JASON BOOCK

Richard Pampuro

Current Position. Graduate student in Chemical and Biomolecular Engineering at Cornell University. Advisor: Matthew DeLisa.

Education. B.S. and M.S.E in Chemical and Biomolecular Engineering at Johns Hopkins University. Advisor: Marc Ostermeier.

Nonscientific Interests. ChemBEasts intramural sports, listening to Grateful Dead tapes, cooking CSA vegetables, wine touring through the Finger Lakes, watching Arrested Development, and Cornell hockey.

I am interested in using natural quality control mechanisms to enhance the engineering of proteins. Production of next-generation biotech products will hinge on expression of recombinant protein pathways; however, often this transfer does not go as expected, resulting in poorly folded and inactive enzymes. We use the innate ability of organisms to recognize well-folded proteins to eliminate this bottleneck and focus protein libraries. Our work here highlights a unique strain-engineering approach to enhance the production of active proteins outside of cells, providing numerous advantages over intracellular expression. Furthermore, this work lays the foundation and provides a screening tool for the understanding the fundamentals of protein export and the quality control mechanisms involved. (Read Boock's article; DOI: 10.1021/sb400142b).

SUNIL CHANDRAN

Sunil Chandran

Current Position. Associate Director, Head of the Automated Strain Engineering group, Amyris Inc., Emeryville, California.

Education. Postdoctoral fellowship, University of Wisconsin-Madison, Advisor: Prof. Ronald Raines. Ph.D. in Organic Chemistry, Michigan State University, Advisor: Prof. John Frost. M.S. in Organic Chemistry, Indian Institute of Technology, Mumbai. B.S. in Chemistry, Mumbai University.

Nonscientific Interests. Photography, hiking, cycling.

My primary interests lie in the field of metabolic engineering for the microbial production of chemicals and fuels. While the metabolic engineering community has been extremely successful in commercializing microbial processes, optimization of microbes for economical industrial-scale production of target molecules requires numerous changes to the genetic code of the microbe, which is extremely time-consuming. The goal of my group is to accelerate the design-build-test cycle within any strain engineering endeavor by reducing the cost and effort of performing molecular biology while simultaneously increasing throughput. A key step in the engineering of strains is the assembly of DNA constructs from individual DNA parts. Current methods for DNA assembly are either limited in the number of DNA parts that can be assembled with high success rates or are laborious. The ligase cycling reaction (LCR) method we describe in our manuscript addresses these concerns and is well-suited to small-scale laboratory manipulations or high-throughput operations that require rapid, highly efficient methods. (Read Chandran's article; DOI: 10.1021/sb4001992).

STEFAN DE KOK

Elva Huang

Current Position. Project Manager, Department of Biotechnology, Delft University of Technology, The Netherlands.

Education. Industrial postdoc at Amyris Inc. in California (2011−2013). Ph.D. in Biotechnology at Delft University of Technology (2012). Advisor: Prof. Jack Pronk. B.S. and M.S. in Life Science and Technology at Delft University of Technology and Leiden University (2007).

Nonscientific Interests. Cycling, ice-skating, hiking, and climbing.

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I am interested in metabolic engineering of microorganisms for high-level production of biochemicals and biofuels. Genetic engineering of microorganisms comprises many steps, including DNA construct design, DNA part amplification, DNA construct assembly, and transformation of the assembled DNA constructs. To facilitate metabolic engineering of microbes, we optimized ligase cycling reaction (LCR) for efficient assembly of DNA constructs. LCR enables one-step assembly of up to 20 DNA parts into DNA constructs up to 20 kb via a cheap, rapid, and convenient workflow. LCR assembly thereby outperforms existing methods for scarless, sequence-independent assembly of DNA constructs and is expected to become the method of choice for DNA assembly. (Read de Kok's article; DOI: 10.1021/sb4001992).

CHARLES HAITJEMA

Kevin Solomon

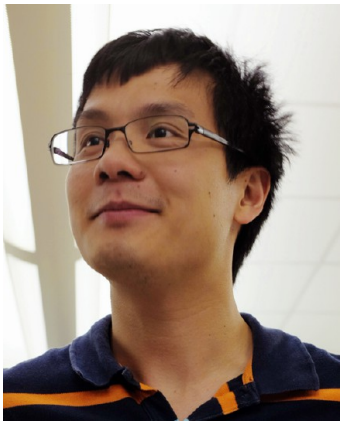
Current Position. Postdoctoral Scholar, Department of Chemical Engineering, University of California, Santa Barbara. Advisor: Dr. Michelle O'Malley.

Education. Ph.D. Microbiology, Cornell University (2012). Advisor: Dr. Matthew DeLisa. B.S. Microbiology, Indiana University (2007). B.A. Spanish, Indiana University (2007)

Nonscientific Interests. Playing the piano and drums, tennis, cycling, and traveling.

I am interested in controlling microbial protein machinery to find solutions in bioenergy and medicine. *Escherichia coli* is the most common host for preparative protein production, but it is severely limited in the ability to deliver proteins to the extracellular medium. Instead, proteins must be isolated from the crowded intracellular environment, leading to impurities, low yields, and high costs. This problem is compounded by the lack of high-throughput screening methods to engineer extracellular secretion machinery. This paper describes a universal genetic assay that enables the engineering of diverse secretory pathways directly in *E. coli*. Using this assay, we isolated superior expression hosts capable of high titer secretion of proteins to the extracellular space. Currently, as a postdoctoral scholar, I am studying cellulose-degrading protein complexes of anaerobic fungi. (Read Haitjema's article; DOI: 10.1021/sb400142b).

JING LIANG



Jing Liang

Current Position. Graduate student at the University of Illinois at Urbana−Champaign, Department of Chemical and Biomolecular Engineering. Advisor: Dr. Huimin Zhao.

Education. B.SE in Biomedical Engineering at the University of Michigan at Ann Arbor.

Nonscientific Interests. Chemical and physical transformation of caloric sources for human consumption, oxidation kinetics of fermentation products from *Vitis vinifera*, biomechanics of aerobic lower extremity locomotion, and did you say nonscientific?

Traditionally, making specific genome modifications in mammalian cells have been a daunting challenge if not an incredibly tedious task. However, recent advances in TALE (and CRISPR) technology have enabled researchers to make such modifications readily. Here, we introduce a scalable high-throughput TALE synthesis platform that can produce hundreds of TALEs per day per liquid handling robot. In contrast to previously reported synthesis platforms, we can produce transfection ready TALEs in a single day without the need for clonal isolation. In the near future, I hope to explore the possibility of using a library of TALEs as a genetic screening tool in mammalian cells to identify genes involved in cell differentiation. (Read Liang's article; DOI: 10.1021/sb400109p).

NICHOLAS ANDREW ROEHNER

Nicholas Andrew Roehner

Current Position. Graduate student, Department of Bioengineering, University of Utah. Advisor: Prof. Chris J. Myers.

Education. B.S. in Bioengineering, University of Washington (2010).

Nonscientific Interests. I enjoy challenging myself outdoors with running, cross-country skiing, and white water rafting. My hobbies include reading and playing/designing board games.

My primary research interest is in biodesign automation. In particular, I am most interested in the development of algorithms and techniques for the automated design of biological systems from abstract behavioral specifications. I am also interested in the development of standards and the reconciliation of biodesign automation tools with laboratory practice in the field of synthetic biology. I plan to apply my research to the design and construction of biological systems ranging from genetic regulatory networks for biosensing and biocomputation to metabolic networks for biosynthesis and bioremediation. (Read Roehner's article; DOI: 10.1021/sb400066m).

LESLIE STANTON

Leslie Stanton

Current Position. Scientist, Amyris Inc., Emeryville, California

Education. Ph.D. Molecular and Cellular Biology, University of California, Berkeley (2010). Advisor: Karsten Weis. B.S. Biochemistry and Molecular Biology, University of Georgia, Athens (2002).

Nonscientific Interests. Running, baking, hiking, and going to the beach.

My interests range from investigating the cell biology of synthetic biology hosts to developing tools to improve engineering of these hosts. At Amyris, we strive to decrease the iteration time of the design–build–test cycle for strain improvement. DNA assembly is often a limiting step in this process since some methods are rapid but lack reliability, while others are reliable yet time-consuming. The improvements made to LCR in this paper have transformed LCR into a method that is both reliable and rapid for constructing large DNA assemblies. Our hope is for LCR to be a universal tool for strain engineers. (Read Stanton's article; DOI: 10.1021/sb4001992).