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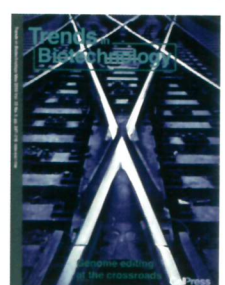
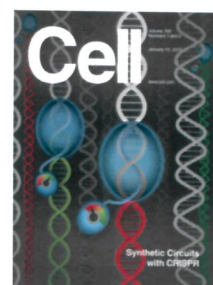
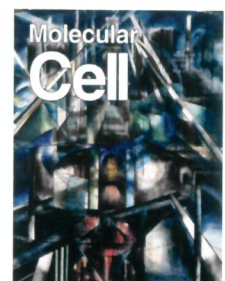
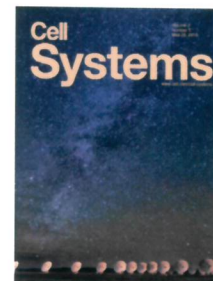
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Supporting Publications



[P14]	<b>Strong cooperation between homotopic brain areas is a prominent feature of motor control for unilateral limb movement</b> P. Wei*, Z. Lu, T. Zhang, <i>National Research Center for Rehabilitation Technical Aids, China</i>
[P15]	<b>Uncovering the hidden layers of the cells through deep learning</b> A. Sharifi-Zarchi <sup>1,2</sup> , F. Abdolhosseini <sup>3</sup> , A. Maazallahi <sup>3</sup> , H. Chitsaz <sup>1</sup> , <sup>1</sup> <i>Colorado State University, USA</i> , <sup>2</sup> <i>Royan Institute, Iran</i> , <sup>3</sup> <i>Sharif University of Technology, Iran</i>
[P16]	<b>Agonist muscle stimulation during movement changes the brain network via switching on several links between the sensory relay stations and motor cortex</b> P. Wei <sup>1</sup> , R. Bao <sup>2</sup> , Z. Lu <sup>1</sup> , T. Zhang <sup>1</sup> , <sup>1</sup> <i>National Research Center for Rehabilitation Technical Aids, China</i> , <sup>2</sup> <i>China Rehabilitation Research Center, China</i>
[P17]	<b>The architecture and evolution of a fission yeast genome revealed from itself</b> K. Yoshida, <i>Sony Computer Science Laboratories, Inc., Japan</i>
[P18]	<b>Gaussian process mixture modeling of single-cell RNA-seq data resolves a CD4+ T cell fate bifurcation</b> T. Lönnberg <sup>1,2</sup> , V. Svensson <sup>1,2</sup> , K.R. James <sup>3</sup> , A. Haque <sup>4</sup> , S.A. Teichmann <sup>1</sup> , <sup>1</sup> <i>EMBL-EBI, UK</i> , <sup>2</sup> <i>Wellcome Trust Sanger Institute, UK</i> , <sup>3</sup> <i>QIMR Berghofer Medical Research Institute, Australia</i> , <sup>4</sup> <i>The Peter Doherty Institute, Australia</i>
[P19]	<b>The Aspergillus mine—comparative genomics of 300 species</b> T. Vesth <sup>1</sup> , S. Theobald <sup>1</sup> , J. Nybo <sup>1</sup> , I. Kjærboelling <sup>1</sup> , R. de Vries <sup>2</sup> , I. Grigoriev <sup>3</sup> , S. Baker <sup>4</sup> , M.R. Andersen <sup>1</sup> , <sup>1</sup> <i>Technical University of Denmark, Denmark</i> , <sup>2</sup> <i>Fungal Physiology, CBS-KNAW Fungal Biodiversity Centre, Utrecht, The Netherlands</i> , <sup>3</sup> <i>Joint Genome Institute, Walnut Creek, CA, USA</i> , <sup>4</sup> <i>Joint Bioenergy Institute, Berkeley, CA, USA</i>
[P20]	<b>Clustering Toolbox (CLUSTbox) for identifying subtypes of complex diseases in big health data phenotyping studies</b> G. Liu <sup>1</sup> , J. Zee <sup>1</sup> , B.W. Gillespie <sup>1,2</sup> , A. Stefan <sup>1</sup> , R.M. Merion <sup>1</sup> , V.P. Andreev <sup>1</sup> , <sup>1</sup> <i>Arbor Research Collaborative for Health, USA</i> , <sup>2</sup> <i>University of Michigan, USA</i>
[P21]	<b>'Snake vectors' for clustering correlation matrices representing biological systems</b> J. Zee <sup>1</sup> , G. Liu <sup>1</sup> , B.W. Gillespie <sup>1,2</sup> , A. Stefan <sup>1</sup> , R.M. Merion <sup>1</sup> , V.P. Andreev <sup>1</sup> , <sup>1</sup> <i>Arbor Research Collaborative for Health, USA</i> , <sup>2</sup> <i>University of Michigan, USA</i>
[P22]	<b>Identifying progressive network perturbation in differentiation from single-cell RNA-seq data</b> S. Mukherjee*, A. Carignano, S. Lee, G. Seelig, <i>University of Washington, USA</i>
[P23]	<b>Inferring metabolic tasks of cancer cells from transcriptomics data</b> S. Gao <sup>1</sup> , Z. Dai <sup>1</sup> , L. Lai <sup>1,2</sup> , <sup>1</sup> <i>Center for Quantitative Biology, Academy for Advanced Interdisciplinary Studies, Peking University, China</i> , <sup>2</sup> <i>BNLMS, State Key for Structural Chemistry of Unstable and Stable Species, College of Chemistry and Molecular Engineering, Peking University, China</i>
[P24]	<b>Transomics reveal CSC metabolism</b> M.K. Konno*, J.K. Koseki, H.M. Matsui, A.A. Asai, N.N. Nishida, K.K. Kawamoto, Y.D. Doki, M.M. Mori, H.I. Ishii, <i>Osaka University, Japan</i>
[P25]	<b>Predicting a metabolome from a genome sequence: a case study of <i>M. tuberculosis</i> identifies variations during dormancy</b> R. Bhagavat, A. Mohan, P. Baloni, N. Chandra*, <i>Indian institute of Science, India</i>
[P26]	<b>Data analysis of CDC data of death: education, an important factor in the increase of suicide rates in USA</b> G. Diaz <sup>1</sup> , T. Brandt <sup>1</sup> , J. Jones <sup>1</sup> , T. Gary <sup>1,2</sup> , A. Yenamandra <sup>1,3</sup> , <sup>1</sup> <i>Lipscomb University, Nashville, TN, USA</i> , <sup>2</sup> <i>Middle Tennessee State University, Nashville, TN, USA</i> , <sup>3</sup> <i>Vanderbilt University Medical Center, Nashville, TN, USA</i>
[P27]	<b>Metabolic rerouting in drug-resistant mycobacteria identified by integrating phenotypic microarrays, transcriptome, and metabolic networks</b> P. Baloni*, J. Padiadpu, N. Chandra, <i>Indian institute of Science, Bangalore, India</i>
[P28]	<b>The dynamic transcriptional and translational landscape of the model antibiotic producer <i>Streptomyces coelicolor</i> A3(2)</b> Y. Jeong, B.K. Cho, N. Lee*, <i>Korea Advanced Institute of Science and Technology, Republic of Korea</i>