

Fundamental forces in protein structure revisited

July 12 2010



Photo by Chrystal Cherniwchan

(PhysOrg.com) -- Research scientists from Bristol have joined forces with colleagues from America to unravel one of the fundamental problems of molecular biology, paving the way for better engineering of biological systems.

Proteins are considered the workhorses of biology, performing a wide variety of tasks including transporting oxygen around blood vessels, contributing to the fabric of tissues such as skin, and mediating most of the chemical reactions in the body.

These and other functions rely on proteins, which are initially made as linear flexible polymers, adopting well-defined and stable 3-dimensional

structures. Understanding what holds protein structures together, and the process of folding from the flexible to the functional forms is one of the outstanding problems of molecular biology.

Discovering the detail of the process would lead to better engineering of [biological systems](#), and could help to improve our understanding and treatment of disease.

In a paper now published in [Nature Chemical Biology](#), researchers from the University of Bristol and the University of Wisconsin, outline their findings.

“One of the issues is that protein 3D structures are stabilised by many, possibly thousands of weak interactions. Though they add up to give stable proteins, their inherent weakness makes them difficult to pin down,” explains Dek Woolfson, Professor of Chemistry and Biochemistry at Bristol.

The two research teams, led by Prof Woolfson and Prof Ron Raines (Wisconsin) used a combination of computer searches of known proteins structures and [theoretical calculations](#) to test for a new type of interaction, which they call n-to-pi-star interactions.

N-to-pi-star interactions are cousins of the more-famous [hydrogen bonds](#), which revolutionised understanding of biological chemistry in the second half of the last century.

Co-workers on the research, Drs Gail Bartlett and Amit Choudhary, found the new interactions in all [protein](#) structures. Moreover, they were able to show that theoretical calculations and the observations of real proteins matched astonishingly well given the intrinsic weak nature of these types of interaction.

Prof Woolfson added: “Whether the n-to-pi-star interaction will have such an impact as the hydrogen bond remains to be seen, but what is certain is that we will have to consider these and similarly less-established forces if we are to understand fully the workings of biology.”

More information: www.nature.com/nchembio/index.html

Provided by University of Bristol

Citation: Fundamental forces in protein structure revisited (2010, July 12) retrieved 9 April 2024 from <https://phys.org/news/2010-07-fundamental-protein-revisited.html>

<p>This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.</p>
--