



**Date:** 20<sup>th</sup> Sept 2019

**Time:** 11 am - 12 pm

**Venue:** Seminar Room Level 6, Neuros  
8 Biomedical Grove  
A\*STAR, 138665

**Host:** Dr. Charles JOHANNES, Ph.D.

President, P<sup>2</sup>S<sup>2</sup>

Principal Scientist, P53 lab

Principal Investigator, Peptide

Engineering Programme, A\*STAR

## Accelerating synthetic combinatorial discovery



**Dr. Zachary Gates**  
Postdoctoral Scientist  
Department of Chemistry  
Massachusetts Institute of  
Technology (MIT)  
Cambridge, MA, USA

### Speaker:

Zak was born and raised in the midwestern United States, where he discovered scientific research as an undergraduate at The University of Chicago. He completed his graduate studies in 2014 under the supervision of Prof. Stephen Kent, and has since been engaged in postdoctoral studies in the laboratory of Prof. Bradley Pentelute at the Massachusetts Institute of Technology. Zak is broadly interested in protein molecules – their atomic-level structures, how and why they fold, how they interact, and how mutations disrupt their normal function to cause disease – and in the use of chemical methods to facilitate their study.

### Abstract:

Combinatorial libraries have revolutionized the fields of peptide and protein engineering. Generally, successful combinatorial approaches employ genetic encoding to determine the amino acid sequences of compounds identified by selection procedures. In this talk, I will describe the development of a proteomics-inspired, tandem mass spectrometry-based sequencing approach applicable to complex mixtures of synthetic peptides. This approach enables the use of selection procedures that operate directly in solution, without the need for solid support beads or encoding tags. For example, by the use of LC-MS/MS sequencing, we have extended the diversity of libraries amenable to size exclusion chromatography-based affinity selection by 5 orders of magnitude, up to ~10<sup>6</sup> members. Immunoproteomics-inspired approaches have increased accessible diversities even further, to 10<sup>8</sup>–10<sup>9</sup>. These diversities are on par with those achieved by early phage display, and are expected to significantly extend the utility of synthetic libraries for identifying peptide and miniprotein-based binding molecules.

No registration is required.

We encourage you to be there early to get a seat as spaces are limited

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