

All posters should be set up  
before Tuesday's poster session

Poster Session Assignment sheet  
1 is for Session I on Tuesday  
2 is for Session II on Thursday

Please Note that these  
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change due to schedule conflict

#	Authors	Title	Session #
1	Xiaochu Li, Floricel Gonzalez, Birgit Scharf and Jing Chen	Spatiotemporal model for pattern formation in phage-bacteria system	1
2	Mohit Kumar Jolly, Jason George, Dongya Jia, Satyendra Tripathi, Samir Hanash and Herbert Levine	Quantifying epithelial-mesenchymal plasticity in cancer and its association with patient survival	2
3	Pavel Kraikivski, Gengjie Jia, Ilya Mayzus, Andrey Rzhetsky and John Tyson	Computational Model of Melanoma Cancer	1
4	Tongli Zhang	Understanding the self-renewal, differentiation and death of intestinal cells	2
5	Akram Mohammed, Greyson Biegert, Jiri Adamec and Tomáš Helikar	Identification of potential tissue-specific cancer biomarkers and development of cancer versus normal genomic classifiers	1
6	Dieanira Erudaitius, Andrew Huang, Jacqueline Mantooth, Garry R. Buettner and Victor G. J. Rodgers	Systematic Approach to Understanding Selective Cancer Susceptibility to Pharmacological Ascorbate Therapy	2
7	Jeong-Ryeol Gong, Dongkwan Shin, Jonghoon Lee and Kwang-Hyun Cho	Analysis of phenotypic network changes along with the sequential occurrence of driver mutations during colorectal tumorigenesis	1
8	Bo Zhou, Yiwu Yan, Kikuye Koyano, Yi Zhang, Xinshu Xiao, Michael Freeman and Wei Yang	Comprehensive Proteogenomic Characterization of Human Prostate Cancer Cells Reveals Many Missing Proteins and Novel Protein Variants	1
9	Sang-Min Park, Chae Young Hwang, Daewon Lee, Jeong-Ryeol Gong and Kwang-Hyun Cho	Cell-type specific optimized therapy for colorectal cancer based on dynamical analysis of variant network models	1
10	Dirk Fey, David R Croucher, Axel Kuehn, Laura Tuffery, Melinda Halasz, Walter Kolch and Boris N Kholodenko	Patient-specific modelling and cell-to-cell variability of the JNK-p53 activation dynamics in primary and relapsed tumours.	2
11	Verena Koerber, Bernhard Radlwimmer, Pankaj Barah, Matthias Schlesner, Katrin Lamszus, Guido Reifenberger, Michael Weller, Peter Lichter and Thomas Höfer	Clonal evolution in glioblastoma	1
12	Wei He, Ayesha N. Shajahan-Haq, Diane M. Demas, Robert Clarke and William T. Baumann	Mathematical modeling of the unfolded protein response in different breast cancer cell lines	2
13	Andrej Bugrim	Dynamic network entropy as predictor of drug response in cancer cells.	1
14	Amrisha Bhosle and Nagasuma Chandra	Co-target identification from context specific kinetic models of folate metabolism in methotrexate resistant cancers	2
15	Richard Ballweg and Tongli Zhang	A Simple Formula for Fractional Killing	1
16	Nidhi Menon and Caroline N. Jones	Heparin-based hydrogel as a biomimetic 3D matrix for solid-phase growth factor presentation and cultivation of breast cancer cells	2

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17	Alice Yu, Andrew Gentles, Angela Hui, Joe Shrager, Maximillian Diehn and Sylvia Plevritis	Extracting dysregulated subnetworks in the non-small cell lung carcinoma tumor microenvironment	1
18	Xubin Li and Anil Korkut	Phosphoproteomics-Guided Discovery of Effective Combination Therapies in Cancer	2
19	Kyla A.L. Collins, Timothy J. Stuhlmiller, Jon S. Zawistowski, Michael P. East, Trang T. Pham, Claire R. Hall, Daniel R. Goulet, Samantha M. Bevill, Steven P. Angus, Sara H. Velarde, Noah Sciaky, Lee M. Graves, Gary L. Johnson and Shawn M. Gomez	Defining subtype taxonomies and functional architectures of the breast cancer kinome	1
20	Sarah Maddox	Characterizing Phenotypic Heterogeneity in Small Cell Lung Cancer	2
21	Dorjsuren Battogtokh, Shihoko Kojima and John Tyson	Modeling the Interactions of Sense and Antisense Transcripts in the Mammalian Circadian Clock Network	1
22	Zhengda Li, Ye Guan and Qiong Yang	Incoherent inputs enhance robustness of biological oscillators	2
23	Michael Hopkins, John Tyson and Bela Novak	A common role for stoichiometric inhibitors in cell cycle transitions	1
24	Gabriel Neurohr, Rachel Terry, Bela Novak, John Tyson and Angelika Amon	Cell size homeostasis is critical for maintaining a permissive DNA: Cytoplasm ratio	2
25	Bronson Weston, John Tyson and Liwu Li	A Dynamic Model of Granulocyte-Monocyte Progenitor Differentiation	1
26	Swati Dubey, Sheela Joshi and Rajendra Prasad	Simulation of a Petri net Based Model of the Menthol Biosynthesis	2
27	Akram Mohammed, Bhanwar Lal Puniya and Tomas Helikar	A comprehensive dynamical network model of the human immune system	2
28	Frank S. Heldt, Reece Lunstone, John J. Tyson and Bela Novak	Dilution of the cell cycle inhibitor Whi5 alone cannot account for size control in budding yeast	2
29	Michael Flossdorf, Veit Buchholz, Yi-Li Cho, Lorenz Kretschmer and Thomas Höfer	Dynamics of T cell memory generation inferred from single cell fate mapping in vivo	1
30	Matthias Guenther, Sumit Deswal, Wolfgang Schamel and Thomas Höfer	Specificity and sensitivity of antigen sensing by the T cell receptor is enhanced by the co-receptor CD8	2
31	James Lee, Pei-Yin Shih, Oren Schaedel, Porfirio Quintero-Cadena, Alicia Rogers and Paul Sternberg	Stress-adaptive decision-making and dispersal behaviors in nematodes involve coordinated neuropeptide signaling	1
32	Toru Matsu-Ura, Andrey Dovzhenok, Sookkyung Lim, Sean Moore and Christian Hong	Intercellular Coupling of the Cell Cycle and Circadian Clock in Adult Stem Cell Culture	2
33	Sean Mack, Daniel Yarmovsky and Daniel Dwyer	Metabolic Modeling the Response to Stress in Bacterial Pathogens	1

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34	Brittany Boribong, Mark Lenzi, Sarah Kadelka, Stanca Ciupe, Liwu Li and Caroline Jones	Measuring neutrophil migration patterns using microfluidic devices and ODE modeling of the mechanistic molecular pathways	2
35	Jignesh Parmar and Pedro Mendes	A mathematical model of iron dynamics in a mouse	1
36	Bo Huang, Ruizhen Yang, Yanting Zhu, Yang Li, Feng Liu and Jue Shi	Coupled feed-forward and feedback of ATM/p53/Mdm2/Wip1 control cell type-dependent bimodal p53 dynamics and cell fate response	2
37	Geena Idefonso, Michael Irvin and Carlos Lopez	Building a Mechanistic Understanding of Cell Death or Survival Decisions in L929 Cells	1
38	Jingyu Zhang, Xiao-Jun Tian, Yi-Jiun Chen, Weikang Wang, Simon Watkins and Jianhua Xing	Cells read TGF-beta temporal information through a nested relay mechanism	2
39	Amogh Jalihal, Pavel Kraikivski, Murali T.M. and John Tyson	Modeling the nutrient signaling network in <i>Saccharomyces cerevisiae</i>	1
40	Nikoleta Tsvetanova and Mark von Zastrow	Functional diversification of signaling by GPCR localization	2
41	Xia Wang, Sarah Jungeun Kwon and Guang Yao	Circadian clock protein Cry regulates cellular quiescence depth	1
42	Chu Chen, Ian Whitney, Anand Banerjee, Palak Sekhri, David Kern, Adrienne Fontan, John Tyson, Iain Cheeseman and Ajit Joglekar	The biochemical design of the mitotic checkpoint	2
43	Simon Mitchell, Koushik Roy, Thomas Zangle and Alexander Hoffmann	Identifying non-genetic origins of cell-to-cell variability in B-lymphocyte proliferation through systems biology	1
44	Shirin Fallahi, Rune Kleppe, Anders Goksøyr, Guttorm Alendal and Hans J. Skaug	Mathematical modeling of regulatory interactions in the fatty acid synthesis pathway	2
45	Willian Da Silveira, Ludivine Renaud, Jonathan Simpson, Matthew Huff, William B Glen, E. Starr Hazard, Dongjun Chung and Gary Hardiman	miRNA expression shifts as an initiator event in carcinogenesis induced by Bisphenol A in human prostate cells	1
46	Jean-Michel Arbona, Arach Goldar, Olivier Hyrien, Alain Arneodo and Benjamin Audit	Modeling the spatio-temporal replication program	2
47	Sarah Kwon, Xia Wang and Guang Yao	Controlling Quiescence Heterogeneity by an Rb-E2F Network Switch	1
48	Alberto Giaretta, Gianna Maria Toffolo and Timothy Charles Elston	Stochastic model of HPV early promoter predicts bursts like pattern of gene expression	2
49	Bhanwar Lal Puniya, Robert Todd and Tomas Helikar	Systems modeling of interplay among extracellular cytokines regulating phenotypic plasticity of CD4+ T-cell differentiation	1
50	Subrata Dev	Optimal methylation noise for best chemotactic performance of <i>E. coli</i>	2
51	Anand Banerjee, John Tyson and Ajit Joglekar	Mathematical modeling of an "ectopic" spindle assembly checkpoint	1

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52	Johannes Borgqvist and Marija Cvijovic	Large scale simulations of a damage accumulation model in <i>Saccharomyces cerevisiae</i> reveal the benefit of dynamic damage retention in unicellular ageing	2
53	Heidi Klumpe, Yaron Antebi and Michael Elowitz	Mapping BMP pairwise interactions describes how cells compute responses to BMP mixtures	1
54	Ping Wang and Xiao-Peng Zhang	The link between dynamic modes of p53 and cell-fate decision in the DNA damage response	2
55	Geysson Javier Fernandez Garcia, Jayson Gutierrez, Diane Lafaundex, Supriya Sen, Yu Hsin Chen, Zhang Cheng and Alexander Hoffmann	Integrated regulation of mRNA synthesis and decay decodes TNF signaling during inflammatory muscle-atrophy.	1
56	Elin Nyman, Hao Li, William Lövfors, Thirza Poot, Niclas Bergqvist, Peter Strålfors and Gunnar Cedersund	An expandable, multi-level, and multi-scale model to simulate drug simulations for type 2 diabetes and its complications	2
57	Sahand Jamal Rahi, Johannes Larsch, Kresti Pecani, Alexander Y. Katsov, Nahal Mansouri, Krasimira Tsaneva-Atanasova, Eduardo D. Sontag and Fred R. Cross	Oscillatory stimuli differentiate adapting circuit topologies	1
58	Katherine Bland, Weihua Guo, Jiayuan Sheng and Xueyang Feng	Investigate metabolic reprogramming of <i>Saccharomyces cerevisiae</i> for xylose-based fatty alcohol production via <sup>13</sup> C metabolic flux Analysis	2
59	Cemal Erdem, Alison M. Nagle, D. Lansing Taylor, Adrian V. Lee and Timothy R. Lezon	Insulin receptor substrate (IRS) dictates differential responses to insulin and insulin-like growth factor I (IGF1) stimulation	1
60	Jeffrey Law, Sophia Orbach, Bronson Weston and T. M. Murali	Network Toxicology: Connecting the Dots in Protein Interaction Networks	2
61	Karol Nieniałowski, Katarzyna Andryka, Karolina Zakrzewska, Tomasz Jetka and Michał Komorowski	Quantitative methods for detecting origins of interferons signalling sensitivity	1
62	Carlos Contreras, Gustavo Carrero and Gerda de Vries	Understanding the effect of radiation on the cell cycle through mathematical modelling	2
63	Ryan Suderman, John Bachman, Adam Smith, Peter Sorger and Eric Deeds	Fundamental Trade-offs between Information Flow in Single Cells and Cell Populations	1
64	Zhaleh Ghaemi and Zaida Luthey-Schulten	mRNA Production Noise in Eukaryotic Cells	2
65	Uchenna Anyaegbunam, Stefan Legewie and Silke Hauf	Evaluating the Robustness of the Temporal Order of Anaphase Events using an Ensemble of Single Cell Models	2
66	Hao Ge, Hong Qian and Xiaoliang Sunney Xie	Nonequilibrium stochastic dynamics at single cell level	2
67	Xi-Ming Sun, Anthony Bowman, Samuel Marguerat and Vahid Shahrezaei	Global regulation of transcription by cell size	1

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68	Shangying Wang, Kai Fan, Nan Luo, Yangxiaolu Cao, Carolyn Zhang and Lingchong You	Emulating mechanism-based models with artificial neural networks for applications in synthetic biology and systems biology	2
69	Aditya Pratapa, Neil Adames, Pavel Kraikivski, John Tyson, Jean Peccoud and T. M. Murali	CrossPlan: Systematic Planning of Genetic Crosses to Validate Mathematical Models	1
70	Egils Stalidzans, Vitalijs Komasilovs and Agris Pentjuss	Total enzyme activity constraint and homeostatic constraint impact on the best adjustable parameter sets of a kinetic model	2
71	Yuta Tokuoka, Noriko Hiroi, Tetsuya Kobayashi, Kazuo Yamagata and Akira Funahashi	Segmenting four-dimensional fluorescence microscopic image using Convolutional Neural Network	1
72	Mansoor Ahmadian, Shuo Wang, John Tyson and Young Cao	Hybrid ODE/SSA Model of the Budding Yeast Cell Cycle Control Mechanism with Mutant Case Study	2
73	Younghyun Han, Juntae Kim and Kwang-Hyun Cho	Predicting anticancer drug responses using deep learning based on cancer cell line gene expression profiles and drug molecular fingerprints	1
74	So-Yeong Jang, Jonghoon Lee, Yunseong Kim, Dongsan Kim and Kwang-Hyun Cho	Predicting the perturbation effects in biological networks based on linear system approximation modeling	2
75	Moritz Beber, Svetlana Galkina, Henning Redestig, Nikolaus Sonnenschein, Peter St. John and Christian Diener	Fast, easy, interoperable and reusable – the cobrapy infrastructure for constraints-based analysis of metabolic flux	1
76	Nello Blaser, Shirin Fallahi and Håvard G. Frøysa	Model reduction under parameter uncertainty	1
77	Håvard G. Frøysa, Hans J. Skaug and Guttorm Alendal	Structural identifiability of kinetic parameters	1
78	Christian Lieven, Moritz Beber and Nikolaus Sonnenschein	Memote - A testing suite for constraint-based metabolic models	2
79	Yosef Roth and Jonathan Karr	KineticDatanator: Tools for Aggregating Data for Biochemical Modeling	1
80	Tom Thorne	Sequential Monte Carlo learning of Bayesian gene regulatory network models from RNA-seq data	2
81	Janaka Edirisinghe, José Faria, Filipe Liu, Joana Xavier, Samuel Seaver, Pamela Weisenhorn, James Jeffryes, Tian Gu, Qizh Zhang, Isabel Rocha and Christopher Henry	Automated pathway curation and improving metabolic model reconstruction based on phylogenetic analysis of pathway conservation	1
82	Anca Stefan, Michelle Wong, Gang Liu, John Hartman, Ronald Pisoni, Bruce Robinson and Victor Andreev	A Black Box Model of Patient Response to Hemodialysis	2
83	Vincent Noël, Marcelo S. Reis, Matheus H.S. Dias, Lulu Wu, Amanda S. Guimarães, Daniel F. Reverbel, Junior Barrera and Hugo A. Armelin	SigNetSim : A web platform for building and analyzing mathematical models of molecular signaling networks	1

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84	Gang Liu, Jarcy Zee, Lisa Henn, Joshua Shimony, Anca Stefan, Brenda Gillespie, Robert Merion and Victor Andreev	Clustering Biological Systems Using Correlation Matrices	2
85	Xiao Ma, Onur Dagliyan, Klaus Hahn and Gaudenz Danuser	An Adaptive Spatiotemporal Spectrum Decomposition Approach for Cellular Morphodynamic Profiling	1
86	Leonie Amstein, Jennifer Scheidel, Jörg Ackermann and Ina Koch	Detection of all possible signaling pathways in complex networks at steady state using Manatee invariants	2
87	Andreas Weidemann, Ulrike Wittig, Maja Rey, Martin Golebiewski and Wolfgang Müller	Kinetics data information retrieval from the literature as public service	1
88	Martin Golebiewski, Steffen Brinkmann, Olga Krebs, Hadas Leonov, Quyen Nguyen, Stuart Owen, Natalie Stanford, Andreas Weidemann, Ulrike Wittig, Katy Wolstencroft, Jacky L. Snoep, Wolfgang Müller and Carole Goble	Data Needs Structure: Data and Model Management for Distributed Systems Biology Projects	2
89	Jungsik Noh, Mihai Azoitei, Philippe Roudo, Klaus Hahn and Gaudenz Danuser	GEF-H1 regulation by microtubule dynamics unveiled by fluctuation analysis of biosensor images	1
90	Abdul Salam Jarrah	Reverse-Engineering Gene regulatory Networks as Threshold Boolean Networks	2
91	Karsten Kuritz, Daniela Stöhr, Nadine Pollak, Markus Rehm and Frank Allgower	Reconstructing dynamic processes from high dimensional snap-shot data	1
92	Min Roh	dwSSA++: efficient rare event probability estimation algorithm with leaping	2
93	Jose Cadena, Andrew Warren, Rebecca Wattam, Allan Dickerman and Anil Vullikanti	Finding coordinated expression motifs in RNA-seq data	1
94	Matěj Troják, David Šafránek, Jakub Hrabec, Matěj Hajnal, Jakub Šalagovič, Františka Romanovská and Jan Červený	E-cyanobacterium.org: A Web-based Platform for Systems Biology of Cyanobacteria	2
95	Nicholas Franzese, Anna Ritz and Adam Groce	Practicality and Relaxation of Shortest Hyperpath Analysis on Biological Networks	1
96	Yunseong Kim, Jung-Min Yang and Kwang-Hyun Cho	Identifying synergistic control targets of a biological network based on a merged state transition map	2
97	Xili Liu, Seungeun Oh and Marc Kirschner	Proliferating mammalian cells modulate growth rate to reduce size variability	1
98	Dola Sengupta and Sandip Kar	Deciphering the dynamical origin of mixed population during neural stem cell development	2
99	Jian-Geng Chiou, Timothy Elston, Thomas Witelski, David Schaeffer and Daniel Lew	Principles that govern competition or co-existence in Rho-GTPase driven polarization	1
100	Lei Zhang and Feng Liu	Exploring the inhibitory effect of membrane tension on cell polarization	2
101	Tian Hong, Chung-Jung Li, Qing Nie and Jun-An Chen	The dual role of microRNA in boundary formation of the spinal cord	1

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102	Yi-Jiun Chen, Weikang Wang, Xiaojun Tian, Daniel E Lefever, David A Taft and Jianhua Xing	An efficient procedure to generate plasmid for endogenous CRISPR-based knockin	2
103	Weikang Wang, Yi-Jiun Chen, Jingyu Zhang, Min Xu and Jianhua Xing	Automating cell segmentation and tracking with deep learning algorithms	1
104	Jens Roessler, Weike Pei, Xi Wang, Thorsten B. Feyerabend, Daniel Postrach, Claudia Quedenau, Wei Chen, Sascha Sauer, Hans-Reimer Rodewald and Thomas Höfer	Computational framework for endogenous barcoding of hematopoietic stem cells in vivo	2
105	Akshay Malwade, Angel Nguyen, Peivand Sadat-Mousavi and Brian Ingalls	Predictive modelling of a batch filter mating process	2
106	Adrián César-Razquin, Enrico Girardi, Mi Yang, Justyna Konecka, Giuseppe Fiume, Marc Brehme, Julio Saez-Rodriguez and Giulio Superti-Furga	In-silico prioritization of transporter-drug relationships from drug sensitivity screens	2
107	Elin Nyman, Markus Karlsson, William Lövfors, Mikael Forsgren, Rasmus Magnusson, Fredrik Eklund, Peter Lundberg, Mika Gustafsson and Gunnar Cedersund	From omics to decision-support using hybrid mechanistic and machine-learning models	1
108	Bert Huttanus, Jiayuan Sheng and Xueyang Feng	A Synthetic Biosensor to Determine Peroxisomal Acetyl-CoA Concentration for Compartmentalized Metabolic Engineering.	2
109	Mojdeh Faraji and Eberhard Voit	Compartmentalization of lignin biosynthesis using either phenylalanine or tyrosine in <i>Brachypodium distachyon</i>	1
110	Wei-Feng Xue	Nano-scale imaging and systems modelling of amyloid protein self-assembly	2
111	Jae-Seung Yeom, Tanya Kostova-Vassilevska, Peter Barnes, David Jefferson and Tomas Ooppelstrup	Simulating the Evolutionary Dynamics of Single-stranded RNA Virus Populations	1
112	Ciaran Welsh and Daryl Shanley	PyCoTools: A Python Toolbox For COPASI	1
113	Ciaran Welsh	Towards a Computational Model of the Dermal Extracellular Matrix in Ageing	1
114	Christian Lieven, Krist Gernaey, Markus Herrgård and Nikolaus Sonnenschein	Modeling Methanotrophy: A genome-scale metabolic model of <i>Methylococcus capsulatus</i>	2
115	Nurhezreen Iqbal, Ai Muto, Nozomu Yachie, Barry Wanner and Hirotada Mori	Global Outlook on Survival of <i>Escherichia coli</i> Mutants during Long-Term Stationary Phase	2
116	Debraj Ghose, Timothy Elston and Daniel Lew	Chemotropism in yeast	2
117	Manish Kumar, Boyang Ji, Parizad Babaei and Jens Nielsen	A systems biology approach to understand the association between gut microbiota and malnutrition	1
118	Mor Miodovnik, Axel Künstner, Ewan Langan, Detlef Zilikens, Regine Gläser, Eli Sprecherq, John Baines, Enno Schmidt and Saleh Ibrahim	A distinct cutaneous microbiota profile in autoimmune bullous disease patients	2
119	Samantha Herath, Mark Ebeid and Daniel Lobo	Automatic Inference of Dynamic Regulatory Networks Controlling Shape And Form	1

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120	John Tyson	The Undergraduate Degree in Systems Biology at Virginia Tech	2
121	Xiao-Jun Tian, Dong Zhou, Youhua Liu and Jianhua Xing	The Transition from Acute Kidney Injury to Chronic Kidney Diseases Comes from Evolutionary Compromise	1
122	Brian Ji and Dennis Vitkup	Ecological Dynamics of Gut Microbiota	2
123	Neil Adames, Pavel Kraikivski, Aditya Pratapa, T. M. Murali, John Tyson and Jean Peccoud	Using high-throughput genetics to test mathematical models of the yeast cell cycle	1
124	Gang Yang, Colin Campbell and Réka Albert	Compensatory interactions to stabilize multiple steady states or mitigate the effects of multiple deregulations in biological networks	2
125	Pavel Kraikivski, T.M. Murali and John Tyson	Cell Cycle Control in Budding Yeast: Robustness of Model Predictions	1
126	Ron Henkel, Fabienne Lambusch, Dagmar Waltemath and Wolfgang Müller	Identifying frequent patterns in biochemical reaction networks using graph-mining	2
127	Federico Reali	Mechanistic interplay between ceramide and insulin resistance	1
128	Xiao Gan and Reka Albert	Analysis of a dynamic model of guard cell signaling reveals the stability of signal propagation	2
129	Kun Xiong, Alex Lancaster, Mark Siegal and Joanna Masek	Overrepresentation of coherent type 1 feed forward loops in transcriptional regulatory networks may be driven by intrinsic noise in gene expression	1
130	Christoph Kommer, Qin Zhang, Ahmed Hegazy, Max Löhning and Thomas Höfer	A data-driven correlation measure model for epigenetic network inference in T cells	2
131	Scott Rata, Stephy Joseph, Helfrid Hochegger and Bela Novak	Two interlinked bistable mechanisms generate a robust M phase	1
132	Heather Deter, Roderick Jensen, William Mather and Nicholas Butzin	Analysis and classification of differential production within toxin-antitoxin systems using large datasets	2
133	Emily Miraldi, Maria Pokrovskii, Jason A. Hall, Dayanne Martins de Castro, Ren Yi, Nick De Veaux, Nicholas Carriero, Aaron Watters, Dan R. Littman and Richard Bonneau	Transcriptional regulatory network inference from gene expression and chromatin accessibility measurements	1
134	Minghan Chen, John J. Tyson and Young Cao	A Model of the Control Mechanism for the Genetic Circuit in Caulobacter Cell Cycle	2
135	Caterina Thomaseth, Dirk Fey, Tapesht Santra, Oleksii Rukhlenko, Boris Kholodenko and Nicole Erika Radde	Evaluating the effects of measurement noise on the inference of biological regulatory networks using Modular Response Analysis	1
136	Qi Song, Ruth Grene, Lenwood Heath and Song Li	CoReg: Identification of co-regulators in genome scale transcription regulatory	2

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137	Sen Liu	A Dynamic KaiA-KaiC Interaction Maintains the Oscillation of the KaiABC Circadian Clock	1
138	Julia Kamenz, Tamara Mihaljev, George Murray, Saahil Golia, Tatiana Boluarte, Stefan Legewie and Silke Hauf	Exploring the dynamic regulation underlying synchronous chromosome splitting in anaphase	2
139	Byeongwook Lee, Uiryong Kang, Hongjun Chang and Cho Kwang-Hyun	The minimum dominating sets in a brain network critically determine the efficiency of local communication of the network	1
140	Hongjun Chang, Byeongwook Lee, Uiryong Kang and Kwang-Hyun Cho	A study on frequency-dependent state transition patterns in brain networks using energy landscape analysis	2
141	Uiryong Kang, Byeongwook Lee, Hongjun Chang and Kwang-Hyun Cho	Increasing the network communicability of a damaged brain network for rehabilitation	1
142	Sebastian Sten, Karin Lundengård, Fredrik Elinder, Maria Engström and Gunnar Cedersund	Multi-level modelling for a new physiologically based interpretation of fMRI data	2
143	Gianluca Selvaggio and Robert Pearlstein	Using action potential simulations to explore the possible cause-effect relationships between gain and loss of cardiac ion channel function and generation of proarrhythmic early afterdepolarizations	1
144	Kjersti Rise, Finn Drabløs and Morten Beck Rye	Aggregating RNA-Seq reads from multiple genes in KEGG metabolic pathways improves interpretability in gene expression pathway analysis	2
145	Marian Breuer, Clyde A. Hutchison Iii., John I. Glass and Zan Luthey-Schulten	The metabolic reconstruction of a minimal cell	1
146	Akinori Nishi, Katsuya Ohbuchi, Hirotaka Kushida, Takashi Matsumoto, Keiko Lee, Haruo Kuroki, Shigeki Nabeshima, Kazuhiro Hanazaki, Chika Shimobori, Nagisa Komokata, Hitomi Kanno, Naoko Tsuchiya, Makoto Zushi, Ayako Yachie, Yukiko Matsuoka, Hiroaki Kitano and Masahiro Yamamoto	Systems Biology of Herbal Medicine: Pharmacological property of complex herbal formulation	2
147	Hitomi Kanno, Akinori Nishi, Katsuya Ohbuchi, Hirotaka Kushida, Takashi Matsumoto, Chika Shimobori, Haruo Kuroki, Shigeki Nabeshima, Nozomu Sakurai, Ayako Yachie, Yukiko Matsuoka, Hiroaki Kitano and Masahiro Yamamoto	Systems biology of multi-herbal formulations: Addressing condition-dependent prescription selection by comparing pharmacological and compound traits of related formulations	1
148	Sandeep Kaur, Jenny Vuong and Sean O'Donoghue	A strategy for modelling and visualising phosphoproteomic datasets	2
149	Yin Hoon Chew, Arthur Goldberg and Jonathan Karr	Toward A Whole-Cell Model of H1 Human Embryonic Stem Cells (hESCs): A Genome-Scale Metabolic Model	1

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150	Agris Pentjušs and Egils Stalidzans	Genome scale metabolic model of Arabidopsis thaliana for isoprenoid production	2
151	Ghofran Othoum, Magbubah Essack, Salim Bougouffa, Rozaimi B. Mohamad Razali, Ameerah Bokhari, Soha Alamoudi, Maged M Saad, Feras F. Lafi, Andre Antunes, Heribert Hirt and Vladimir B. Bajic	Genome mining of Bacillus licheniformis strains from the Red Sea with focus on the biosynthesis of antimicrobial products	1
152	Iulia M. Lazar, Ina Hoeschele and Shreya Ahuja	Cell Cycle Model System for the Identification of Molecular Markers of Cancer	2
153	Daniel Sevin and Uwe Sauer	Nontargeted in vitro metabolomics identifies wide-spread enzyme promiscuity in Escherichia coli	1
154	Nicholas Butzin and Will Mather	Crosstalk between diverse synthetic protein degradation tags in Escherichia coli	1
155	Snorre Sulheim, Tjasa Kumelj, Alexander Wentzel and Eivind Almaas	Extended GEM of Streptomyces Coelicolor for production of secondary metabolites	1
156	Udaya Sree Datla, William H. Mather, Sheng Chen, Isaac W. Shoultz, Uwe C. Tauber, Caroline N. Jones and Nicholas C. Butzin	The spatiotemporal network dynamics of acquired resistance in an engineered microecology	2
157	Hunter Flick, Jiayuan Sheng and Xueyang Feng	Systematic Optimization of Protein Secretory Pathways in Saccharomyces cerevisiae to Increase Expression of Hepatitis B Small Antigen	1
158	Henning Redestig, Moritz Beber, Svetlana Galkina, Danny Dannaher, Markus Herrgård and Nikolaus Sonnenschein	Data-Driven Design of Cell Factories and Communities	2