Poster Presentations

- 1. Glucose transport engineering allows mimicking fed-batch performance in batch mode and selection of superior producer strains Alvaro R. Lara, Universidad Autónoma Metropolitana, Mexico
- ATLASx and ARBRE: New computational tools for biosynthetic pathway prediction 2. Anastasia Sveshnikova, Ecole Polytechnique Fédérale de Lausanne, Switzerland
- 3. Prediction of strategies for integration of computationally designed biosynthetic pathways into industrial host organisms Anastasia Sveshnikova, Ecole Polytechnique Fédérale de Lausanne, Switzerland
- Community science designed ribosomes with beneficial phenotypes 4. Antje Kruger, Northwestern University, USA
- 5. A computational framework to explore the kinetic and thermodynamic landscape of optimal enzyme utilization Asli Sahin, Ecole Polytechnique Fédérale de Lausanne, Switzerland
- A computational workflow to reconstruct interaction networks in microbial 6. communities Asli Sahin, Ecole Polytechnique Fédérale de Lausanne, Switzerland
- 7. High-throughput screening of gas fermenting microorganism by combining 3D printing and an open-source programmable microcontroller Axayacatl Gonzalez, The University of Queensland, Australian Institute for Bioengineering and Nanotechnology, Australia
- Enhancing cell-free production of complex proteins and biomaterials 8. Caleb Lay, Northwestern University, USA
- 9. Co-expression of thermostable pectinases for cost-effective pectin bioconversion Carol Nathali Flores Fernandez, University College London, United Kingdom
- 10. A high-throughput screen of protein-protein interactions responsible for proper bacterial microcompartment formation Carolyn Mills, Northwestern University, USA
- 11. Methylation as an important epigenetic factor in the heterogeneity of CHO cell subclones producing a recombinant MAb César Coria, Universidad Nacional Autónoma de México, Instituto de Biotecnología, Mexico
- 12. Computational engineering of transcription factor biosensor specificity for metabolic pathway optimization Chester Pham, University of Toronto, Canada
- 13. Developing cell-free workflows for lasso peptide biodiscovery Derek Wong, Northwestern University, USA
- 14. Development of a high-throughput assay to discover PET-biodegrading microbes and microbial consortia

Erica Gardner, University of Michigan, USA

- 15. **in silico Analysis and comparison of the metabolic capabilities of different organisms by reducing metabolic complexity** Evangelia Vayena, Ecole Polytechnique Fédérale de Lausanne, Switzerland
- 16. **Optimisation of a CRISPR-Cas9 deletion screen for the identification of essential genomic targets in CHO cells** Federico De Marco, Austrian Centre of Industrial Biotechnology, Austria
- 17. Single-cell RNA sequencing: Characterization of high-producer and non-producer CHO cells Giulia Borsi, BOKU, Austria
- 18. Building a synthetic formate assimilation pathway for carbon-negative cell-free biomanufacturing Grant Landwehr, Northwestern University, USA
- 19. Engineering cell-free biosensors for water quality diagnostics Holly Ekas, Northwestern University, USA
- Adaptive laboratory evolution of Clostridium autoethanogenum to enhance CO2 valorization James Kemp Heffernan, The University of Queensland, Australian Institute for Bioengineering and Nanotechnology, Australia
- 21. Engineering glycosyltransferases to manufacture non-toxic antifungals Jonathan Bogart, Northwestern University, USA
- 22. Syntrophic cocultures of Clostridium organisms to produce isopropanol and C6-C8 alcohols and carboxylic acids Jonathan Otten, University of Delaware, USA
- 23. Towards the rational engineering and directed evolution of chloroalkane dehalogenases to manipulate substrate preferences Katherine Picott, University of Toronto, Canada
- 24. A low-cost, thermostable, cell-free protein synthesis platform for on-demand production of glycoconjugate vaccines Katherine Warfel, Northwestern University, USA
- Simplified methods for orthogonal tRNA expression in cell-free systems for protein engineering Kosuke Seki, Northwestern University, USA
- 26. **Emerging microbial patterns under fluid flow conditions** Liliana Angeles Martinez, Ecole Polytechnique Fédérale de Lausanne, Switzerland
- 27. Development of a cell-free platform for point of care synthesis of peptide hormones Madison DeWinter, Northwestern University, USA
- SLAM-Seq reveals early transcriptomic adaptation mechanisms upon glutamine deprivation in Chinese Hamster Ovary cells Maja Papež, ACIB GmbH, Austria
- Systems biology approaches to investigate the metabolic mechanisms underlying cancer
 Maria Masid, Ecole Polytechnique Fédérale de Lausanne, Switzerland

- 30. **Understanding fungal cell wall stress response using a multiomics approach** Mark Marten, University of Maryland, Baltimore County, USA
- 31. Engineering E. coli for the utilization of CO2-derived ethylene glycol for bioproduction Michelle Feigis, University of Toronto, Canada
- 32. Exploiting narrow-spectrum bacteriocins as probes to study and engineer microbial communities Nikhil Nair, Tufts University, USA
- 33. Integration of metabolism and regulation identifies constraints and pitfalls to engineering synthetic heterotrophy Nikhil Nair, Tufts University, USA
- 34. Data-informed catastrophic and harmonious protein coding choices for multigene expression Nikhil U. Nair, Tufts University, USA
- Capturing the plasmid metabolic burden using metabolic and expression models (MEmodels)
 Omid Oftadeh, Ecole Polytechnique Fédérale de Lausanne, Switzerland
- Systems metabolic engineering and bioprocess engineering strategies for 3hydroxypropionic acid production in Pichia pastoris Pau Ferrer, Universitat Autonoma de Barcelona, Spain
- 37. Accurate prediction of mRNA degradation at nucleotide resolution with deep learning Qing Sun, Texas A&M, USA
- Engineering a novel Pichia pastoris cell-free protein synthesis platform for vaccine production Rochelle Aw, Northwestern University, USA
- 39. Identification, isolation and characterization of compounds present in aqueous extracts of scaptotrigona aff. postica propolis, with antiviral action against avian coronavirus, zicavirus, mayaro virus and chikungunya virus Ronaldo Mendonça, Instituto Butantan, Brazil
- 40. Using CRISPR-Cas9 hosts to engineer BGCs for novel antibiotc production and discovery Rosemary Gillane, AIBN, University of Queensland, Australia
- 41. **PgIB mutagenesis towards the development of shigella glycoconjugate vaccines** Sarah Sobol, Northwestern University, USA
- 42. Regenerative effect of combined laser and human stem cell-conditioned medium therapy on hypertrophic burn scar Seung Yeol Lee, Soonchunhyang University Bucheon Hospital, South Korea
- 43. Effect of hypertrophic scar fibroblast-derived exosomes on keratinocytes of normal human skin So Young Joo, Hangang Sacred Heart Hospital, South Korea
- 44. Model-guided development of self-remodeling protein complexes from fungal cellulosome parts Stephen Lillington, University of California, Santa Barbara, USA

- 45. **Dicovering transcription factor promoters for portable, on-demand diagnostics** Steven Fleming, Northwestern University, USA
- 46. **REKINDLE a method for REconstructing KINetic models using Deep LEarning** Subham Choudhury, Ecole Polytechnique Fédérale de Lausanne, Switzerland
- 47. Genetically stable CRISPR-based kill switches for engineered microbes Tae Seok Moon, Washington University in St. Louis, USA
- 48. **Engineering ligand-specific biosensors for aromatic amino acids and neurochemicals** Tae Seok Moon, Washington University in St. Louis, USA
- 49. **Transient and integrating systems for heterologous expression in anaerobic gut fungi** Tejas Navaratna, University of California, Santa Barbara, USA
- 50. Computational biochemistry with NICE-tools: Advances and applications for synthetic biology and metabolic engineering Vassily Hatzimanikatis, Ecole Polytechnique Fédérale de Lausanne, Switzerland
- 51. NICEdrug.ch, a workflow for rational drug design and systems-level analysis of drug metabolism Vassily Hatzimanikatis, Ecole Polytechnique Fédérale de Lausanne, Switzerland
- 52. Using machine learning approaches to estimate novel substrate activity and kinetic parameters of enzymes Veda Sheersh Boorla, The Pennsylvania State University, USA
- Sequential activation of multiple gene copies facilitates adaptation of CHO cells to increased productivity Victor Jimenez Lancho, BOKU, Austria
- 54. Using machine learning approaches to estimate novel substrate activity and kinetic parameters of enzymes Vikas Upadhyay, The Pennsylvania State University, USA
- 55. The effect of upstream conditions on the performance of primary recovery operations in antibody producing mammalian cell cultures Viktoria Gkoutzioupa, University College London, United Kingdom
- 56. Using high fidelity metabolic models for Clostridium thermocellum to resolve knowledge gaps in phosphate metabolism and role in a co-culture Wheaton Schroeder, the Pennsylvania State University, USA