Catalytic Efficiencies of Alkaline Proteinases from Microorganisms

Dessislava Georgieva[a], Nicolay Genov[b], Wolfgang Voelter[c], and Christian Betzel[a,*]

[a] Department of Biochemistry and Molecular Biology, University of Hamburg, Martin-Luther-King-Platz 6, 20146 Hamburg, Germany. Fax: +49-40-8998-4747. E-mail: Betzel@unisgi1.desy.de
[b] Institute of Organic Chemistry, Bulgarian Academy of Sciences, 1113 Sofia, Bulgaria
[c] Institute of Physiological Chemistry, University of Tübingen, Hoppe-Seyler-Str. 4, 72076 Tübingen, Germany

[*] Author for correspondence and reprint requests

Z. Naturforsch. **61c**, 445–452 (2006); received January 13/February 22, 2006

Catalytic efficiencies of proteinase K and mesentericopeptidase were determined using series of peptide-4-nitroanilide substrates and compared with those of subtilisin DY, savinase and esperase. For each enzyme the subsites S1–S4 were characterized. The data for the enzyme specificities were related to our high resolution X-ray models of the five enzymes and their complexes with peptides. The catalytic efficiencies of the alkaline proteinases are modulated by the hydrophobicity, solvent accessibility, flexibility and electrostatic effects in the substrate binding sites. The longer and nonpolar S1 loop offers more possibilities for hydrophobic interactions and increases the enzyme efficiency. S2 is a small narrow cleft which limits the possibilities for effective substitutions in P2. The wide specificity of S3 is due to its location on the protein surface of all investigated proteinases. The affinity of S4 for aromatic groups depends on the nature of the residues building the hydrophobic cavity.

Key words: Protease Efficiency, Enzyme Kinetic, Substrate Recognition, X-Ray Models