

Researcher shows proteins have controlled motions

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(PhysOrg.com) -- Iowa State University researcher Robert Jernigan believes that his research shows proteins have controlled motions. Most biochemists traditionally believe proteins have many random, uncontrolled movements.

Research conducted by Jernigan, director of the L.H. Baker Center for Bioinformatics and Biological Statistics together with Guang Song, an assistant professor in computer science and graduate student Lei Yang, over a 10-year period shows that not only are protein motions more restricted, but also that these restricted, controlled motions are part of the function of the proteins.

The group's findings were recently published in the journal "*Structure*."

Using as an example a protein from HIV virus, Jernigan conducted his research using a simple model and tested to see how the proteins moved. The large number of reported structures show exactly the motions that are required for their function, and exactly the same motions as computed by Jernigan's model.

"This is one experimental case that is indicative, but there are many others," he said.

Jernigan believes this research is the first step to better understanding proteins and cell behaviors.

"There is the possibility of creating designer drugs with this newly discovered information," he said.

"These are models that conform to the point of view that the structures have been designed to exert very strong control of their motions," he said. "Those motions correspond closely to the motions needed for their function."

For instance, HIV virus protein structures that Jernigan studied did not move randomly, but actually opened and closed to allow access to other structures.

There is a binding site that must open to permit access to the protein and then close again to allow the protein to function, he said.

Because the protein structure opens and closes as part of its function, Jernigan believes that the motion is controlled and part of the function of the protein.

Jernigan's studies used the HIV virus, but he believes that the results are relevant to many other protein structures.

Source: Iowa State University

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