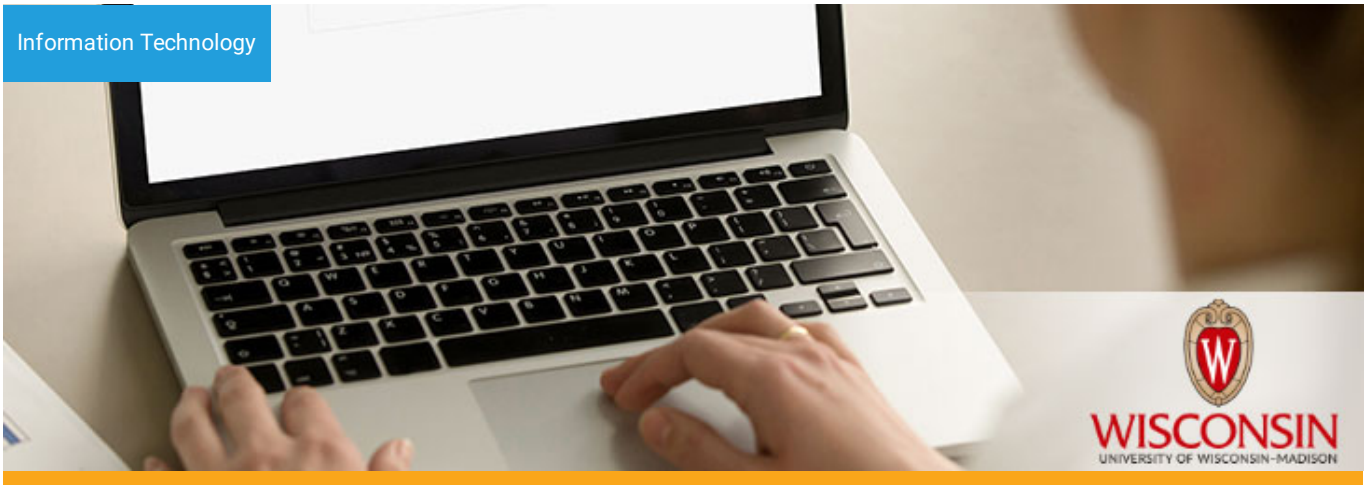
Information Technology



Predicting Protein Hot Spot Residues

WARF: P140357US01

Inventors: Julie Mitchell, Xiaolei Zhu, Steven Darnell

The Wisconsin Alumni Research Foundation (WARF) is seeking commercial partners interested in developing the most accurate software to date for modeling hot spot mutagenesis in proteins.

Overview

Most biological processes involve multiple proteins interacting with each other. While the principles governing protein-protein interactions are not fully understood, it is known that a small subset of 'hot spot' residues play a key role in binding.

In practice, the site-directed mutation of hot spots is an effective means of disrupting and studying protein interactions. This typically involves replacing the amino acid of interest with an alanine. The process requires major time and resources to identify hot spots in a systemic fashion.

Predictive models can dramatically improve efficiency.

The Invention

UW–Madison researchers have created the most accurate program ever developed to predict hot spot residues in proteins and model the effects of alanine substitution on each of the amino acids. The program uses a modified Knowledge-based FADE and Contacts (or KFC2) approach.

Applications

- Software for predicting hot spots and alanine mutagenesis
- Determining sites to target with small molecule drug design

Key Benefits

- Outperforms other programs
- Makes experimental design more efficient

Stage of Development

The program currently is in use.

Additional Information

For More Information About the Inventors

- Julie Mitchell

Tech Fields

- Information Technology : Computing methods, software & machine learning

- Research Tools : Protein interactions & function

For current licensing status, please contact Jennifer Gottwald at jennifer@warf.org or 608-960-9854