ACS SyntheticBiology

Introducing Our Authors

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ERAN BRAM

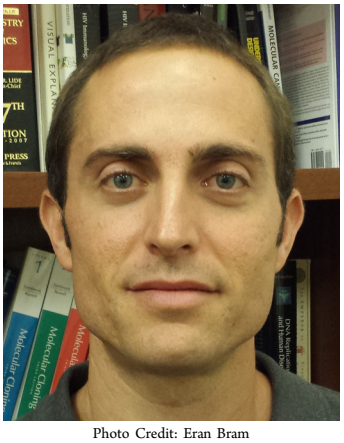

Photo Credit: Eran Bram

Current Position. Senior Scientist I, Diagnostics Research and Technology Development, Asuragen, Inc.

Previous Position. Founder and CSO at Piercell Bio, Ltd.

Education. Postdoctoral fellowship, Weiss lab for Synthetic Biology, Department of Biological Engineering, MIT (2013). Advisor: Ron Weiss. Ph.D. Molecular Biology, Technion—Israel Institute of Technology, Haifa, Israel (2009). Advisor: Yehuda G. Assaraf. B.A. Life Sciences, The Open University, Tel Aviv, Israel (2004).

Nonscientific Interests. I enjoy spending time with my wife and two daughters, hiking, exercising, and reading cheap contemporary sci-fi books.

My Ph.D. research focused on identifying molecular mechanisms of cancer drug resistance and on developing a diagnostic assay for assessing drug resistance in cancer cells. I am currently working as a Sr. Scientist at Asuragen, Inc. on developing next-generation diagnostic tools for cancer and other human genetic diseases.

My postdoctoral research focused on engineering probiotic bacterial sentinel/killer cells that detect pathogens in their environment and respond by producing a pathogen-specific toxin. These systems may potentially expand the natural intestinal immune system capabilities and continuously protect the body from various foodborne pathogens. The current publication represents a significant step in this direction, demonstrating a proof-of-concept *in vitro E. coli* system, that specifically detects and eradicates the opportunistic pathogen *P. aeruginosa*. For me, working at the application level presented a great opportunity to integrate many fundamental facets of synthetic biology such as genetic circuits, cell−cell communication, and protein engineering into one working biological system that has come to fruition within the current publication. (Read Bram's article, DOI: 10.1021/sb4000417).

BERNHARD PAETZOLD

Photo Credit: Jana Seyfang

Current Position. Ph.D. student, EMBL/CRG research unit in Systems Biology, Barcelona. Advisor: Luis Serrano

Education. Diploma in Biochemistry (combined B.S. and M.S.), University of Tuebingen, Germany. Thesis Advisor: Prof. Thilo Stehle.

Nonscientific Interests. Kite surfing, snowboarding, traveling, entrepreneurship, and EU research politics.

My research is focused on applying synthetic biology to engineer *Mycoplasma pneumoniae* for applications in the health sector. However, time and quality is often compromised due to outdated techniques. Part of my main project as a Ph.D. student was to make a set of complicated constructs. By blending two methods developed by Daniel Gibson, we developed a shortcut to success. Our strategy allows the simultaneous assembly and synthesis of DNA in one reaction step; we demonstrated that the overhangs needed for assembly, and even longer stretches, could be synthesized from oligonucleotides during the assembly itself.

I want to also take this opportunity to thank Daniel Gibson who invented the underlying, and my favorite, DNA assembly technique. I will be graduating with my Ph.D. at the end of 2013 and am looking for an exciting job or Postdoctoral position anywhere around the world. (Read Paetzold's article, DOI: 10.1021/sb400067v).

MATTHEW SMITH

Photo Credit: Matthew Smith

Received: November 26, 2013
Published: December 20, 2013

Current Position. Insight Data Science Fellow, Mountain View, CA.

Education. Ph.D. in Bioengineering, California Institute of Technology (2013). Advisor: Prof Frances Arnold. M. Phys in Physics, University of Oxford, England (2008).

Nonscientific Interests. Surfing, skiing, and hiking.

I am interested in computational approaches to help navigate the vast combinatorial spaces of biology. My research focused on evolutionary protein design methods, specifically tools for homologous protein recombination. We developed a novel computational method for identifying fragments of protein structure that preserve protein function when swapped between two or more homologous proteins. In this paper, we demonstrate one potential application of this method by efficiently identifying stabilizing mutations from several homologous fungal cellulases. Using a small, maximally informative subset of chimeric proteins and a simple machine learning algorithm, we were able to accurately predict the most stabilizing protein fragments and uncover a number of stabilizing point mutations. In the future, I hope other protein engineers will find these tools useful. (Read Smith's article, DOI: 10.1021/sb400010m).