Poster Presentation

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Structural studies of biomass degrading enzyme systems

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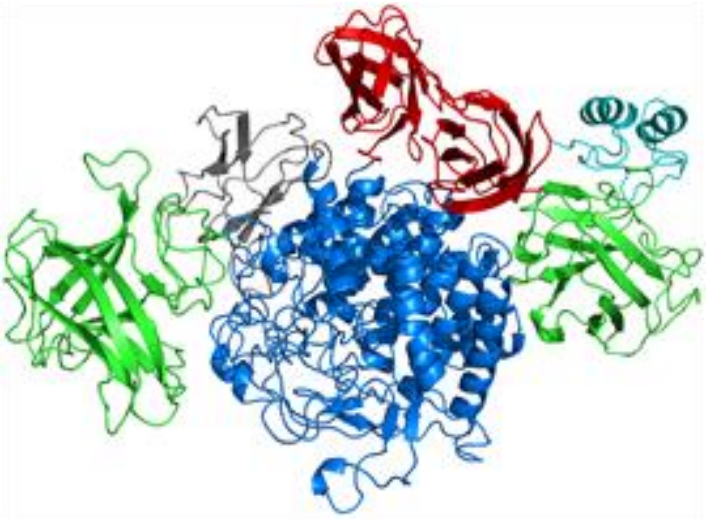
Renewable energy today comprises wind, photovoltaics, geothermal, and biofuels. Biomass is the leading source of renewable, sustainable energy used for the production of liquid transportation fuels. While the focus is shifting today from the ethanol towards next generation or advanced biofuels the real challenge however remains the same: reducing the recalcitrance of biomass to deconstruction, which yields the sugars needed for further processing. NREL's Biosciences Center conducts studies of the fundamental nature of the plant cell wall; as well as those enzyme systems utilized in Nature to deconstruct it. These systems could be classified in two ways: the "free enzymes" and the "cellulosomes." Cellulosomes are self-assembling, multi-enzyme machinery that can include dozens and hundreds of catalytic domains and cellulose binding modules interconnected by linker peptides. We will present a structural overview of the biomass degrading enzymes from fungi using Trichoderma reesei and Penicillum funiculosum as examples. The bacterial cellulosome system discussed will be from a thermophile Clostridium thermocellum and bacterial free enzyme example will be the hyperthermophile, Caldicellulosiruptor bescii. To study these systems, we combined classical biochemistry and molecular biology, mass spectrometry, electron microscopy, high throughput robotics, macromolecular crystallography, and molecular dynamics. We seek to understand the properties and structure of biomass and plant cell walls, the structure-function relationships of the relevant hydrolytic enzymes, and the ways these enzymes interact with and alter the biomass during the degradation. Thorough understanding of the details of the molecular machinery at work has led to the development of improved enzyme cocktails that have reduced the cost of biomass conversion to renewable fuels so that today, this technology is becoming competitive with traditional fossil fuels.



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