

103 年 2 月 通過 學術審查

年 級：博七 (93 博士班入學)

著作列表

Journal Papers

1. **Chia-Yang Cheng**, Chia-Han Chu, Hung-Wei Hsu, Fang-Rong Hsu, Chung Yi Tang, Wen-Ching Wang, Hsing-Jien Kung, Pei-Ching Chang: An improved ChIP-seq peak detection system for simultaneously identifying post-translational modified transcription factors by combinatorial fusion, using SUMOylation as an example. *BMC Genomics* 2014, 15(Suppl 1):S1
(SCI; IF=4.4, subject categories BIOTECHNOLOGY & APPLIED MICROBIOLOGY (21/160=13.1%))
2. Pei-Ching Chang, **Chia-Yang Cheng**, Mel Campbell, Yi-Cheng Yang, Hung-Wei Hsu, Ting-Yu Chang, Chia-Han Chu, Yi-Wei Lee, Chiu-Lien Hung, Shi-Mei Lai, Clifford G Tepper, Wen-Ping Hsieh, Hsei-Wei Wang, Chuan-Yi Tang, Wen-Ching Wang and Hsing-Jien Kung: The chromatin modification by SUMO-2/3 but not SUMO-1 mediates the epigenetic silencing of key immune-related genes during Kaposi's sarcoma associated herpesvirus reactivation. (**Chia-Yang Cheng is co-first author**)
BMC Genomics 2013, 14:824
(SCI; IF=4.4, subject categories BIOTECHNOLOGY & APPLIED MICROBIOLOGY (21/160=13.1%))
3. Chun-Chi Lai, Yung-Hsin Yeh, Wen-Ping Hsieh, Chi-Tai Kuo, Wen-Ching Wang, Chia-Han Chu, Chiu-Lien Hung, **Chia-Yang Cheng**, Hsin-Yi Tsai, Jia-Lin Lee, Chuan-Yi Tang, Lung-An Hsu: Whole-Exome Sequencing to Identify a Novel LMNA Gene Mutation Associated with Inherited Cardiac Conduction Disease *PLOS ONE* Published: December 12, 2013 DOI: 10.1371/journal.pone.0083322
(SCI; IF=3.7, subject categories MULTIDISCIPLINARY SCIENCES 7/56=12.5%)
4. F.R. Hsu, H.Y. Chang, Y.L. Lin, Y.T. Tsai, H.L. Peng, Y.T. Chen, **C.Y. Cheng**, M.Y. Shih, C.H. Liu, and C.F. Chen, "AVATAR: A database for genome-wide alternative splicing event detection using large scale ESTs and mRNAs," *Bioinformatics*, Vol.1 No.1, PP. 16~18, 2005-04.

Conference Papers

1. **Chia-Yang Cheng**, Chia-Han Chu, Fang-Rong Hsu, Chung Yi Tang, Wen-Ching Wang, Hsing-Jien Kung, Pei-Ching Chang: An improved ChIP-seq peak detection system for simultaneously identifying post-translational modified transcription factors by combinatorial fusion, using SUMOylation as an example. The 12th Asia Pacific Bioinformatics Conference (Shanghai, China, 17-19 January, 2014)
2. **Chia-Yang Cheng**, Fang-Rong Hsu, Chuan Yi Tang: Extracting Alternative Splicing Information from Captions and Abstracts Using Natural Language Processing. SUTC 2008. (IEEE)
3. Che Feng Chen, **Chia-Yang Cheng**, Chia-Hung Liu, Min Yao Shih: Genome-Wide Alternative Splicing Events Detection through Analysis of Large Scale ESTs. BIBE 2004: 310-316