Protein folding: Diverse methods yield clues

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(Aug. 6, 2009) -- Rice University physicists have written the next chapter in an innovative approach for studying the forces that shape proteins -- the biochemical workhorses of all living things.

New research featured on the cover of today's issue of the Journal of Physical Chemistry illustrates the value of studying proteins with a new method that uses the tools of nanotechnology to grab a single molecule and pull it apart. The new method helps scientists measure the forces that hold proteins together. The new study contrasted the findings from Rice's method with a different approach that relies on chemical reactions .

"There is an ongoing discussion among scientists about which of these methods is more relevant," said Ching-Hwa Kiang, assistant professor of physics and astronomy at Rice. "What we've found is that each teaches us something different, but the results from the two are similar enough that we can use them together in the future."

Over the past decades, scientists have discovered that misfolded proteins play an important but mysterious role in diseases like Alzheimer's and Parkinson's. As a result, more laboratories like Kiang's are studying how proteins fold and misfold in the hopes of finding clues that could lead to new treatments.

Kiang's team specializes in studying the forces that hold protein strands together. Her group uses atomic force microscopes (AFM), which operate much like phonograph players. The AFM has a needle that's

suspended from one end of a cantilevered arm. The needle bobs up and down on the arm, randomly grabbing and lifting proteins. By measuring exactly how much force it takes to pull the strands apart, Kiang's group can learn important clues about the protein's behavior.

Kiang's work was recognized in Small Times magazine's 2007 "Best of Small Tech Awards," but it's not the only way to study protein folding. Other groups use chemicals to determine how much energy it takes to unfold proteins, and Kiang's latest paper looks at similarities and differences between the two methods.

"The chemical denaturant method gives very accurate information about the folded and unfolded state of the protein, and our method gives important information about what happens in between," Kiang said.

Proteins are the workhorses of biology. Each protein is a string of amino acids that are attached end to end, like a strand of pearls. The order of the amino acids comes from DNA blueprints, but the order itself doesn't tell scientists what the protein is designed to do. That's because each protein folds in upon itself shortly after its made, much like a strand of pearls curls up as it's dropped into someone's palm.

Unlike the pearls, which might fall this way or that depending upon how they're dropped, proteins fold the same way every time. That's important, because when they misfold, they cannot function properly and in some cases can make people sick.

"This is fundamental research, but it is very important," Kiang said. "We need to answer to these fundamental questions in order to better understand how protein folds correctly, which affects people's health."

Source: Rice University (news : web)