■ CEM ALBAYRAK

Eser Erçin

Current Position. Postdoctoral Fellow, Department of Biosystems Science and Engineering, ETH Zürich; Advisor: Dr. Savaş Tay.

Education. Ph.D. and M.S. in Chemical Engineering, Stanford University; Advisor: Dr. Jim Swartz. B.S. in Biology and B.S. in Chemical Engineering, Massachusetts Institute of Technology (MIT).

Nonscientific Interests. I enjoy cooking, playing soccer, squash, playing the violin, and traveling (particularly road trips).

The overarching theme of my Ph.D. work was the site-specific incorporation of non-natural amino acids (nnAAs) into proteins using cell-free protein synthesis. Here, we incorporated multiple copies of two different nnAAs into green fluorescent protein (GFP) and showed that GFP polymers resulting from direct conjugation of these modified proteins retained their activity. We were thus able to synthesize a biomaterial composed entirely of active proteins. I believe the true power of our method lies in its modularity and generalizability. Even though we only demonstrated it with GFP, in principle, our protocol can be used to create polymers of any protein or of any group of proteins without inactivating them. I sincerely hope this method proves useful to scientists looking to synthesize polymers and materials containing active proteins. (Read Albayrak's article; DOI: 10.1021/sb400116x).

■ DARIO CECCHI

Fabio Chizzolini

Current Position. Ph.D. student, CIBIO, University of Trento, Trento, Italy. Advisor: Dr. Sheref S. Mansy.

Education. M.Sc. Molecular and Industrial Biotechnology, Department of Biology, University of Bologna, Bologna, Italy. Advisor: Dr. Alberto Danielli. Leonardo Fellow at the Centre for Genomic Regulation, Barcelona, Spain. Advisor: Dr. Rory Johnson.

Nonscientific Interests. During my free time I like to cook and to brew my own beer. I also enjoy playing soccer and handball.

I have always been fascinated by the mechanisms that made life arise from fortuity, and I decided to pursue my research on the rational design of chemical systems that can mimic it. Looking at natural genetic regulation as a starting point, I am attempting to build cell-free genetic circuits. The work presented here gives some insight into how this goal can be achieved. Indeed, the gene position within an operon has a profound impact on the performance and regulation of the system as a whole. At the moment I am testing several transcriptional regulators that may be useful for the construction of artificial cells. (Read Cecchi's article; DOI: 10.1021/sb4000977).

■ FABIO CHIZZOLINI

Dario Cecchi

Current Position. Ph.D. Candidate, CIBIO, University of Trento, Italy. Advisor: Sheref S. Mansy.

Education. M.S., Molecular Biology, University of Padua, Italy. Advisor: Tom Ellis. B.S., Life Sciences, University of Florence, Italy. Advisor: Elisabetta Meacci.

**Nonscientific Interests.** Writing short stories, History.

How do you design a DNA sequence if your goal is to synthesize a given amount of a protein? Being always fascinated by the central dogma of molecular biology, working on this problem was an amazing opportunity for me. In this article I explore one of the possible mechanisms that can be used to control protein expression: transcription. I am currently expanding this work by investigating additional mechanisms to control protein expression. Ultimately we hope our work will lead to the construction of artificial cells with predictable behavior. (Read Chizzolini's article; DOI: 10.1021/sb4000977).

■ SEOK HOON HONG
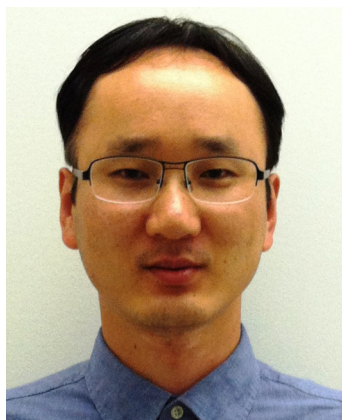
Seok Hoon Hong

Current Position. Postdoctoral fellow, Department of Chemical and Biological Engineering, Northwestern University. Advisor: Dr. Michael C. Jewett.

Education. Ph.D. in Chemical Engineering at Texas A&M University. Advisor: Dr. Thomas K. Wood; M.S. and B.S. in Chemical Engineering at Seoul National University, Korea. Advisor: Dr. Jeyong Yoon.

Nonscientific Interests. Home improvement, history book reading.

I am interested in engineering biological systems to develop as useful platforms for advanced biomanufacturing. I study cell-free synthetic biology for the production of novel protein-based materials *via* site-specific incorporation of nonstandard amino acids. In this research, we characterized cell-free protein synthesis in crude lysates derived from a genomically recoded *E. coli* and demonstrated that the removal of release factor 1 increases nonstandard amino acid incorporation at single and multiple in-frame positions. I am currently working on the development of a high yielding cell-free protein synthesis system *via* advanced genome engineering technology for the production of sequence-defined biopolymers. I imagine cell-free synthetic biology research will provide suitable platforms in the synthesis of advanced biopolymers, proteins, and enzymes. (Read Hong's article; DOI: 10.1021/sb400140t).

■ SUKANYA IYER

Sukanya Iyer

Current Position. Postdoctoral Research Associate, Emory University. Advisor: Dr. Minsu Kim.

Education. Ph.D., Life Science, University of Tennessee, Oak Ridge National Laboratory. Advisor: Dr. Mitchel Doktycz; B.Tech. in Biotechnology, SRM University, India.

Nonscientific Interests. I enjoy hiking, traveling, and attending live music concerts and theater performances.

My graduate work centered on development of molecular tools to harness cell-free systems for synthetic biology. Cell-free extracts provide a flexible and well-characterized context to implement predictable gene circuits. To aid the efforts to enable gene circuits in cell-free systems, we utilized DNA aptamers to develop ligand responsive T7 promoters. Since DNA aptamers can be selected against potentially any molecule of interest, the approach detailed in the paper provides a way forward for designing gene promoters are responsive to any desired molecule. My current postdoctoral research is aimed at providing a quantitative description of gene expression dynamics in stationary phase of growth in *E. coli*, with the aid of simple synthetic gene circuits. In the future, I hope to continue to develop novel molecular tools and take a bottom-up approach to further our understanding of biological design principles. (Read Iyer's article; DOI: 10.1021/sb4000756).

■ WEI-CHENG LU
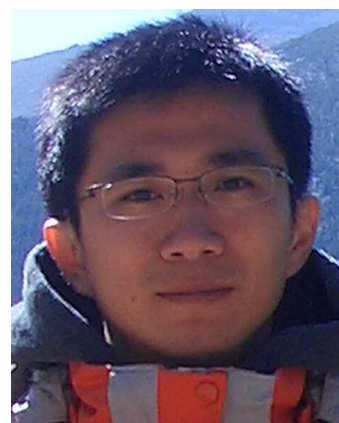
Wei-Cheng Lu

Current Position. As of June 2014: Postdoctoral fellow, Department of Chemical Engineering, University of Texas at Austin. Advisor: Dr. George Georgiou.

Education. Ph.D., Cellular and Molecular Biology, University of Texas at Austin. Advisor: Dr. Andrew Ellington. B.S., Medical Technology, Tzu Chi University, Taiwan.

Nonscientific Interests. My interests outside of science primarily include outdoor and indoor sports, especially badminton, basketball, and hiking.

My scientific interests primarily lie in the evolution of proteins for biotechnology applications, including for therapeutic purposes. Directed evolution in particular has demonstrated the ability to generate a wide variety of useful molecules. In previous papers we focused on biotin ligase and streptavidin, as the biotin:streptavidin interaction is the strongest known noncovalent bonding in nature. Specifically, we attempted to expand the applications of this incredible bond by generating orthogonal pairs of *E. coli* biotin ligase (which I evolved) and streptavidin (which Matthew Levy evolved), *i.e.*, [evolved biotin ligase:desthiobiotin] and [evolved streptavidin:desthiobiotin]. For this paper, we generated four synthetic operons composed of unique variant pairs and selected for the operon(s) that best utilized desthiobiotin. Not only did our experiment demonstrate the coevolution of two proteins, but more importantly, it also revealed the potential for directed evolution applications in more complex pathways. (Read Lu's article; DOI: 10.1021/sb400160m).

■ TAIJI OKANO
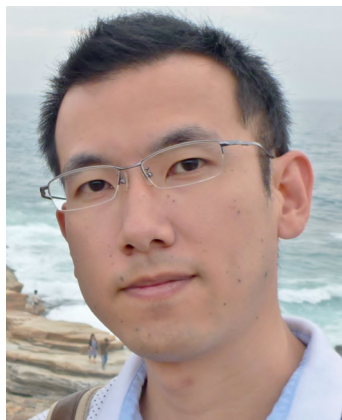
Taiji Okano

Current Position. Assistant Professor, Department of Precision Mechanics, Faculty of Science and Engineering, Chuo University, Japan

Education. Postdoctoral researcher, ERATO Project, Japan Science and Technology Agency. Ph.D. in Science, Fukuoka University, Japan (2009).

Nonscientific Interests. I love music, especially classical.

My current research interests are to develop and apply new microdevices for chemical and biochemical assays. In our previous publication, we fabricated quartz-glass microchambers for conducting protein synthesis using an *in vitro* transcription and translation system. By using the glass as a material, the efficiency of the protein synthesis was enhanced to such an extent that the protein synthesis from a single copy of DNA can be detected. Therefore, our microchamber devices can serve as a powerful tool for the detailed analysis of protein synthesis. In this paper, we studied the effect of the compartment size, which is one of the fundamental variables for reactions occurring in cells, and found the existence of an optimum compartment size for the protein synthesis reaction. (Read Okano's article; DOI: 10.1021/sb400087e).

■ DAN SIEGAL-GASKINS

Dan Siegal-Gaskins

Current Position. Postdoctoral Scholar, Division of Biology and Biological Engineering, California Institute of Technology, Pasadena, California, USA. Advisor: Prof. Richard Murray.

Education. Ph.D. Physics, University of Chicago (2008). Advisor: Prof. Sean Crosson; B.A.Sc. Engineering Science, University of Toronto, Canada (2002).

Nonscientific Interests. Music, cats, and the outdoors.

I am primarily interested in using the tools of synthetic biology to better understand natural gene regulatory circuit behavior. Recent advances in cell-free techniques, developed in large part to improve the synthetic circuit prototyping pipeline, have provided additional tools in the form of simplified *in vitro* testing platforms. In this work we characterize the performance of a cell extract-based "breadboard" using real-time and simultaneous fluorescence measurements of transcriptional and translational activity, identifying specific contributions of essential biomolecular resources. Limits on resources can be clearly seen as the operational demands of a circuit increases. How these resource limits manifest *in vivo* remains an open and intriguing question. (Read Siegal-Gaskin's article; DOI: 10.1021/sb400203p).

■ HARUKA SOGA

Haruka Soga

Current Position. Graduate student, Department of Biotechnology, Graduate School of Engineering, Osaka University. Advisor: Dr. Tomoaki Matsuura.

Education. B.S. in Engineering, Osaka University, Japan. Advisor: Dr. Tomoaki Matsuura.

Nonscientific Interests. Bicycling, travel, drawing pictures.

My research is focused on the effect of a confined reaction volume on the synthesis of membrane protein within it. To understand this we synthesized EmrE, a multidrug transporter from *Escherichia coli*, by encapsulating a cell-free system into giant unilamellar vesicles (GUVs). These vesicles were >1 μm in diameter and composed of 1-palmitoyl-2oleoyl-*sn*-glycero-3-phosphocholine. We found EmrE was synthesized and integrated into the GUV membrane in its active form. Furthermore, we found that the ratio of membrane-integrated EmrE to total synthesized EmrE decreased as the vesicle volume increased. Since protein synthesis inside GUVs may be used for *in vitro* directed evolution, I hope to apply the result of this research to *in vitro* directed evolution of membrane proteins in future studies. (Read Soga's article; DOI: 10.1021/sb400094c).

◼ ZOLTAN TUZA

Zoltan Tuza

Current Position. Ph.D. Candidate, Department of Information Technology at PPCU Budapest, Hungary. Advisor: Gabor Szederkenyi.

Education. M.Sc. in Electrical and Computer Engineering at PPCU Budapest, Hungary (2010).

Nonscientific Interests. Outdoor activities like hiking and camping, landscape photography.

I'm generally interested in system modeling and system identification, with a recent focus on modeling of biomolecular systems. My background in electrical and computer engineering certainly gives me a perspective on complex systems that is different from that of traditional biologists. It was an interesting challenge to develop the tools and experiments required to probe questions like resource limits in a biomolecular system. In our work on the cell-free "breadboard", I am particularly happy about the demonstration of simultaneous real-time measurement of transcription and translation and fine control over inputs, both of which will be of significant help in gathering rich data for first principal modeling and model fitting. (Read Tuza's article; DOI: 10.1021/sb400203p).