



Fall 12-14-2018

## Science in the News

Celine M. Chandler

University of the Pacific, c\_chandler2@u.pacific.edu

Follow this and additional works at: <https://scholarlycommons.pacific.edu/biochem>

---

### Recommended Citation

Chandler, Celine M., "Science in the News" (2018). *CHEM151*. 14.  
<https://scholarlycommons.pacific.edu/biochem/14>

This Article Review is brought to you for free and open access by the Department of Chemistry at Scholarly Commons. It has been accepted for inclusion in CHEM151 by an authorized administrator of Scholarly Commons. For more information, please contact [mgibney@pacific.edu](mailto:mgibney@pacific.edu).

Celine Chandler  
December 14, 2018

### Science in the News: Article Review

The utilization of new technologies has allowed scientists to create artificial proteins. Once protein folding is understood and can be predicted, man-made proteins are possible with the help of a computer program known as Rosetta. This is of great significance because proteins that are not currently found in nature can be designed for specific functions, such as fighting cancer. Atomic forces between amino acids make the folding of proteins particularly difficult to predict strictly by hand. In Dr. Harrison's Biochemistry course, we discussed how complicated various types of folding such as primary, secondary, tertiary, and quaternary structures are. We also studied how hydrophobic and electrostatic interactions, hydrogen bonds, and chemical cross-linking are responsible for stabilizing tertiary structures. Dr. Baker and his team utilized Rosetta by first entering an amino acid sequence into the program and waiting for the computation of likely folded protein structures. The scientists were then able to synthesize genes that encode the designed proteins and grow them in bacteria and yeast (1).

As the technology began to advance, Dr. Baker teamed up with Dr. Wilson to design a protein that could fight the flu. After using the Rosetta software to find a specific structure that would fold and fit in a pocket of the virus that is an epitope for neutralizing antibodies, it was possible to narrow down the list of computed folded structures from Rosetta. By placing this protein in its pocket, the virus would be unable to enter cells and spread further. After finding possible protein folded structures through Rosetta, the team ran experiments on mice and discovered that one of the proteins (HB1.6928.2.3) successfully prevented the spread of the flu. (2) These results assured the scientists that Rosetta was a useful tool and that scientific research coupled with creativity, can lead to life-changing biochemistry. The next steps for this research seem endless, but Dr. Baker hopes to build various molecular machines. For example, in class we discussed a molecular machine known as ATP synthase that builds ATP molecules that are used for energy in the human body. Another possible future applications of Rosetta are the design of proteins that could block the formation of plaque in the brain that are speculated to cause Alzheimer's.

1. Zimmer, C. Scientists Are Designing Artisanal Proteins for Your Body. *New York Times*, Dec 2017, pp D1.

2. Chevalier, A.; Silva, D.; Rocklin, G. J.; Hicks, D.R.; Vergara, R.; Murapa, P.; Bernard, S. M.; Zhang, L.; Lam, K.; Yao, G.; Bahl, C. D.; Miyashita, S.; Goresnik, I./ Fuller, J. T.; Koday, M. T.; Jenkins, C. M.; Colvin, T.; Carter, L.; Bohn, A.; Bryan, C. M.; Fernandez-Velasco, A. D.; Stewart, L.; Dong, M.; Huang, X.; Jin, R.; Wilson, I. A.; Fuller, D. H.; Baker, D. Massively parallel de novo protein design for targeted therapeutics. *Nature International Journal of Science*. Sep 2017.