BIOGRAPHICAL SKETCH

NAME in English Kun-Yi Chien NAME in Chinese 簡昆鎰	POSITION TITLE Associate Professor, Department of Biochemistry and Molecular Biology

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
Soochow University	B.S.	06/87	Microbiology
National Tsing Hua University	Ph.D.	06/93	Physical Biochemistry
National Tsing Hua University	Postdoctoral	12/01	Physical Biochemistry

A. Positions and Honors

Positions and Employment

2002-2003 Assistant Research Professor, Chang Gung Memorial Hospital, Taiwan
2003-2013 Assistant Professor, Chang Gung University, Taiwan

Other Experience and Professional Memberships

2004- Member, Taiwan Proteomics Society
2004- Member, Taiwan Society for Mass Spectrometry
2005- Member, Human Proteome Organization (HUPO)
2008-2011 Council member, Taiwan Proteomics Society

Honors

B. Selected Peer-reviewed Publications (2009-2014) (in chronological order)

1. Huang KY, **Chien KY**, Lin YC, Hsu WM, Fong IK, Huang PJ, Yueh YM, Gan RR, Tang P. A proteome reference map of Trichomonas vaginalis. *Parasitol Res.* 2009, 104(4):927-933.
2. Chi, L. -M., Lee, C. -W., Chang, K. -P., Hao, S. -P., Lee, H. -M., Liang, Y., Hsueh, C., Yu, C. -J., Lee, I. -N., Chang, Y. -J., Lee, S. -Y., Yeh, Y. -M., Chang, Y. -S., **Chien, K. -Y.*** and Yu, J. -S.* Enhanced interferon signaling pathway in oral cancer revealed by quantitative proteome analysis of microdissected specimens using 16O/18O labeling and integrated 2DLC-ESI-MALDI tandem MS. *Mol. Cell. Proteomics* 2009, 8(7):1453-1474.
3. Lin CY, Tan BC, Liu H, Shih CJ, **Chien KY**, Lin CL, Yung BY. Dephosphorylation of nucleophosmin by PP1β facilitates pRB binding and consequent E2F1-dependent DNA repair. *Mol Biol Cell.* 2010, 21(24):4409-4417.
4. Chang KP, Yu JS, **Chien KY**, Lee CW, Liang Y, Liao CT, Yen TC, Lee LY, Huang LL, Liu SC, Chang YS, Chi LM. Identification of PRDX4 and P4HA2 as metastasis-associated proteins in oral cavity squamous cell carcinoma by comparative tissue proteomics of microdissected specimens using iTRAQ technology. *J Proteome Res.* 2011, 10(11):4935-4947.
5. Wu ZZ, Sun NK, **Chien KY**, Chao CC. Silencing of the SNARE protein NAPA sensitizes cancer cells to cisplatin by inducing ERK1/2 signaling, synoviolin ubiquitination and p53 accumulation. *Biochem Pharmacol.* 2011, 82(11):1630-1640.
6. Tsai MH, Wu CC, Peng PH, Liang Y, Hsiao YC, **Chien KY**, Chen JT, Lin SJ, Tang RP, Hsieh LL, Yu JS. Identification of secretory gelsolin as a plasma biomarker associated with distant organ metastasis of colorectal

cancer. *J Molecular Medicine* 2012, 90(2):187-200.

7. Hsieh Y-J, **Chien K-Y**, Lin S-Y, Sabu S, Hsu R-M, Chi L-M, Lyu P-C, and Yu J-S*. Photofrin binds to procaspase-3 and mediates photodynamic treatment–triggered methionine oxidation and inactivation of procaspase-3. *Cell Death Dis.* 2012, 3: e347; doi:10.1038/cddis.2012.85.
8. Chen CY, Weng YH, **Chien KY**, Lin KJ, Yeh TH, Cheng YP, Lu CS, Wang HL. (G2019S) LRRK2 activates MKK4-JNK pathway and causes degeneration of SN dopaminergic neurons in a transgenic mouse model of PD. *Cell Death Differ*. 2012, 19(10):1623-1633.
9. Wang CI, **Chien KY**, Wang CL, Liu HP, Cheng CC, Chang YS, Yu JS, Yu CJ. Quantitative Proteomics Reveals Regulation of Karyopherin Subunit Alpha-2 (KPNA2) and Its Potential Novel Cargo Proteins in Nonsmall Cell Lung Cancer. *Mol Cell Proteomics* 2012, 1(11):1105-1122.
10. Sun NK, Huang SL, **Chien KY,** Chao CC. Golgi-SNARE GS28 potentiates cisplatin-induced apoptosis by forming GS28-MDM2-p53 complexes and by preventing the ubiquitination and degradation of p53. *Biochem J.* 2012, 444(2):303-314
11. Lin SY, Li TY, Liu Q, Zhang C, Li X, Chen Y, Zhang SM, Lian G, Liu Q, Ruan K, Wang Z, Zhang CS, **Chien KY**, Wu J, Li Q, Han J, Lin SC. GSK3-TIP60-ULK1 signaling pathway links growth factor deprivation to autophagy. *Science* 2012, 336(6080):477-481.
12. Feng Y, **Chien KY**, Chen HL, Chiu CH. Pseudogene recoding revealed from proteomic analysis of salmonella serovars. *J. Proteome Res.* 2012, 11(3):1715-1719.
13. Lin SY, Li TY, Liu Q, Zhang C, Li X, Chen Y, Zhang SM, Lian G, Liu Q, Ruan K, Wang Z, Zhang CS, Chien KY, Wu J, Li Q, Han J, Lin SC. Protein phosphorylation-acetylation cascade connects growth factor deprivation to autophagy. *Autophagy* 2012, 8(9):1385-1386.
14. Chen CL, Lai YF, Tang P, **Chien KY**, Yu JS, Tsai CH, Chen HW, Wu CC, Chung T, Hsu CW, Chen CD, Chang YS, Chang PL, Chen YT. Comparative and targeted proteomic analyses of urinary microparticles from bladder cancer and hernia patients. *J. Proteome Res.* 2012, 11(12):5611-56290.
15. Dong YM, **Chien KY**, Chen JT, Lin SJ, Wang TC, Yu JS. Site-specific separation and detection of phosphopeptide isomers with pH-mediated stacking capillary electrophoresis-electrospray ionization-tandem mass spectrometry. *J Sep Sci*. 2013, 36(9-10):1582-1589.
16. Chen JT, Ho CW, Chi LM, **Chien KY**, Hsieh YJ, Lin SJ, Yu JS. Identification of the lamin A/C phosphoepitope recognized by the antibody P-STM in mitotic HeLa S3 cells. *BMC Biochem.* 2013, 14:18; doi: 10.1186/1471-2091-14-18.
17. Chang KP, Wang CL, Kao HK, Liang Y, Liu SC, Huang LL, Hseuh C, Hsieh YJ, **Chien KY,** Chang YS, Yu JS, Chi LM*. Overexpression of caldesmon is associated with lymph node metastasis and poorer prognosis in patients with oral cavity squamous cell carcinoma. *Cancer* 2013, 119(22):4003-4011.
18. Lin SJ, Chang KP, Hsu CW, Chi LM, **Chien KY,** Liang Y, Tsai MH, Lin YT, Yu JS. Low-molecular-mass secretome profiling identifies C-C motif chemokine 5 as a potential plasma biomarker and therapeutic target for nasopharyngeal carcinoma. *J Proteomics* 2013, 94C:186-201.
19. Chen CD, Wang CL, Yu CJ, **Chien KY**, Chen YT, Chen MC, Chang YS, Wu CC, Yu JS. Targeted proteomics pipeline reveals potential biomarkers for the diagnosis of metastatic lung cancer in pleural effusion. *J Proteome Res.* 2014, 13(6):2818-2829.

C. Research Support

Ongoing Research Support

Completed Research Support (2006-2010)

99-2320-B-182-011-MY2 08/01/10-07/31/12
Development of highly sensitive phosphopeptide enrichment systems for quantitative phosphoproteomics
The goal of this project was to develop methodologies of quantitative phosphoproteomics suitable for various types of samples.
Role: PI

101-2320-B-182-012 08/01/12-07/31/13

Investigation of the downstream regulation mechanism of beta-interferon using a high coverage quantitative proteomic workflow

The goal of this project was to establish an analytical workflow for in-depth proteome/phosphoproteome analysis. The established platform was applied to the study of Interferon signaling pathway.

Role: PI