effect over to pro-ABE I suggesting an influence on development of inter-exosite communication. As F1.2 is removed and PT2 is activated to thrombin, pro-ABE I and II become more solvent exposed and mature into the functional exo-sites ABE I and II. HSCQ NMR titrations with GpBalpha (269-286, 15N-labeled L275, 15N-labeled D277) demonstrate that ligand binding affinity at pro-ABE II / ABE II increases as ProT is converted to PT2 and then thrombin. The final thrombin enzyme effectively accommodates substrates at its serine protease active site and utilizes its mature exo-sites to regulate several coagulation related activities.

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**Characterization of Proteases Derived from Nephila Clavata**

Mitsutoshi Fujitaka, Mitsuhito Miyazawa, Shigeru Shimamoto, Yuji Hidaka

Kinki University, Higashi-osaka, Japan, 2National Institute of Agrobiological Sciences, Tsukuba, Japan.

Spiders capture insects using a web net. The fact that they eat them without chewing suggests that spiders possess highly efficient digestive enzymes. Preliminary experiments indicated that a spider protease is able to digest synthetic spider dragline amyloid fibers. Thus, the spider protease has the potential ability to digest amyloid fibrils including pathogenic β-amyloid, such as amyloid fibrils, which are responsible for Alzheimer’s disease. Therefore, we extracted and characterized the enzymes derived from *Nephila Clavata*.

Spider saliva including proteolytic enzymes was prepared from *Nephila Clavata* by electrical stimulation. The extracts were applied to SDS-PAGE and the enzymatic activity of spider proteases was estimated by a casein protease assay. Two protein bands, showing protease activity, were predominantly observed on the assay and their molecular weights were estimated as approximately 21.9 and 19.5 kDa, based on the SDS-PAGE analysis. In order to characterize the enzymes, an inhibition assay for a synthetic peptide substrate was performed using several types of inhibitors, such as PMSF and EDTA. The results suggested that the spider protease can be categorized as a metal-dependent carboxypeptidase although the inhibitors were not able to completely depress the protease activity of the enzyme. The results will be discussed in this paper.

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**Structural and Computational Studies of the Staphylococcus Aureus Sortase B-Substrate Complex Provide New Insight into the Mechanism of Sortase Transpeptidases**

Alex W. Jacobitz, Jeff Weresczynski, Sung Wook Yi, Brendan R. Amer, Grace L. Huang, Angelyn V. Nguyen, Michael R. Sawaya, Michael E. Jung, J Andrew McCammon, Robert T. Clubb

1University of California, Los Angeles, Los Angeles, CA, USA, 2University of California, San Diego, La Jolla, CA, USA.

Staphylococcus aureus sortase B (SrtB) is the gateway leading to the formation of other pyruvate species with more reactive conformational sub-states. The final thrombin enzyme effectively accommodates substrates at its serine protease active site and utilizes its mature exo-sites to regulate several coagulation related activities.

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**The Role of Conformational Collapse in Enzymic Catalysis**

Robert Callender, Huo-Lei Peng, Hua Deng, Brian Dyer

1Albert Einstein School of Medicine, Bronx, NY, USA, 2Emory University, Atlanta, GA, USA.

Lactate dehydrogenase catalyzes the inter-conversion between pyruvate and lactate, using NAD as cofactor. At the chemical step, hydride transfer from NADH to pyruvate C2=O carbon and proton transfer from protonated histidine to C2=O oxygen occur simultaneously on the ca. 20 fs time scale. Here, we investigate how (pig heart) lactate dehydrogenase (pLDH) guides the orientation of substrate to product (P) (i.e. ES$\leftrightarrow$EP), competitive inhibition, and the subsequent conversion of substrate to product (P) (i.e. ES$\rightarrow$E+P), noncompetitive inhibition. These observed effects could be interpreted as different degrees of osmolyte exclusion from regions on alkaline phosphatase critical to these steps. Furthermore, the amount and location of this exclusion would be sensitive to the steric and chemical differences between these solutes. These results highlight the importance taking into consideration the actual complex environment in which enzymes operate.