



◆ 科学研究

◆ 实验室

◆ 研究小组

◆ 青年科学家小组

◆ 科研项目

◆ 发表论文

[1] Li Yang, Gang Wei, Kun Tang, Christine Nardini, Jing-Dong J. Han . Understanding human diseases with high-throughput quantitative measurement and analysis of molecular signatures. *Science China Life Sciences* 2013, Volume 56, Issue 3, pp 213-219, [PDF]

[2] Allison Jones, Andrew E. Teschendorff, Quanxi Li, Jane D. Hayward, Athilakshmi Kannan, Tim Mould, James West, Michal Zikan, David Cibula, Heidi Fieg, Shih-Han Lee, Elisabeth Wik, Richard Hadwinl, Rupali Arora, Charlotte Lemech, Henna Turunen, Päivi Pakarinen, Ian J. Jacobs, Helga B. Salvesen, Milan K. Bagchi, Indrani C. Bagchi, Martin Widschwendter. Role of DNA Methylation and Epigenetic Silencing of HAND2 in Endometrial Cancer Development. *PLoS Med* 2013, 10(11):e1001551 [PDF]

[3] Analysis of a gene regulatory cascade mediating circadian rhythm in zebrafish. Li Y, Li G, Wang H, Du J, Yan J. *PLoS Comput Biol* 2013, 2013, 9(2):e1002940 [PDF]

[4] Banerji CR, Miranda-Saavedra D, Severini S, Widschwendter M, Enver T, Zhou JX, Teschendorff AE. Cellular network entropy as the energy potential in Waddington's differentiation landscape. *Sci Rep* 2013, 2013, 3: 3039

[5] Boyd-Kirkup JD, Green CD, Wu G, Wang D, Han JD. Epigenomics and the regulation of aging. *Epigenomics*. 2013 Apr 2013, 5(2):205-27. doi: 10.2217/epi.13.5. PMID: 23566097 [PubMed – in process]

[6] Cold-induced RNA-binding proteins regulate circadian gene expression by controlling alternative polyadenylation. Liu Y, Hu W, Murakawa Y, Yin J, Wang G, Landthaler M, Yan J. *Sci Rep* 2013, 2013, 3: 2054 [PDF]

[7] Guo J, Mei X, Tang K. Automatic landmark annotation and dense correspondence registration for 3D human facial images. *BMC Bioinformatics* 2013, 14: 232 [PDF]

[8] Haipeng Li, Thomas Wiehe . Coalescent tree imbalance and a simple test for selective sweeps based on microsatellite variation. *PLoS Comput Biol* 2013, 2013, 9(5):e1003060 [PDF]

[9] Hammad Naveed, Jingdong J. Han. Structure-based protein-protein interaction networks and drug design. *Quantitative Biology* 2013, 2013, DOI 10.1007/s40484-013-0018-y. [PDF]

[10] Jialiang Huang, Chaoqun Niu, Christopher D. Green, Lun Yang, Hongkang Mei, Jing-Dong J. Han. Systematic Prediction of Pharmacodynamic Drug-Drug Interactions through Protein-Protein-Interaction Network. *PLoS Computational Biology* 2013, 2013, 9(3): e1002998 [PDF]

[11] Jin W, Li R, Zhou Y, Xu S. Distribution of ancestral chromosomal segments in admixed genomes and its implications for inferring population history and admixture mapping. *Eur J Hum Genet* 2013, doi: 10.1038/ejhg.2013.265

[12] Jin Yang. Chemical sensing by cell-surface chemoreceptor arrays: The roles of receptor cooperativity and adaptation. *Phys Rev E* 2013, 2013 [PDF]

[13] Jin' e Li, Yi Liu., Min Liu, Jing-Dong J. Han. Functional Dissection of Regulatory Models Using Gene Expression Data of Deletion Mutants. *PLoS Genetics* 2013, 2013, 9:e1003757 [PDF]

[14] Junrui Li, Kristan A. Schneider, Haipeng Li. The Hitchhiking Effect of a Strongly Selected Substitution in Male Germline on Neutral Polymorphism in a Monogamy Population. *PLoS ONE* 2013, 10.1371/journal.pone.0071497 [PDF]

[15] Kang L, Zheng HX, Chen F, Yan S, Liu K, Qin Z, Liu L, Zhao Z, Li L, Wang X, He Y, Jin L. MtDNA lineage expansions in Sherpa population suggest adaptive evolution in Tibetan highlands. *Mol Biol Evol* 2013, 2013 [Epub ahead of print] [PDF]

[16] Kao Lin, Andreas Futschik, Haipeng Li*. A fast estimate for the population recombination rate based on regression. *Genetics* 2013, doi:10.1534/genetics.113.150201 [PDF]

[17] Liu Y, Qiao N, Zhu S, Su M, Sun N, Boyd-Kirkup J, Han JD. A novel Bayesian network inference algorithm for integrative analysis of heterogeneous deep sequencing data. *Cell Res* 2013, doi: 10.1038/cr.2013.8

[18] Mazin P, Xiong J, Liu X, Yan Z, Zhang X, Li M, He L, Somel M, Yuan Y, Phoebe Chen YP, Li N, Hu Y, Fu N, Ning Z, Zeng R, Yang H, Chen W, Gelfand M, Khaitovich P. Widespread splicing changes in human brain development and aging. *Mol Syst Biol* 2013, doi: 10.1038/msb.2012.67.

[19] NIU Bing, YUAN Xiaocheng, ROEPER Preston, SU Qiang, PENG Chunrong, YIN Jingyuan, DING Juan, LI Haipeng*, LU Wencong. HIV-1 protease cleavage site prediction based on two-stage feature selection method. *Protein Pept Lett* 2013, 2013, 20(3):290-298 [PDF]

[20] NIU Shen, HUANG Tao, FENG Kaiyan, HE Zhisong, CUI Weiren, GU Lei, LI Haipeng, CAI Yudong, LI Yixue . Inter- and intra-chain disulfide bond prediction based on optimal feature selection. *Protein Pept Lett* 2013, 2013, 20(3):324-335 [PDF]

[21] Peng S, Tan J, Hu S, Zhou H, Guo J, Jin L, Tang K. Detecting genetic association of common human facial

[22] Qian W, Deng L, Lu D, Xu S. Genome-wide landscapes of human local adaptation in Asia. PLoS One 2013, 8(1):e54224 [PDF]

[23] Qiao N, Huang Y, Naveed H, Green CD, Han J-DJ . CoCiter: An Efficient Tool to Infer Gene Function by Assessing the Significance of Literature Co-Citation . PLoS ONE 8(9) 2013, :e74074 doi:10.1371/journal.pone.0074074

[24] Qin P, Li Z, Jin W, Lu D, Lou H, Shen J, Jin L, Shi Y, Xu S. A panel of ancestry informative markers to estimate and correct potential effects of population stratification in Han Chinese. Eur J Hum Genet 2013,doi: 10.1038/ejhg.2013.111 [PDF]

[25] Somel M, Liu X, Khaitovich P. Human brain evolution: transcripts, metabolites and their regulators. Nat Rev Neurosci 2013, 14(2):112-27

[26] Song QF, Zhang G, Zhu XG. Optimal crop canopy architecture to maximise canopy photosynthetic CO₂ uptake under elevated CO₂ – a theoretical study using a mechanistic model of canopy photosynthesis. Funct Plant Biol 2013, 2013, 40, 109-124 [PDF]

[27] Tan J, Yang Y, Tang K, Sabeti PC, Jin L, Wang S. The adaptive variant EDARV370A is associated with straight hair in East Asians. Hum Genet 2013, 2013 Jun 23. [Epub ahead of print] [PDF]

[28] Teschendorff AE. Epigenetic aging: insights from network biology. Aging 2013, 2013, 5(10): 719-20 [PDF]

[29] Wei Zhang, Yi Liu, Na Sun, Dan Wang, Jerome Boyd-Kirkup, Xiaoyang Dou, Jing-Dong Jackie Han. Integrating Genomic, Epigenomic, and Transcriptomic Features Reveals Modular Signatures Underlying Poor Prognosis in Ovarian Cancer. Cell Reports 2013,http://dx.doi.org/10.1016/j.celrep.2013.07.010 [PDF]

[30] Xian B, Shen J, Chen W, Sun N, Qiao N, Jiang D, Yu T, Men Y, Han Z, Pang Y, Kaeberlein M, Huang Y, Han JD. WormFarm: a quantitative control and measurement device toward automated *Caenorhabditis elegans* aging analysis. Aging Cell 2013, 2013 Feb 26. doi: 10.1111/acel.12063. PMID: 23442149

[31] Xin CP, Yang J, Zhu XG. A model of chlorophyll a fluorescence induction kinetics with explicit description of structural constraints of individual photosystem II units. Photosynth Res 2013,DOI 10.1007/s11120-013-9894-2 [PDF]

[32] Xu J, Li Y, Ma X, Ding J, Wang K, Wang S, Tian Y, Zhang H, Zhu XG. Whole transcriptome analysis using next-generation sequencing of model species *Setaria viridis* to support C4 photosynthesis research. Plant Mol Biol 2013, 2013, DOI 10.1007/s11103-013-0025-4. [PDF]

[33] Xu Y, Shao C, Fedorov BV, Goropashnaya VA, Barnes MB, Yan J. Molecular signatures of mammalian hibernation: comparisons with alternative phenotypes. BMC Genomics 2013, 2013, 14:567 [PDF]

[34] Yana G, Kammerov, Sijia Wang, Jingze Tan, Pascale Gerbault, Abigail Wark, Longzhi Tan, Yajun Yang, Shilin Li, Kun Tang, Hua Chen, Adam Powell, Yuval Itan, Dorian Fuller, Jason Lohmueller, Junhao Mao, Asa Schachar, Madeline Paymer, Elizabeth Hostetter, Elizabeth Byrne, Melissa Burnett, Andrew P. McMahon, Mark G. Thomas, Daniel E. Lieberman, Li Jin, Clifford J. Tabin, Bruce A. Morgan, Pardis C. Sabeti. Modeling Recent Human Evolution in Mice by Expression of a Selected EDAR Variant. Cell 2013, 2013, 152(4): 691-702. [PDF]

[35] Yuan Y, Yang L, Shi M, Lu D, Lou H, Chen YP, Jin L, Xu S. Identification of well-differentiated gene expressions between Han Chinese and Japanese using genome-wide microarray data analysis. J Med Genet 2013,doi:10.1136/jmedgenet-2012-101501 [PDF]

[36] Zhang Y, Zhang X0, Chen T, Xiang JF, Yin QF, Xing YH, Zhu S, Yang L and Chen LL. Circular intronic long noncoding RNAs. Mol Cell 2013, 2013, 51: 792-806

[37] Zhu S, Xiang JF, Tian C, Chen LL, Yang L. Prediction of constitutive A-to-I editing sites from human transcriptomes in the absence of genomic sequences. BMC Genomics 2013, 2013, 14: 206

[38] Zhu S, Zhang X0, Yang L. Panning for long noncoding RNAs. Biomolecules 2013, 2013, 3: 226-241 (Review)