1. Annotation and curation of the biochemical engineering literature
   Daniel McShan, University of Colorado School of Medicine
2. Characterization of the cell growth and the distribution of end-products in a batch cultivation of Mannheimia succiniciproducens
   Hyohak Song, KAIST
3. Clustering analyses of complete genomes based on the KEGG orthology for the elucidation of evolutionary relationships among the organisms
   Jin Sik Kim, KAIST
4. Combining experimental data and in silico analysis to model the metabolic network of Lactobacillus plantarum
   Jeroen Hugenholtz, Kluyver Centre for Genomics of Industrial Fermentations
5. Comparative proteomic analysis of GS-NS0 murine myeloma cell lines producing a recombinant monoclonal antibody at varying specific production rate
   David C. James, The University of Queensland
6. Computational flux balance analysis of photoautotrophic metabolism
   John A. Morgan, Purdue University
7. Construction of valine-producing strain and its transcriptome analysis
   Jin Hwan Park, KAIST
8. Genome-wide analysis of the transcriptional response of murine hybridomas to osmotic shock
   Duan Shen, Rensselaer Polytechnic Institute
   Jong Hwan Baek, KAIST
10. Hyaluronic acid production by recombinant Bacillus subtilis strains
    Stephen Brown, Novozymes, Inc.
11. Influence of culture environment on the production of mouse embryonic stem cells
    Muhammad Arshad S. Chaudhry, University of British Columbia
12. Metabolic engineering of Escherichia coli for the improved production of L-threonine based on metabolic flux analysis
    Kwangho Lee, KAIST
13. Proteomic and genomic studies of mammalian cell physiology to optimize production of therapeutic and diagnostic proteins
    Susan Sharfstein, Rensselaer Polytechnic Institute
14. An integrative and probabilistic approach for discovering regulatory modules in molecular interaction networks
    Ana Paula S. Oliveira, Center for Microbial Biotechnology, BioCentrum-DTU
15. Analysis of thermodynamic feasibility in a genome scale metabolic model
   Matthew Jankowski, Northwestern University
16. Bayesian model discrimination analysis for identification of most probable
   biological network
   Ranjan Srivastava, University of Connecticut
17. Dynamic flux balance analysis of cell-free protein synthesis
   Jeffrey D. Varner, Genencor International Inc.
18. Identifying reaction activation/inhibition strategies for strain engineering
   Priti Pharkya, Pennsylvania State University
19. Integration of transcriptomic, proteomic, and metabolic flux information
   for Metabolic Control Analysis in E. coli
   Vassily Hatzimanikatis, Northwestern University
20. Metabolic control analysis on the industrial cultivations of Saccharomyces
   cerevisiae– the interplay between metabolism and growth environment
   Liqing Wang, Northwestern University
21. Metabolic engineering of two pathways, the indole and terpenoid
   pathways, in Catharanthus roseus hairy roots
   Christie A. M. Peebles, Rice University
22. Metabolic network construction for cell growth and glutathione formation
   in batch culture of Saccharomyces cerevisiae
   Shaohong Wen, College of Life Science and Technology
23. Model-driven designs of an oscillating gene network
   Howard Salis, University of Minnesota
24. Optimization of pentose fermentation in Zymomonas mobilis through
   kinetic modeling and experimental analysis
   Dhinakar S. Kompala, University of Colorado
25. Parameter optimization method for a whole cell model
   Mariajosé Castellanos, University of Maryland Baltimore County
26. Quantifying protein expression using amine specific isobaric tags
   Kelvin H. Lee, Cornell University
27. The impact of diffusion on the design and use of DNA microarrays
   Jacob Borden, Northwestern University
28. The large-scale transcriptional program in human megakaryocytic
   differentiation
   Peter G. Fuhrken, Northwestern University
29. Transcriptional responses of recombinant Escherichia coli to spatial DOT
   gradients simulated in a two-compartment scale-down system
   Alvaro R. Lara, Universidad Nacional Autónoma de México
30. Uncovering transcriptional regulation of metabolism by using metabolic
   network topology
   Kiran Raosaheb Patil, Technical University of Denmark
31. Application of metabolic flux analysis to identify the pathways of free fatty
   acid toxicity to liver cells
   Shireesh Srivastava, Michigan State University
32. Enhanced production of bioactive compounds in plant cell cultures by signal transduction
   Jian-Jiang Zhong, East China University of Science and Technology
33. Generation of alloreactive T cell in-vitro for subsequent depletions before transplantations
   Mei Shao, The Ohio State University
34. Inactivation of p44/42 MAPK reduces HEK 293 cell aggregation
   Wai Lam W. Ling, Schering-Plough Research Institute
35. Network analysis and redesign of signal transduction networks
   Costas D Maranas, Pennsylvania State University
36. Signal transduction systems for adult neural stem cell proliferation
   David Schaffer, University of California at Berkeley
37. Trafficking, signaling, and cell responses of a mutant form of the epidermal growth factor receptor, EGFRvIII
   Catherine M Cresson, Massachusetts Institute of Technology
38. Detection of circulating tumor cells in human peripheral blood using RT-PCR technology
   Xiaodong Tong, The Ohio State University
39. Effect of anticancer drugs on human lymphoma cell growth with different expression of Hsp70
   Tatiana Korolenko, Institute of Physiology RAMS
40. Endogenous inhibitors of cysteine proteases as prognostic markers of tumor development
   Tatiana Korolenko, Institute of Physiology RAMS
41. Ganoderic acid from bioreactor-cultivated mycelia of medicinal mushroom Ganoderma lucidum and study on its anti-tumor mechanism
   Jian-Jiang Zhong, East China University of Science and Technology
42. Targeting the unique metabolic environments of tumors
   Neil Forbes, University of Massachusetts
43. Biodegradable hollow fibre scaffolds for minimising mass transfer limitations in tissue engineering
   Julian B Chaudhuri, University of Bath
44. Embryonic stem cell-derived endothelial cells as a cell source in the development of pre-vascularized materials
   Kara E McCloskey, Georgia Institute of Technology
45. A systems biology approach for metabolic engineering of E. coli sugar-utilization regulatory systems
   Ramon Gonzalez, Iowa State University
46. Analysis and modeling of the unfolded protein response during heterologous protein expression
   Anne Skaja Robinson, University of Delaware
47. Effect of the methanol utilization (Mut) phenotype on recombinant protein production and cultivation strategies in Pichia pastoris fed-batch cultures
   Pau Ferrer, Universitat Autònoma de Barcelona
48. Engineering Escherichia coli to improve culture performance and overcome by-product formation during recombinant protein production under oscillating DOT conditions
Alvaro R. Lara, Universidad Nacional Autónoma de México

49. Expression of functional mussel adhesive protein in Escherichia coli
Hyung Joon Cha, Pohang University of Science and Technology

50. Expression of the gene coding for the rabies virus glycoprotein (GPV) in Drosophila melanogaster (S2) cells
Carlos Augusto Pereira, Instituto Butantan, Laboratorio de Imunologia Viral

51. Influence of down-regulated cold-inducible RNA-binding protein on hypothermic growth of Chinese Hamster Ovary cells producing erythropoietin
Gyun Min Lee, KAIST

52. Large scale fermentation and purification of human leptin expressed in periplasmic space of Escherichia coli
Chao-Min Liu, Roche Discovery Technologies Dept., Hoffmann-La Roche Inc.

53. Unbiased exploration of the protein folding landscape in bacteria
Adam C. Fisher, Cornell University

54. Cholesterol supplementation during production increases the infectivity of retroviral and lentiviral vectors pseudotyped with VSV-G
William M. Miller, Northwestern University

55. Engineering Chinese Hamster Ovary cells to improve sialylation
Frederyk Ngantung, Massachusetts Institute of Technology

56. Improved strategies for the simultaneous production of various proteins by insect cells: a flow cytometry study
Laura A. Palomares, Universidad Nacional Autónoma de México

57. Molecular characterisation of the Unfolded Protein Response in NS0 myeloma cells
Alan J Dickson, University of Manchester

58. Optimizing heavy and light chain gene dose for efficient antibody production by CHO cells
David C. James, The University of Queensland

59. Optimizing the sialic acid metabolic pathway for producing humanized glycoproteins in insect cells
Someet Narang, Johns Hopkins University

60. Protein engineering to understand specificity versus cross-reactivity in cellular immune recognition
Jennifer A. Maynard, University of Minnesota
Poster Session #2

61. A prototype process for rotavirus-like particles purification from insect cell-baculovirus expression system
   Marco Rito-Palomares, Biotechnology Center, Tec de Monterrey

62. Accelerating biocatalyst stability through rigorous predictions of stability
   Andreas S. Bommarius, Georgia Institute of Technology

63. Analysis of temperature in monoclonal antibody producing CHO cell lines: strategies for shifting temperature to improve cell viability and protein production
   Kirin Malik Jamison, Genentech, Inc.

64. Efficient isolation of high producing cells using fluorescence activated cell sorting
   Nicholas R. Abu-Absi, Chiron

65. Fermentation development of a recombinant botulinum vaccine candidate, Serotype C expressed in Pichia pastoris
   Jayanta Sinha, University of Nebraska-Lincoln

66. From laboratory to manufacturing facility: development and scale-up of a multi-valent vaccine fermentation process
   Tsu-shun Lee, Wyeth Research

67. Lessons learned from technology transfer to contract manufacturer
   Keri Mills, Genentech, Inc.

68. Manufacturing perspective on large scale centrifugation of mammalian cell cultures
   Ken Green, Lonza Biologics

69. Modeling and control of fed-batch processes for proteolytically sensitive recombinant proteins: a case-study with recombinant streptokinase
   M. Velu, Indian Institute of Technology Madras

70. Optimization of fed batch parameters and harvest time of CHO cell cultures for a glycosylated product with multiple mechanisms of inactivation
   M. Nazmul Karim, Texas Tech University

71. Optimization of human serum albumin production in methylotrophic yeast Pichia pastoris by repeated fed-batch fermentation
   Tomoshi Ohya, Mitsubishi Pharma Corporation

72. Timesaving approach for multi-valent vaccine fermentation process development
   Brian Bahler, Wyeth Research

73. Application of a novel oscillatory flow screening micro-reactor to a biotransformation in a two-phase medium
   Nuno Reis, University of Minho, Dept. Biological Engineering

74. Comparative effects of reaction kinetics and mass transfer limitation in micro enzyme fuel cell bioreactors
   Michael Cooney, Hawaii Natural Energy Institute
75. High throughput cell culture experimentation with BioProcessors SimCell platform
   Ache Stokelman, Amgen, Inc.

76. Microscale process evaluation of recombinant biocatalysts libraries: application to baeyer-villiger monooxygenase catalysed lactone synthesis
   Claudia Ferreira-Torres, University College London

77. Parallel bioreactors on a mL-scale for high-throughput bioprocess design
   Dirk Weuster-Botz, Technical University of Munich

78. The characterisation and application of a novel miniature stirred bioreactor for the scale down of industrially relevant microbial fermentations
   Jonathan I. Betts, University College London

79. Biofabrication techniques for probing cellular physiology
   Colin Herbert, University of Maryland

80. Design and delivery of oligonucleotides for antisense and rna interference in mammalian cells
   Charles M. Roth, Rutgers University

81. Directed metallization of single enzyme molecules with preserved enzymatic activity
   Amihay Freeman, Tel Aviv University

82. Engineering the biology at a device interface: towards micromolecular biomanufacturing
   Angela Lewandowski, University of Maryland

83. Fractionation of immunomagnetically labeled human cord blood hematopoietic progenitor cells using a novel dipole magnetic flow cell sorter
   Jeffrey J Chalmers, The Ohio State University

84. Microtissue culture for high throughput screening applications
   Lars Keld Nielsen, The University of Queensland

85. Novel nanofiber structure by electrospinning and its use in microvascular tissue engineering
   Dong Han, State University of New York

86. pH and expansin action on single suspension-cultured tomato cells
   CR Thomas, University of Birmingham

87. The effect of magnetic nanoparticles on the binding affinities of Ab's
   Jeffrey Chalmers, The Ohio State University

88. Bioengineering of microbial enzymes and regulator proteins to enhance carbon sequestration
   F. Robert Tabita, The Ohio State University

89. Computational approaches for optimally allocating diversity in directed evolution studies
   Costas D. Maranas, Pennsylvania State University

90. Directed evolution of human estrogen receptor
   Huimin Zhao, University of Illinois
91. Directed evolution of novel adeno-associated virus gene therapy vehicles
   David Schaffer, University of California at Berkeley
92. Engineered in vivo biosensors for nuclear hormone receptor ligands
   David W. Wood, Princeton University
93. Engineering of a Tat-dependent filamentous phage display platform
   Danielle Tullman-Ercek, University of Texas at Austin
94. Engineering of highly soluble Fab fragments in the periplasm of
   Escherichia coli by anchored periplasmic expression (APEX)
   Min Jeong Seo, University of Texas at Austin
95. Fragmentation and reassembly of aminoglycoside phosphotransferase
   (3')-IIa transforms the relationship between sequence and function
   Marc Ostermeier, Johns Hopkins University
96. High-throughput protease screening using optimized fluorescent protein
   fret
   Annalee W. Nguyen, University of California Santa Barbara
97. Optimising industrial bioprocesses: developing and screening specificity-
   enhanced proteases by directed evolution of bovine trypsin
   Janahan Paramesvaran, University College London
98. Photochemical selection of positive metagonomic library
   Joon Kim, KAIST
99. Protease substrate specificity profiling using bacterial substrate display
   Patrick Daugherty, University of California Santa Barbara
100. Random strand transfer recombination (RSTM): a similarity-independent
    method for molecular recombination of nucleotide sequences
    Birgit Reiter, Applied Biocatalysis Research Centre
101. Rational strategies for randomized directed evolution using L-Shuffling
    Jean-Marie SONET, Protéus
102. Towards a combinatorial approach for the analysis of membrane protein
    expression at the blood-brain barrier
    Eric V. Shusta, University of Wisconsin
103. A high throughput method for screening enzyme libraries
    Mag. Pohn Brigitte, Applied Biocatalysis Research Centre
104. Biocatalytic synthesis of amino-alcohols using an engineered transketolase
    and b-alanine:pyruvate transaminase pathway in Escherichia coli
    C.U.Ingram, University College London
105. Expression, screening and mutagenesis of nitrile hydratases
    Christoph Reisinger, Applied Biocatalysis Research Centre
106. Metabolic engineering of the phenylpropanoid pathway for the synthesis
    of flavonoids
    John A. Morgan, Purdue University
107. Nanobiocatalysts: enabling multienzyme biotransformations involving
    cofactor regeneration
    Ping Wang, The University of Akron
108. Production of thermostable protease from Bacillus licheniformis LBBL-II isolated from traditonally fermented locust beans (Parkia biglobosa) in south western nigeria  
Folasade M. Olajuyigbe, Federal University of Technology, Akure, Nigeria

109. Development of efficient Escherichia coli succinate production systems  
Ka-Yiu San, Rice University

110. Engineering E. coli to maximize the flux of reducing equivalents available for cofactor-dependent transformations  
Patrick C. Cirino, Pennsylvania State University

111. Statistically designed optimization for monoclonal antibody production in CHO fed-batch culture  
Eric J. Hayduk, CuraGen Corporation

112. Use of transcriptome analysis to identify factors that define clonal productivity in recombinant mammalian cell lines  
Louise M Barnes, University of Manchester

113. Ionic liquids as solvents for whole cell biocatalysis with in situ product removal  
Dirk Weuster-Botz, Technical University of Munich

114. Isolation of angiotensin-I converting enzyme inhibitory peptide by using antipeptide antibody column  
Md. Fida Hasan, Kobe University

115. New bioseparations techniques using self-cleaving affinity tags  
David W. Wood, Princeton University

116. Production of the natural aroma compounds 2-phenylethanol and 2-phenylethylacetate from L-phenylalanine by coupling whole-cell biocatalysis with organophilic pervaporation  
Jens Schrader, DEHEMA e.V., Karl-Winnacker-Institut, Biochemical Engineering Group

117. Protein recovery from high biomass recombinant systems  
Ian Sellick, Pall Life Sciences

118. Cell culture scale-down model development through impeller agitation rate optimization  
Yasunori Hashimura, Amgen, Inc.

119. Relationship between protein stability and biological activity of beta amyloid, a disease causing protein  
Theresa Good, UMBC

120. Biochemical engineering laboratory: undergraduate laboratory course for chemical engineering students  
Claire Komives, San Jose State University