SEMINAR

ALL ARE WELCOME

TEMASEK LIFESCIENCES LABORATORY

05 October 2017 (Thursday), 11am
The Auditorium (Level 1)

Hosted by: Dr Jang In-Cheol

Sequence Similarity Networks (SSNs) and Genome Neighborhood Networks (GNNs): Web Tools for the Discovery of Novel Enzymes in Novel Metabolic Pathways

Professor John A. Gerlt
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Professor John Gerlt is a mechanistic enzymologist and an expert in structure/function studies of numerous metabolic enzymes. He has made numerous significant contributions to the field of mechanistic enzymology and physical organic chemistry, and his seminal work in the enolase superfamily and the crotonase superfamily has established a new and important discipline of genomic enzymology. Professor Gerlt is the Program Director of the Enzyme Function Initiative (EFI), a Large-Scale Collaborative Project (Glue Grant) from the National Institute of General Medical Sciences. The EFI is formed from approximately 80 researchers at 9 academic institutions in the US and Canada. Professor Gerlt has won numerous awards, including the Repligen Award, the A. Ian Scott Medal, the Arthur C. Cope Scholar Award, and is a Fellow of the American Association for the Advancement of Science. He currently holds the Gutgsell Chair, a prestigious University Endowed Chair. He is currently the Associate Editor for the ACS journal, Biochemistry, and is on the Editorial Board of a number of journals. He has published extensively in prestigious journals such as Science, Nature, Nature Chemical Biology, Proceedings of the National Academy of Sciences, Journal of the American Chemical Society and Biochemistry, etc.

The number of proteins in the UniProt database (>89M sequences in Release 2017_08) is increasing with a doubling time of 2.5 yrs; however, ≥50% of the proteins have uncertain or unknown functions. This lecture will describe two publicly accessible web tools for generation of protein sequence similarity networks (SNNs; EFI-EST; efi.igb.illinois.edu/efi-est/) and genome neighborhood networks (GNNs; EFI-GNT; efi.igb.illinois.edu/efi-gnt/) that can be used to 1) synergistically leverage the large amounts of sequence data and 2) guide formulation of experimental strategies for assigning functions to uncharacterized proteins in novel metabolic pathways. Examples will be provided of the use of SSNs and GNNs to discover novel metabolic pathways in species in the human gut microbiome. The lecture also will describe how SSNs can be used to prioritize targets in large protein families for functional assignment based on metagenome sequence datasets.

Recent Publications:

1.Purification, Crystallization, and Structural Elucidation of D-Galactaro-1,4-lactone Cycloisomerase from *Agrobacterium tumefaciens* Involved in Pectin Degradation, M. W. Vetting, J. T. Bouvier, **J. A. GERLT**, and S. C. Almo, *Acta. Cryst. Section F* **2015**, *72*, 36-41. PMID: 26750482

2.A General Strategy for the Discovery of Metabolic Pathways: D-Threitol, L-Threitol, and Erythritol Utilization in *Mycobacterium smegmatis*, H. Huang, M. S. Carter, M. W. Vetting, N. Al-Obaidi, Y. Patskovsky, S. C. Almo, and **J. A. GERLT**, *J. Am. Chem. Soc*. **2015**, *137*, 14570-14573. PMID: 26560079

3.Assignment of Function to a Domain of Unknown Function (DUF): DUF1537 is a Novel Kinase Family in Catabolic Pathways for Acid Sugars, X. Zhang, M. S. Carter, M. W. Vetting, B. San Francisco, S. Zhao, N. Al-Obaidi, J. O. Solbiati, J. Thiaville, V. de Crécy-Lagard, M. P. Jacobson, S. C. Almo, and **J. A. GERLT**, *Proc. Nat. Acad. Sci. USA*, **2016** *113*, E4161-9. doi: 10.1073/pnas.1605546113. PMID: 27402745