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**EDUCATION :**

2000: *M.S. (Major: Epidemiology)*, National Taiwan University, Taipei, Taiwan  
1997: *B.S. (Major: Public Health)*, Taipei Medical University, Taipei, Taiwan

**RESEARCH EXPERIENCE :**

2012-Present *Chief of Staff*  
Taiwan Biobank, Institute of Biomedical Sciences, Academia Sinica

2006-2012 *Project Manager*  
Taiwan Biobank, Institute of Biomedical Sciences, Academia Sinica  
**Specimen collection, Laboratory management**

2000-2006 *Research Assistant*  
Institute of Biomedical Sciences, Academia Sinica  
**Cancer Genetics of Breast Cancers**

**SELECTED PUBLICATIONS.**

Hu LY, Chang CC, Huang YS, Chou WC, Lin YM, Ho CC, Chen WT, Shih HM, Hsiung CN, **Wu PE**, Shen CY. SUMOylation of XRCC1 activated by poly (ADP-ribosyl)ation regulates DNA repair. *Hum Mol Genet.* 2018;27:2306-2317

Chen CH, Yang JH, Chiang CWK, Hsiung CN, **Wu PE**, Chang LC, Chu HW, Chang J, Song IW, Yang SL, Chen YT, Liu FT, Shen CY. Population structure of Han Chinese in the modern Taiwanese population based on 10,000 participants in the Taiwan Biobank project. *Hum Mol Genet.* 2016;25:5321-5331.

Yang SY, Hsiung CN, Li YJ, Chang GC, Tsai YH, Chen KY, Huang MS, Su WC, Chen YM, Hsiung CA, Yang PC, Chen CJ, **Wu PE**, Yu JC, Shen CY, Hsu HM. Fanconi anemia genes in lung adenocarcinoma- a pathway-wide study on cancer susceptibility. *J Biomed Sci.* 2016;23:23.

Cheng CW, Chen PM, Hsieh YH, Weng CC, Chang CW, Yao CC, Hu LY, **Wu PE**, Shen CY. Foxo3a-mediated overexpression of microRNA-622 suppresses tumor metastasis by repressing hypoxia-inducible factor-1 $\alpha$  in ERK-responsive lung cancer. *Oncotarget.* 2015;6:44222-38.

Hsiung CN, Chu HW, Huang YL, Chou WC, Hu LY, Hsu HM, **Wu PE**, Hou MF, Yu JC, Shen CY. Functional variants at the 21q22.3 locus involved in breast cancer progression identified by screening of genome-wide estrogen response elements. *Breast Cancer Res.* 2014;16:455.

Chu HW, Cheng CW, Chou WC, Hu LY, Wang HW, Hsiung CN, Hsu HM, **Wu PE**, Hou MF, Shen CY, Yu JC. A novel estrogen receptor-microRNA 190a-PAR-1-pathway regulates breast cancer progression, a finding initially suggested by genome-wide analysis of loci associated with lymph-node metastasis. *Hum Mol Genet.* 2014;23:355-67.

Cheng CW, Liu YF, Yu JC, Wang HW, Ding SL, Hsiung CN, Hsu HM, Shieh JC, **Wu PE**, Shen CY. Prognostic significance of cyclin D1,  $\beta$ -catenin, and MTA1 in patients with invasive ductal carcinoma of the breast. *Ann Surg Oncol.* 2012;19:4129-39.

Yu JC, Hsiung CN, Hsu HM, Bao BY, Chen ST, Hsu GC, Chou WC, Hu LY, Ding SL, Cheng CW, **Wu PE**, Shen CY. Genetic variation in the genome-wide predicted estrogen response element-related sequences is associated with breast cancer development. *Breast Cancer Res.* 2011;13:R13

**Wu PE**, Shen CY. 'Hide-then-hit' to explain the importance of genotypic polymorphism of DNA repair genes in determining susceptibility to cancer. *J Mol Cell Biol.* 2011;3:59-65.

Hsu MS, Yu JC, Wang HW, Chen ST, Hsiung CN, Ding SL, **Wu PE**, Shen CY, Cheng CW. Synergistic effects of polymorphisms in DNA repair genes and endogenous estrogen exposure on female breast cancer risk. *Ann Surg Oncol.* 2010; 17:760-71.

Ding SL, Yu JC, Chen ST, Hsu GC, Hsu HM, Ho JY, Lin YH, Chang CC, Fann CSJ, Cheng CW, **Wu PE**, Shen CY. Diverse associations between ESR1 polymorphism and breast cancer development and progression. *Clin Cancer Res* 2010;16:3473-84.

Cheng CW, Yu JC, Wang HW, Huang CS, Shieh JC, Fu YP, Chang CW, **Wu PE**, Shen CY. The clinical implications of MMP-11 and CK-20 expression in human breast cancer. *Clinica Chimica Acta* 2010;411:234-241.

Yu JC, Ding SL, Chang CH, Kuo SH, Chen ST, Hsu GC, Hsu HM, Hou MF, Jung LY, Cheng CW, **Wu PE**, Shen CY. Genetic susceptibility to the development and progression of breast cancer associated with polymorphism of cell-cycle and ubiquitin ligase genes. *Carcinogenesis* 2009;30:1562-70.

Gaudet MM, et al. (Shen CY is listed as the 95th among 117 authors) Five Polymorphisms and Breast Cancer Risk: Results from the Breast Cancer Association Consortium. *Cancer Epidemiol Biomarker Prev* 2009;18:1610-1616.

Udler MS, et al. (Shen CY is listed as the 23rd among 35 authors). FGFR2 variants and breast cancer risk: fine-scale mapping using African American studies and analysis of chromatin conformation. *Human Mol Genet* 2009;18:1692-703.

Ahmed S, et al. (Shen CY is listed as the 119th among 139 authors). Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. *Nat Genet* 2009;41:585-590.

Dunning AM, et al. (Shen CY is for TWBCS listed in the authors). Association of ESR1 gene tagging SNPs with breast cancer risk. *Human Mol Genet* 2009;18:1131-1139.

Ding SL, Yu JC, Chen ST, Hsu GC, Kuo SJ, Lin YH, **Wu PE**, Shen CY. Genetic variants of BLM interact with RAD51 to increase breast cancer susceptibility. *Carcinogenesis* 2009;30:43-9.

Chou WC, Wang HC, Wong FH, Ding SL, **Wu PE**, Shieh SY, Shen CY. Chk2-dependent phosphorylation of XRCC1 in the DNA damage response promotes base excision repair. *EMBO J.* 2008; 27:3140-50.

Cheng CW, Yu JC, Huang CS, Shieh JC, Fu YP, Wang HW, **Wu PE**, Shen CY. Polymorphism of cytosolic serine hydroxymethyltransferase, estrogen and breast cancer risk among Chinese women in Taiwan. *Breast Cancer Res* 2008;11:145-55.

Huang CS, Shen CY, Wang HW, **Wu PE**, Cheng CW. Increased expression of SRp40 affecting CD44 splicing is

associated with the clinical outcome of lymph node metastasis in human breast cancer. *Clin Chim Acta.* 2007;384:69-74.

Bau DT, Mau YC, Ding SI, **Wu PE**, Shen CY. DNA double-strand-break repair capacity and risk of breast cancer. *Carcinogenesis* 2007;28:1726-30.