

■ ROBERT PENCHOVSKY



Image courtesy of Robert Penchovsky.

Current position: Assistant Professor of Genetics at the Faculty of Biology, Sofia University, “St. Kliment Ohridski” in Bulgaria

Education: Postdoctoral Researcher at Yale University, New Haven, CT; advisor: Ronald R. Breaker. Ph.D. in Genetics, University of Cologne, Germany in the laboratory of John S. McCaskill at the former National Institute of Germany for Mathematics and Informatics (*Gesellschaft für Mathematik und Datenverarbeitung* mbH - GMD), later part of Fraunhofer-Gesellschaft (FhG), at Schloss Birlinghoven, Sankt Augustin, Germany. M.Sc. in Biochemistry and Microbiology with specialization of genetics and an Associate degree in applied computer sciences from Sofia University, “St. Kliment Ohridski”, Bulgaria

Nonscientific interests: Playing chess and tennis, swimming, boxing, cycling and many other sports. I am a fan of F1 motor racing and also like to watch so-called independent films from USA, Germany, Bulgaria, and Russia in their native languages

RNA is a unique biopolymer because it plays very diverse roles in nature. RNA is much more than a messenger between genomic DNA and proteins; it is also a powerful catalytic biopolymer that is directly responsible for the peptide bond formation during protein synthesis in the most advanced cellular machine, the ribosome. These findings inspired us to engineer functional RNA assemblies. We use computational modeling of secondary RNA structures to design catalytic RNAs that can sense the length of their substrate molecules and response to specific nucleic acid sequences. As a result, we have built multiple RNA assemblies with the functionality of integrated digital circuits. Our findings demonstrate that research within the framework of RNA synthetic biology can be used to build *de novo* complex molecular machines. (Read Penchovsky’s article; DOI: 10.1021/sb300053s)

■ ARTHUR PRINDLE

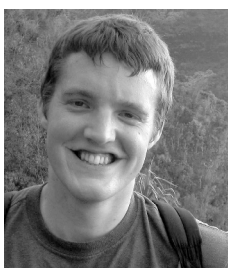


Image courtesy of Arthur Prindle.

Current position: Ph.D. student at the University of California, San Diego. Advisor: Jeff Hasty

Education: B.S. in Chemical Engineering, Caltech, Pasadena, CA

Nonscientific interests: Keeping my wife happy, playing with our parrotlet Widget

For me, bacteria are the ideal platform for exploring and engineering biology. They are small, extremely hardy, inexpensive to maintain, reproduce quickly, and comprise a vast array of species with unique properties. The majority of synthetic biology efforts have utilized *E. coli* out of tradition, ease of genetic manipulation, and a prevalence of available tools and methods. A next generation of *integrated* synthetic biology will utilize the native networks of diverse microbial species in concert with engineered gene circuits. Achieving this vision will require the development of microbial “shopping catalogues” complete with strain-specific pros, cons, and lists of parameters that define their circuit compatibility. And, of course, a willingness to accept that most will not work as intended the first time. (Read Prindle’s article; DOI: 10.1021/sb300060e)

■ ARUN STEPHEN RAJKUMAR



Image courtesy of Henrike Niederholtmeyer.

Current position: Ph.D. student in the Laboratory of Biological Network Characterization, Institute of Bioengineering, Ecole Polytechnique Fédérale de Lausanne, Switzerland; advisor: Prof. Sebastian J. Maerkl

Education: M.S. (by research) in Biophysics from Anna University, Chennai, India

Nonscientific interests: Literature, scale modeling, and popular science

My research focuses on studying transcriptional regulation through synthetic biology. The work involved is a hybrid and collaborative endeavor involving standard molecular cloning, synthetic biology, microfluidics and mathematical modeling. The published article describes some of the groundwork required. I want to understand how eukaryotic promoters are designed, and have been doing so by synthesizing variants of a known promoter and inferring the role of each regulatory element in the promoter of interest from observed changes in regulatory function. I hope to understand how regulatory elements which can be studied *in vitro*, such as transcription factor binding sites or nucleosome-disfavoring sequences, are integrated into promoters *in vivo*, ultimately providing us with “rules” of promoter construction and culminating in robust, quantitative models of transcriptional regulation. (Read Rajkumar’s article; DOI: 10.1021/sb300045j)

■ CALVIN SCHMIDT

Current position: Undergraduate student at Rice University, Houston, TX, majoring in Biochemistry and Cell Biology; advisor: Dr. Matthew Bennett

Education: J.K. Mullen High School, Denver, Colorado