALOVIRUS PROTEASE.** Ping Chen, Robert Almasy, Hideald Tsoe, Dave Matthews, Chris Finko, Cindy Garbukov, and Chen-Chen Kuo, Agouron Pharmaceuticals Inc., 3565 General Atomics Court, San Diego, CA92121, 1Japan Tobacco Inc., Pharmaceutical Division, Minato, Tokyo, Japan

Human cytomegalovirus (HCMV) is a beta herpes virus. HCMV, like all other members of the Herpes virus family, encodes a protease that is essential for capsid maturation and production of infectious virus. The catalytic domain of the HCMV protease was produced in E.coli as a single-chain protein and was crystallized in space group C222 1 at 2.5 Å resolution using the high resolution crystal structures of the catalytic domain of the HCMV protease was produced in E.coli as a single-chain protein and was crystallized in space group C222 1 at 2.5 Å resolution using the high resolution crystal structures of the catalytic domain of the HCMV protease was produced in E.coli as a single-chain protein and was crystallized in space group C222 1 at 2.5 Å resolution using the high resolution crystal structures of the catalytic domain of the HCMV protease was produced in E.coli as a single-chain protein and was crystallized in space group C222 1 at 2.5 Å resolution using the high resolution crystal structures of the catalytic domain of the HCMV protease was produced in E.coli as a single-chain protein and was crystallized in space group C222 1 at 2.5 Å resolution using the high resolution crystal 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