Symposium Agenda

Thursday, October 21st

3:00 p.m. – 7:00 p.m.   Arrival and Registration

5:30 p.m. – 7:00 p.m.   Dinner

7:00 p.m. – 8:00 p.m.   **Keynote Lecture**

1. Post-translational Modifications in Cancer and the DNA Damage Response  
   **Tony Hunter**, The Salk Institute for Biological Sciences

8:00 p.m. – 9:00 p.m.   Opening Reception

Friday, October 22nd

7:00 a.m. – 8:30 a.m.   Breakfast

8:30 a.m. – 11:50 a.m.   **Session I: Glycosylation**  
   *Chair: Al Burlingame*

8:30 – 9:10 a.m.   2. Recent advances in ETD internal energy deposition technology provides a new robust analytical platform for global studies of labile O-GlcNAcylation and S/T phosphorylation  
   **Al Burlingame**, University of California, San Francisco

9:10 – 9:30 a.m.   3. Regulation of IRS-1/2 Mediated Insulin Signaling by O-GlcNAc Modification  
   **Lauren Ball**, Medical Univ of South Carolina

9:30 – 10:10 a.m.   4. Extensive Crosstalk Between O-GlcNAcylation & Phosphorylation: A New Paradigm for Nutrient Regulation of Signaling, Transcription and Mechanisms Underlying Chronic Disease  
   **Gerald Hart**, Johns Hopkins University Medical School
10:10 a.m. – 10:30 a.m.  Coffee Break

10:30 – 10:50 a.m.  5.  Metabolic Labeling of C. Elegans Primary Embryonic Cells as a Tool for Glycoprotein Discovery  
Amanda Marusich, University of Nevada, Reno

10:50 – 11:10 a.m.  6.  Non Consensus Sequence Motifs for Gln- and Asn-Linked Glycosylation in Human Antibodies Revealed by Selective Enrichment and Detection Techniques  
John Valliere-Douglas, Amgen

11:10 – 11:50 a.m.  7.  O-Glycan Modifications of Proteins Important for Cellular Regulation and Homeostasis  
Richard Cummings, Emory University School of Medicine

12:00 p.m. – 4:00 p.m.  Lunch and Free Time

4:00 p.m. – 6:00 p.m.  Session II: Explorations into Various PTM Functions  
Chair: Kevin Moore

4:00 – 4:40 p.m.  8.  Exploring the Importance of Protein-Tyrosine Sulfation in Male Fertility  
Kevin Moore, Oklahoma Medical Research Foundation

4:40 – 5:00 p.m.  9.  Functional regulation of DNMT1 by deacetylation  
Lirong Peng, H.Lee Moffitt Cancer Center & Research Institute

5:00 – 5:40 p.m.  10.  Examining the Histone Code Using Peptide Microarrays  
Stephen Fuchs, University of North Carolina-Chapel Hill

5:40 – 6:00 p.m.  11.  Elucidation of post-translational modification impact on the p53 conformational state using proximity ligation assay  
Tina Settineri, Life Technologies

6:00 p.m. – 7:30 p.m.  Dinner

7:30 p.m. – 9:00 p.m.  Poster Session I (Odd program numbers manned)
Saturday, October 23rd

7:00 a.m. – 8:30 a.m.  Breakfast

8:30 a.m. – 11:50 a.m.  Session III: Sumoylation/Phosphorylation
  *Chair: Pierre Thibault*

  8:30 – 9:10 a.m.  **12.** A novel proteomics approach to identify SUMOylated proteins and their modification sites in mammalian cells
  *Pierre Thibault*, Universite de Montreal - IRIC

  9:10 – 9:30 a.m.  **13.** Site-Specific Identification of SUMO-2 Conjugation Sites in Cells Reveals Novel SUMOylation Motifs
  *Joost Schimmel*, Leiden University Medical Center

  9:30 – 9:50 a.m.  **14.** Quantitative phosphoproteomic analysis of T cell signaling
  *Arthur Salomon*, Brown University

  9:50 – 10:10 a.m.  **15.** Phosphoprotein profiling of Tamoxifen Response in Breast Cancer Cells
  *Kolbrun Kristjansdottir*, University of Chicago

10:10 a.m. – 10:30 a.m.  Coffee Break

10:30 – 10:50 a.m.  **16.** Inhibition of RIP2’s tyrosine kinase activity limits NOD2-driven cytokine responses
  *Derek Abbott*, Case Western Reserve University

10:50 – 11:10 a.m.  **17.** Role of Tyrosine Phosphorylation in the Crosstalk between O-GlcNAc Modification and Serine/Threonine Phosphorylation
  *Suresh Mishra*, University of Manitoba

11:10 – 11:50 a.m.  **18.** The evolution of phosphotyrosine and methylarginine signaling
  *Anthony Pawson*, Samuel Lunenfeld Research Institute

12:00 p.m. – 4:00 p.m.  Lunch and Free Time
4:00 p.m. – 6:00 p.m.  
**Session IV: Cys Modifications and Oxidative Damage**
*Chair: Stuart Lipton*

4:00 – 4:40 p.m.  
19. **Quantitative Chemical Proteomics of Dynamic Palmitoylation**  
*Brent Martin*, Scripps Research Institute

4:40 – 5:00 p.m.  
20. **Sulfenic Acid Modification of Kv1.5 is a Redox Sensitive Fate Switch for Channel Surface Expression and Degradation**  
*Laurie Svoboda*, University of Michigan

5:00 – 5:40 p.m.  
21. **S-Nitrosylation/Redox Control of Protein Misfolding, Mitochondrial Fragmentation, and Neuronal Synaptic Damage in Neurodegenerative Diseases**  
*Stuart Lipton*, Sanford-Burnham Medical Research Institute

5:40 – 6:00 p.m.  
22. **Selective Chemoprecipitation as an Enabling Method or Discovery-Driven Nitroproteomics Using Liquid Chromatography-Tandem Mass Spectrometry**  
*Laszlo Prokai*, University of North Texas Health Science Center

6:00 p.m. – 7:30 p.m.  
Dinner

7:30 p.m. – 9:00 p.m.  
Poster Session II (Even program numbers manned)

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**Sunday, October 24th**

7:00 a.m. – 8:30 a.m.  
Breakfast

8:30 a.m. – 11:50 a.m.  
**Session V: Bioinformatics + Bioinformatics and Cell Signaling**
*Chair: Robert Chalkley*

8:30 – 9:10 a.m.  
23. **PTM Detection and Site Identification: The Data Analysis Challenge**  
*Robert Chalkley*, University of California, San Francisco
9:10 – 9:30 a.m. **24.** QuickMod: A spectral library search tool for rapid unsupervised identification of modified peptides in MS/MS data  
**Erik Ahrné**, Swiss Institute of Bioinformatics

9:30 – 9:50 a.m. **25.** Estimating False Discovery Rates of Post-Translational Modification Site Assignments  
**Nuno Bandeira**, University of California, San Diego

9:50 – 10:10 a.m. **26.** Misidentification of PTMs as observed in practice and found in the literature  
**Katalin Medzihradszky**, University of California, San Francisco

10:10 a.m. – 10:30 a.m. Coffee Break

10:30 – 11:10 a.m. **27.** Meta-analyses of Phosphorylation Signatures (MAPS): Analysis of Signaling Pathways and Subcellular Compartments  
**Peter Hornbeck**, Cell Signaling Technology

11:10 – 11:50 a.m. **28.** Global Analysis of Signaling Pathways  
**Akhilesh Pandey**, Johns Hopkins University

12:00 p.m. Box Lunch and Departures (Hotel Check Out is 11:00 a.m.)
Poster Session

Odd program numbers manned Friday and Even program numbers manned Saturday

29. Mass spectrometrical analysis of the mitochondrial carrier aralar1 from mouse hippocampus  
Seok Heo, Medical University of Vienna

30. Various Novel Modifications in Redox-Active Cysteine and Their Cellular Functions  
Kong-Joo Lee, Ewha Womans University College of Pharmacy

Eunok Paek, Univ. of Seoul

32. An Integrated Proteomic and Transcriptomic Approach Reveals new insight into Beta methylthiolation of Escherichia coli Ribosomal Protein S12  
Michael Strader, National Institute of Mental Health

33. Mass spectrometric profiling of post translational modifications in NF-kB proteins  
Francesco Lanucara, University of Manchester

34. Post-translational modification of aminoacyl-tRNA synthetase-interacting multifunctional proteins regulates their functional versatilities  
Jung Min Han, Seoul National University

35. Bioinformatics and phosphoproteomic analysis of membrane fractions of Arabidopsis thaliana and Oryza sativa in subjection to salt treatment  
Ing-Feng Chang, National Taiwan University

36. Proteomics Analysis of O-GlcNAc–Modified Proteins in Cerebral Cortex from Normal and 3xTg-AD Alzheimer’s Disease Mouse Model  
Joshua Alfaro, Pacific Northwest National Laboratory

37. The effects of mitogen activated protein kinases (MAPKs) on TZF1-mediated plant stress responses  
Thushani Rodrigo-Peiris, Ohio State University
38. Cellular localization and functional diversity of human lysyl-tRNA synthetase are controlled by site-specific post-translational modification
   **Dae Gyu Kim**, Seoul National University

39. PTM profiling of serum proteins by ERLIC chromatography
   **Zsuzsanna Darula**, Biological Research Centre, Hungarian Academy of Science

40. Click chemistry enrichment of total cell surface glycoproteins
   **Tamara Nyberg**, Life Technologies

41. On the Primary Structure of the Substrates of the O-GlcNAc Transferase
   **Samuel Myers**, University of California, San Francisco

42. Role of MSH2 acetylation in DNA mismatch repair
   **Rangasudhagar Radhakrishnan**, Moffitt Cancer Center

43. Characterization of the tropomyosin-related receptor kinase A (TrkA) downstream phosphoproteome
   **Jordane Biarc**, University of California, San Francisco

44. A Summary of Computational Resources for Protein Phosphorylation
   **Xinjiao Gao**, University of Science & Technology of China

45. Bridging the Glycome to the Glycoproteome
   **Vernon Reinhold**, University of New Hampshire

46. Enrichment and Proteomic Analysis of Protein Fatty Acylation
   **Li Jing**, UCLA

47. The HSF1 transcriptional competence is elevated via stabilizing membrane rafts by the heat shock protein co-inducer BGP-15
   **Tim Crul**, Biological Research Center, Hungarian Academy of Sciences