

PROGRAM

WEDNESDAY, August 27—2:30 PM

SESSION 1 TRANSCRIPTIONAL AND POST-TRANSCRIPTIONAL GENE REGULATORY NETWORKS

Chairperson: **R. Albert**, Pennsylvania State University, University Park

Walhout, A.J.M., Program in Gene Function and Expression and
Program in Molecular Medicine, University of Massachusetts
Medical School, Worcester: A genome-scale, integrated
transcriptional and post-transcriptional microRNA network. 1

Furlong, E., European Molecular Biology Laboratory, Heidelberg,
Germany: Gene regulatory networks during development—
Dissecting the logic. 2

Bozek, K.,¹ Dame, C.,² Kramer, A.,³ Religio, A.,⁴ Herzog, H.,⁴ ¹Dept. of
Computational Biology and Applied Bioinformatics, Max Planck
Institute for Informatics, Saarbrücken, ²Dept. of Neonatology,
³Laboratory of Chronobiology, Charité Universitätsmedizin Berlin,
⁴Institute for Theoretical Biology, Humboldt University, Berlin,
Germany: Regulation of clock controlled genes in mammals. 3

Luo, O.,¹ Cotsapas, C.,² Williams, R.,¹ ¹John Curtin School of Medical
Research, Australian National University, Canberra; ²Center for
Human Genetic Research, Massachusetts General Hospital,
Boston: Uncovering the regulatory architecture of coordinated
control of gene expression. 4

Baliga, N.S., Institute for Systems Biology, Seattle, Washington: A
predictive model of adaptive responses to environmental changes. 5

Lee, E.,¹ Bussemaker, H.J.,^{1,2} ¹Dept. of Biological Sciences, ²Center
for Computational Biology and Bioinformatics, Columbia University,
New York, New York: Association analysis of inferred transcription
factor activity reveals regulatory networks. 6

Wilson, M., Barbosa-Morais, N., Schmidt, D., Conboy, C., Vanes, L., Tybulewicz, V., Fisher, E., Tavaré, S., Odom, D., Cancer Research UK Cambridge Research Institute: Tissue-specific transcription is directed by genome sequence in an aneuploid mouse strain carrying human chromosome 21.

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WEDNESDAY, August 27—5:40 PM

KEYNOTE SPEAKER

Pawson, T., Samuel Lunenfeld Research Institute, Toronto, Canada: The evolution and function of domain-based protein interaction networks.

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WEDNESDAY, August 27—6:30 PM

Wine and Cheese Reception

THURSDAY, August 28—9:00 AM

SESSION 2 SIGNALING AND MACHINERY NETWORKS

Chairperson: **E. Furlong**, European Molecular Biology Laboratory, Heidelberg, Germany

Vidal, M., Center for Cancer Systems Biology (CCSB) and Dept. of Cancer Biology, Dana-Farber Cancer Institute, Dept. of Genetics, Harvard Medical School, Boston, Massachusetts.

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Thakar, J., Saadatpour-Moghaddam, A., Harvill, E.T., Zhang, R., Loughran, T., Albert, R., Pennsylvania State University, University Park: Modeling the dynamics of heterogeneous networks—Immune regulation and LGL leukemia.

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Akiva, E., Itzhaki, Z., Margalit, H., Dept. of Molecular Genetics and Biotechnology, Faculty of Medicine, Hebrew University of Jerusalem, Israel: Intra-domain loops define an additional level of modularity in protein interaction networks.

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- Boxem, M.,^{1,2} Maliga, Z.,³ Klitgord, N.,¹ Li, N.,¹ Lemmens, I.,⁴ Mana, M.,⁵ de Lichtervelde, L.,¹ Mul, J.,¹ van de Peut, D.,¹ Devos, M.,¹ Simonis, N.,¹ Yildirim, M.A.,¹ Cokol, M.,⁵ Kao, H.-L.,⁶ de Smet, A.-S.,⁴ Wang, H.,⁷ Schlaitz, A.-L.,³ Hao, T.,¹ Center for Cancer Systems Biology (CCSB) and Dept. of Cancer Biology, Dana-Farber Cancer Institute and Dept. of Genetics, Harvard Medical School, ²Massachusetts General Hospital, ⁵Harvard Medical School, Boston, Massachusetts; ³Max Planck Institute, Dresden, Germany; ⁴VIB, Ghent, Belgium; ⁶New York University, ⁹Rockefeller University, New York; ⁷Stanford University, California; ⁸Utrecht University, The Netherlands; ¹⁰Indiana University, Indianapolis: A protein domain-based interactome network for *C. elegans* early embryogenesis. 12
- Gavin, A.-C., European Molecular Biology Laboratory, Heidelberg, Germany: The social network of a cell—Dynamic protein interactions. 13
- Cahill, D.J., School of Medicine and Medical Sciences, Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Ireland: Understanding disease processes by profiling the natural and diseased antibody repertoire. 14
- Carmi, S.,^{1,2} Levanon, E.Y.,³ Eisenberg, E.,⁴ ¹Minerva Center and Dept. of Physics, Bar-Ilan University, Ramat Gan, ⁴Raymond and Beverly Sackler School of Physics and Astronomy, Tel Aviv University, Israel; ²Center for Polymer Studies, Boston University, ³Dept. of Genetics, Harvard Medical School, Boston, Massachusetts: Efficiency of complex production in changing environment. 15
- Lievens, S.,^{1,2} Van der Heyden, J.,^{1,2} Vanderroost, N.,^{1,2} Vidal, M.,³ Tavernier, J.,^{1,2} ¹Dept. of Medical Protein Research, VIB, ²Dept. of Biochemistry, Ghent University, Belgium; ³Center for Cancer Systems Biology (CCSB) and Dept. of Cancer Biology, Dana-Farber Cancer Institute, Dept. of Genetics, Harvard Medical School, Boston, Massachusetts: Array MAPPIT—High-throughput interactome analysis in mammalian cells. 16

SESSION 3 METABOLIC NETWORKS

Chairperson: **E. Schadt**, Rosetta Inpharmatics, Merck & Co.,
Seattle, Washington

Palsson, B., University of California, San Diego.

Katari, M.S.,¹ Nowicki, S.D.,¹ Nero, D.,¹ Kelfer, J.,¹ Thompson, L.P.,¹
Chiaromonte, F.,^{1,3} Shasha, D.E.,³ Coruzzi, G.M.,¹ Gutiérrez,
R.A.,^{1,2} ¹Center for Genomics and Systems Biology, Dept. of
Biology, ³Courant Institute of Mathematical Sciences, New York
University, New York; ²Departamento de Genética Molecular y
Microbiología, Pontificia Universidad Católica de Chile, Santiago: A
systems approach to nitrogen regulatory networks and the
"VirtualPlant". 17

Mithani, A.,¹ Preston, G.,² Hein, J.,¹ Depts. of ¹Statistics, ²Plant
Sciences, University of Oxford, United Kingdom: Calculating the
likelihood of two homologous metabolic networks with neighbor
dependence using a Gibbs sampler. 18

Hillenmeyer, M.E.,^{1,2} Hoon, S.,¹ Erikson, E.,³ Arnoldo, A.,^{4,5} Moffatt,
J.,^{4,5} Nislow, C.,^{4,5,6} Giaever, G.,^{3,4,5} ¹Stanford Genome Technology
Center, ²Program in Biomedical Informatics, Stanford University,
Palo Alto, California; ³Dept. of Pharmaceutical Sciences, ⁴Donnelly
Centre for Cellular and Biomolecular Research, ⁵Dept. of Molecular
Genetics, ⁶Banting and Best Department of Medical Research,
University of Toronto, Canada: The chemical portrait of yeast—
Uncovering a phenotype for all genes. 19

Shlomi, T.,¹ Cabili, M.N.,¹ Herrgård, M.J.,² Palsson, B.Ø.,² Ruppin, E.,¹
¹Tel Aviv University, Israel; ²University of California, San Diego:
Network-based prediction of human tissue-specific metabolism. 20

SESSION 4a NETWORK PROPERTIES AND PERTURBATION

- Zhong, Q.,¹ Li, Q.-R.,¹ Simonis, N.,¹ Klitgord, N.,¹ Tam, S.,¹ Mou, D.,¹ Venkatesan, K.,¹ Milstein, S.,¹ Benoit, C.,² Lin, C.,¹ Szeto, D.,¹ Dricot, A.,¹ Yan, H.,¹ Hill, D.H.,¹ Cusick, M.E.,¹ Vidal, M.,¹ Center for Cancer Systems Biology (CCSB) and Dept. of Cancer Biology, Dana-Farber Cancer Institute, Dept. of Genetics, Harvard Medical School, Boston, Massachusetts; ²Faculté Universitaire des Sciences Agronomiques de Gembloux, Centre de Biophysique Moéculaire Numérique, Gembloux, Belgium: Edge-specific network perturbation in disease. 21
- Ewing, R.M., Song, J., Yang, T., Center for Proteomics, School of Medicine, Case Western Reserve University, Cleveland, Ohio: Spokes and matrices—Revealing network topology by mining human AP-MS data. 22
- Dotan-Cohen, D., Melkman, A.A., Dept. of Computer Science, Ben Gurion University, Beer Sheva, Israel: Fuzzy-N-rich—Testing statistical enrichment of semantically similar GO-annotations. 23

THURSDAY, August 28—5:30 PM

POSTER SESSION I

- Ahnert, S.E.,¹ Fink, T.M.A.,² Zinovyev, A.,³ ¹Theory of Condensed Matter, Cavendish Laboratory, University of Cambridge, United Kingdom; ²CNRS UMR 144, ³Bioinformatics, Institut Curie, Paris, France: Network growth model predicts minimum amount of non-coding DNA in eukaryotes. 24
- Bocu, R., Tabirca, S., Chen, Y.J., University College Cork, Ireland: Interactome networks and cancer growth. 25
- Chen, P.-Y., Hamer, R., Armitage, J., Reinert, G., Deane, C., Dept. of Statistics and Oxford Centre for Integrative Systems Biology, Oxford University, United Kingdom: Examining the chemotaxis pathways across species. 26

- Derow, C., Anand, P., Aranda, B., Kerrien, S., Khadake, J., Montecchi-Palazzi, L., Orchard, S., Quinn, A., Thorneycroft, D., Hermjakob, H., European Molecular Biology Laboratory (EMBL)—European Bioinformatics Institute, Hinxton, United Kingdom: Intact molecular interaction database and the analysis of protein-protein interaction networks of candidate cancer proteins. 27
- Dotan-Cohen, D.,¹ Kasif, S.,²⁻⁵ Melkman, A.A.,¹ ¹Dept. of Computer Science, Ben Gurion University, Beer Sheva, Israel; ²Dept. of Biomedical Engineering, ³Center for Advanced Genomic Technology, ⁴Bioinformatics Program, Boston University, ⁵Harvard/MIT Program in Health Sciences and Technology, Children's Hospital, Boston, Massachusetts: Integrating semantic-similarity into hierarchical clustering of expression data. 28
- Edwards, R.J.,¹ Davey, N.E.,² Shields, D.C.,² ¹School of Biological Sciences, University of Southampton, United Kingdom; ²UCD Complex and Adaptive Systems Laboratory, UCD Conway Institute of Biomolecular and Biomedical Sciences, University College Dublin, Ireland: Large scale prediction of protein-protein interaction motifs in the human interactome. 29
- Ericsson, O., Nong, R.Y., Pardali, K., Landegren, U., Dept. of Genetics and Pathology, Uppsala University, Sweden: Microarray profiling of endogenous protein interaction networks via proximity ligation. 30
- Iacucci, E., K.U. Leuven, Belgium: Cis Regulatory Module in networks—Detection by way of orthologous co-expression. 31
- Krysiak-Baltyn, K., Edsgard, D., Gupta, R., Jensen, T.S., Brunak, S., Center for Biological Sequence Analysis, Technical University of Denmark, Lyngby: Linking phenotypes with genes—A case study with cryptorchidism. 32
- Kühner, S., Beltran, P., Rode, M., Racké, I., Gavin, A.-C., Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany: Characterizing a minimal molecular machinery. 33

- Lo, F.-Y.,¹ Facciotti, M.T.,^{1,2} Pan, M.,¹ Kaur, A.,¹ Vuthoori, M.,¹ Reiss, D.J.,¹ Baliga, N.S.,^{1,3,4} ¹Institute for Systems Biology, ³Depts. of Microbiology, and Molecular and Cellular Biology, ⁴Molecular and Cellular Biology Program, University of Washington, Seattle; ²Genome and Biomedical Sciences Facility, University of California, Davis: Hybrid bacterial/eukaryotic mechanisms in global transcriptional regulation of archaeal physiology. 34
- Miyamoto-Sato, E., Ishizaka, M., Fujimori, S., Hirai, N., Masuoka, K., Yanagawa, H., Graduate School of Science and Technology, Keio University, Yokohama, Japan: Toward refining protein interactome for human transcription factor complexes using in vitro virus (IVV). 35
- Nitsch, D., Moreau, Y., SCD-ESAT, Katholieke Universiteit Leuven, Belgium: Ab initio gene prioritization. 36
- Pardali, K.,¹ Zieba, A.,¹ Spångberg, L.,¹ Nyström, E.,² Wälby, C.,^{1,3} Moustakas, S.,⁴ Heldin, C.-H.,⁴ Landegren, U.,^{1,1} ¹Dept. of Genetics and Pathology, ³Center of Image Analysis, Uppsala University, ⁴Ludwig Institute for Cancer Research, ²Olink Bioscience, Uppsala, Sweden: Monitoring the dynamics of Smad complex formation using proximity ligation. 37
- Richter, K., Klopffleisch, K., Uhrig, J.F., Botanical Institute III, University of Cologne, Germany: SNC, an algorithm for rapid and stringent clustering of large protein interaction networks. 38
- Salehi-Ashtiani, K., Center for Cancer Systems Biology (CCSB) ORFeome Group, Center for Cancer Systems Biology (CCSB), Dept. of Cancer Biology, Dana-Farber Cancer Institute, Boston, Massachusetts: An update on the CCSB orfeome and isoform discovery projects. 39
- Setty, Y.,^{1,2} Cohen, I.R.,² Dor, Y.,³ Kugler, H.,¹ Harel, D.,^{2,1} Microsoft Research, Cambridge, United Kingdom; ²Weizmann Institute of Science, Rehovot, ³Hebrew University of Jerusalem, Israel: A four dimensional model of pancreatic organogenesis. 40
- Souiai, O., Becker, E., Brun, C., Institut de Biologie du Développement de Marseille-Luminy, CNRS-Université de la Méditerranée, Marseille, France: Tissue-specificity and protein-protein interaction networks. 41

Stein, A.,¹ Aloy, P.,^{1,2} ¹Institute for Research in Biomedicine (IRB) and Barcelona Supercomputing Center (BSC), ²Institució Catalana de Recerca i Estudis Avançats (ICREA), Spain: Contextual specificity in peptide-mediated protein interactions—Gaining new insights from structure. 42

FRIDAY, August 29—9:00 AM

SESSION 4b FROM NETWORK TO PROTEIN PROPERTIES

Chairperson: **A.-L. Barabasi**, Northeastern University, Boston, Massachusetts

Gorna, M., Nurmohamed, S., Chandran, V., Titman, C., Griffin, J., Callaghan, A.J., Luisi, B.F., Dept. of Biochemistry, University of Cambridge, United Kingdom: The structure and function of the *E. coli* RNA degradosome, and its potential contribution to hierarchical network control. 43

Kortemme, T., University of California, San Francisco and California Institute for Quantitative Biosciences (QB3): Design of selective and multi-specific protein-protein interfaces. 44

Kerrien, S.,¹ Montecchi-Palazzi, L.,¹ Reisinger, F.,¹ Aranda, B.,¹ Jones, A.R.,² Oesterheld, M.,³ Martens, L.,¹ Hermjakob, H.,¹ ¹European Molecular Biology Laboratory (EMBL)—European Bioinformatics Institute, Hinxton, ²Liverpool University, United Kingdom; ³Institute for Bioinformatics, GSF national Research Center for Environment and Health, Neuherberg, Germany: The PSI semantic validators—How compliant is your proteomics data? 45

Schelhorn, S.-E., Lengauer, T., Albrecht, M., Dept. of Computational Biology and Applied Algorithmics, Max-Planck Institute for Informatics, Saarbrücken, Germany: Integrative prediction and analysis of protein region interactions. 46

Lim, W.A., Dept. of Cellular and Molecular Pharmacology, University of California, San Francisco: Evolution and engineering of cell signaling networks. 47

Teichmann, S., MRC Laboratory of Molecular Biology, Cambridge, United Kingdom: Evolution of protein complexes and protein interaction networks. 48

Leach, S.M., Tranchevent, L.-C., Moreau, Y., Dept Electrical Engineering, ESAT-SCD, Bio I, Katholieke Universiteit Leuven, Belgium: Benchmarking probabilistic interaction networks in human. 49

Szklarczyk, R.,¹ Huynen, M.,¹ Snel, B.,^{2,1} Centre for Molecular and Biomolecular Informatics, NCMLS, Radboud University Medical Centre, Nijmegen,² Bioinformatics, Dept. of Biology,³ Academic Biomedical Centre, Utrecht University, The Netherlands: Complex fate of paralogs. 50

FRIDAY, August 29—2:10 PM

SESSION 5 GENETIC NETWORKS

Chairperson: **B. Palsson**, University of California, San Diego

Piano, F., New York University, New York: Modules in development and evolution in nematode early embryos. 51

Ideker, T., University of California, San Diego: Mapping gene regulatory pathways by assembly of physical and genetic interactions. 52

de Bono, B.,¹ Vastrik, I.,¹ D'Eustachio, P.,^{2,3} Schmidt, E.,¹ Derow, C.,¹ Hermjakob, H.,¹ Orchard, S.,¹ Gopinath, G.,² Croft, D.,¹ Gillespie, G.,^{2,4} Jassal, B.,¹ Lewis, S.,⁵ Matthews, L.,² Wu, G.,² Birney, E.,¹ Stein, L.,^{2,1} European Bioinformatics Institute, Hinxton, United Kingdom;² Cold Spring Harbor Laboratory, ³ New York University School of Medicine, ⁴ College of Pharmacy and Allied Health Professions, St. John's University, Queens, New York; ⁵ Lawrence Berkeley National Laboratory, Berkeley, California: Casting the cancer net—Joining curated pathways and experimentally determined protein interaction data with ontological relevance. 53

Pache, R.A.,¹ Madan Babu, M.,² Aloy, P.,^{1,3,1} Institute for Research in Biomedicine (IRB) and Barcelona Supercomputing Center (BSC), ³ Institutió Catalana de Recerca i Estudis Avançats (ICREA), Spain; ² MRC Laboratory of Molecular Biology, Cambridge, United Kingdom: Exploiting gene deletion fitness effects in yeast to understand the modular architecture of protein complexes under different growth conditions. 54

Barbasi, A.-L., Northeastern University, Boston, Massachusetts:
Network medicine—From the human disease to comorbidity
patterns. 55

Iyer, V., University of Texas, Austin: Transcriptional regulatory
networks and mechanisms in yeast and human cells. 56

Tasan, M.,¹ Tian, W.,¹ Oestergaard, M.,² Tyrer, J.,³ Morrison, J.,³ Hill,
D.P.,⁴ Blake, J.A.,⁴ Ponder, B.A.J.,³ Easton, D.F.,⁵ Pharoah, P.D.,³
Roth, F.P.,¹ Dept. of Biological Chemistry & Molecular
Pharmacology, Harvard Medical School, Boston, Massachusetts;
²Dept. of Public Health and Primary Care, ³Cancer Research UK
Dept. of Oncology, ⁵Cancer Research UK Genetic Epidemiology
Group, Strangeways Research Laboratories. Cambridge, United
Kingdom; ⁴Jackson Laboratory, Bar Harbor, Maine: Mouse
functional linkage graphs and complex human disease. 57

FRIDAY, August 29—5:30 PM

POSTER SESSION II

Please see Poster Session I for list of posters.

SATURDAY, August 29—9:00 AM

SESSION 6 NETWORK MEDICINE I

Chairperson: **F. Piano**, New York University, New York

Andrews, B.J., Kainth, P., Sharifpoor, S., van Dyk, D., Sassi, H., Pena-
Castillo, L., Kostic, A., Frey, B., Hughes, T., Banting and Best Dept.
of Medical Research, Terrence Donnelly Centre for Cellular and
Biomolecular Research, University of Toronto, Canada: Mapping
cell cycle transcription and kinase pathways using yeast functional
genomics. 58

Westerhoff, H.V., Manchester Centre for Integrative Systems Biology,
University of Manchester, United Kingdom; Netherlands Institute for
Systems Biology, Vrije Universiteit, Amsterdam, The Netherlands:
Targeting the networks of life and their elusive fragilities. 59

- Evers, B.,¹ Demajo Meseguer, S.,¹ Schut, E.,¹ van der Burg, E.,¹ Wade-Martins, R.,² Bouwman, P.,¹ Ovaa, H.,³ Egan, D.,⁴ Jonkers, J.,¹ Divs. of ¹Molecular Biology, ³Cellular Biochemistry, ⁴Molecular Carcinogenesis, Netherlands Cancer Institute, Amsterdam; ²Wellcome Trust Centre For Human Genetics, Oxford, United Kingdom: High throughput compound screens in an in vitro model for BRCA2 deficient breast cancer. 60
- Koegl, M.,¹ Baiker, A.,² Friedel, C.,³ Dong, Y.-A.,² von Brunn, A.,² Fossum, E.,² Kasmapour, B.,¹ Schwarz, F.,¹ Zimmer, R.,³ Haas, J.,² Korn, B.,^{1,1} Deutsches Krebsforschungszentrum, Heidelberg, ²Max-von-Pettenkofer Institut, ³Institut für Informatik, LMU München, Germany: High-throughput screening for virus-host interactions. 61
- Cai, L., Dalal, C.K., Elowitz, M.B., Div. of Biology, California Institute of Technology, Pasadena: Frequency modulated stochastic localization bursts coordinately regulate downstream genes. 62
- Schadt, E.E., Dept. of Genetics, Rosetta Inpharmatics, Merck & Co., Seattle, Washington: Elucidating the circuits of metabolic diseases. 63
- Xin, X.,¹ Thierry-Mieg, N.,² Rual, J.-F.,³ Hirozane-Kishikawa, T.,³ Hill, D.,³ Vidal, M.,³ Boone, C.,¹ Banting and Best Department of Medical Research, University of Toronto, Canada; ²TIMC-IMAG Laboratory, CNRS, Grenoble, France; ³Center for Cancer Systems Biology, Dana-Farber Cancer Institute, Boston, Massachusetts: Smart-pooling for proteome-scale interactome mapping using the shifted transversal design. 64
- Lappe, M., Max-Planck Institute for Molecular Genetics, Berlin, Germany: Systems Biology = networks + structures? 65
- Tafelmeyer, P.,¹ Rain, J.-C.,¹ Guédât, P.,¹ Pecquery-Texier, A.,¹ Moisant, F.,¹ Collura, V.,¹ Meil, A.,¹ Emiliani, S.,² Barbey, S.,³ Paris, J.-M.,³ Benarous, R.,³ ¹Hybrigenics SA, ²Institut Cochin, Paris, ³CellVir SA, Evry, France: Targeting the HIV-1 host cell interactome to identify new anti-HIV drug candidates. 66

SESSION 7 NETWORK MEDICINE II

Chairperson: **B. Luisi**, MRC Institute of Virology, Glasgow, United Kingdom

Brunak, S., Center for Biological Sequence Analysis, Technical University of Denmark, Lyngby: Linking clinical phenotypes to human genes and their variation. 67

Wanker, E.E., Max-Delbruck-Center for Molecular Medicine, Berlin, Germany: The first protein interaction networks for human in health and disease. 68

Zhang, R.,¹ Shah, M.V.,¹ Yang, J.,¹ Nyland, S.B.,¹ Liu, X.,¹ Yun, J.K.,² Albert, R.,³ Loughran, T.P.,¹ ¹Pennsylvania State University Hershey Cancer Institute, ²Dept. of Pharmacology, Jake Gittlen Cancer Research Foundation, Pennsylvania State University College of Medicine, Hershey ³Dept. of Physics, Pennsylvania State University, University Park: Modeling for a cure—A survival signaling network model of CTL in T-LGL leukemia. 69

Xu, Y.,^{1,2} Wang, Y.,¹ Zhang, M.,² Lu, J.,² Dave, V.,¹ Whitsett, J.A.,¹ Divs. of ¹Pulmonary Biology, ²Biomedical Informatics, Cincinnati Children's Hospital Medical Center and University of Cincinnati, Ohio: A systems approach to mapping genetic networks controlling surfactant homeostasis. 70

Juan, D.,¹ Pazos, F.,² Valencia, A.,¹ ¹Structural Biology and BioComputing Programme, Spanish National Cancer Centre (CNIO), ²Spanish National Biotechnology Centre, CNB-CSIC, Madrid, Spain: Co-evolution in the analysis and prediction of protein interaction networks. 71

Braun, P., Center for Cancer Systems Biology (CCSB) and Dept. of Cancer Biology, Dana-Farber Cancer Institute, Dept. of Genetics, Harvard Medical School, Boston, Massachusetts: Binary interactome network mapping of *S. cerevisiae*, *A. thaliana* and *H. sapiens* as a foundation for systems biology. 72

Ortutay, C., Vihinen, M.,^{1,2} ¹Institute of Medical Technology, University of Tampere, ²Tampere University Hospital, Finland: Systems biology studies of immunome interactome.

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SATURDAY, August 29

CONFERENCE DINNER

Pre-dinner Drinks 5:40 PM

Dinner 7:00 PM