System and Method for Designing Stable Proteins

Summary:
The invention includes methods for designing thermostable proteins using predictive models implemented as computer software programs.

Contact Information: Matt Koenig, J.D.
KU Innovation & Collaboration (785)864-1774 mekoenig@ku.edu

Benefits:
- Accurate
- Robust
- Fast
- 3D structure is optional

Applications:
Designing proteins with enhanced thermo-stability has been a main focus of protein engineering because many native proteins are only marginally stable under both normal physiological and storage conditions. It is particularly relevant today and will continue to gain more importance as protein-based drugs and vaccines become increasingly attractive because of their high efficiency and low side effects. In addition, enzymes with enhanced stability are also very useful in many biotechnological applications.

Computational methods for designing proteins with enhanced thermo-stability are very useful because of their potential low cost and time-saving properties over current experimental approaches.

Overview:
The models were built based on mining very large-scale heterogeneous data using state-of-the-art machine learning algorithms. It is also a process of identifying single or multiple mutations for a given base protein for developing more stable mutants of the base protein without losing its functional activity.

Why it is better:
Extensive comparative studies have been conducted to validate the advantage of the invention over other existing computational methods. The invention has been applied to design stable mutants for several proteins. Experimental data have shown that the computational methods in the invention are accurate, robust, and capable of predicting stabilizing mutations on the surface as well as in the core of the protein.

Patents:
US 2012/0265513

Additional Web Content:
Contact the inventor, Jianwen Fang, Yunqi Li, C. Russell Middaugh.