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- Wei-Chung Cheng

**Title**

- Assistant Professor

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**Resume**

- Degree:  
2003-2011 Ph.D., Department of Biomedical Engineering and Environmental Sciences, National Tsing-Hua University. Research topic: The database construction for microarray clinical meta-analysis and inter/intra individual variance gene expression study. Advisor: Dr. Ian C. Hsu
- Experiences:  
2011-2014 Postdoctoral Fellow, Institute of Biomedical Informatics, National YangMing University. Research topic: The database construction for cancer driver genes and miRNAs. Advisor: Dr. Hsei-Wei Wang.  
2014-2015 Assistant Research Fellow, Research Center of Tumor Medical Science, China Medical University  
2015-2016 Assistant Professor, Graduate Institute of Cancer Biology, China Medical University  
2015- Assistant Professor, Graduate Institute of Biomedical Science, China Medical University

**Fields of Specialty**

- Molecular biology
- Genomics
- Bioinformatics

## Research

- Cancer genomics
- Next generation sequencing
- Biological database

## Paper & Project

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1. Lai HC, Yeh CC, Jeng LB, Huang SF, Liao PY, Lei FJ, **Cheng WC**, Hsu CL, Cai X, Chang C\*, Ma WL\*. Androgen receptor mitigates postoperative disease progression of hepatocellular carcinoma by suppressing CD90+ populations and cell migration and by promoting anoikis in circulating tumor cells. *Oncotarget* 2016 Jun (Epub ahead of print)
2. Chung IF, Chen CY, Su SC, Li CY, Wu KJ, Wang HW\*, **Cheng WC\***. DriverDBv2: a database for human cancer driver gene research. *Nucleic Acids Res.* 2016 Jan 4;44(D1):D975-9.
3. **Cheng WC**, Chung IF, Tsai CF, Huang TS, Cheng CY, Wang SC, Chang TY, Sun HJ, Chao YC, Cheng CC, Wu CW and Wang HW. YM500v2: A small RNA sequencing (smRNA-seq) database for human cancer miRNome research. *Nucleic Acids Research*, 2015 JAN:43(D1):D862-867
4. Wang HW, Sun HJ, Chang TY, Lo HH, **Cheng WC**, Tseng GC, Lin CT, Chang SJ, Pal N, and Chung IF. Discovering monotonic stemness marker genes from time-series stem cell microarray data. *BMC Genomics*, 2015 JAN:16 Suppl 2:S2
5. Tsai YP, Chen HF, Chen SY, **Cheng WC**, Wang HW, Shen ZJ, Song C, Teng SC, He C, Wu KJ. TET1 regulates hypoxia-induced epithelial-mesenchymal transition by acting as a co-activator. *Genome Biol.* 2014 DEC:15(12):513.
6. Huang HN, Chen SY, Hwang SM, Yu CC, Su MW, Mai W, Wang HW, **Cheng WC**, Schuyler SC, Ma N, Lu FL, Lu J. miR-200c and GATA binding protein 4 regulate human embryonic stem cell renewal and differentiation. *Stem cell research.* 2014 MAR:12(2):338-353
7. Chen KH, Wang KJ, Tsai ML, Wang KM, Adrian AM, **Cheng WC**, Yang TS, Teng NC, Tan KP, Chang KS. Gene selection for cancer identification: a decision tree model empowered by particle swarm optimization algorithm. *BMC Bioinformatics.* 2014, FEB:15(1):49.
8. **Cheng WC**, Chung IF, Chen CY, Sun HJ, Fen JJ, Teng WC, Chang TY, Wong TT\*, Wang HW\*. DriverDB: A exome sequencing (exome-seq)

database for cancer driver gene identification. *Nucleic Acids Research*, 2014, JAN:42(D1):D1048-1054

9. **Cheng WC**, Chung IF, Huang TS, Chang ST, Sun HJ, Wong TT\*, Wang HW\*. YM500: A small RNA Sequencing (smRNA-Seq) database for miRNA research. *Nucleic Acids Research*, 2013, JAN:41(D1): D285-D294.
10. Li CY, Chiang CS, **Cheng WC**, Chen CR, Shu WY, Tsai ML, Huang CL, Chang HZ, Hseu RS, Chang CW, Fang SH, Hsu IC. Gene expression profiling of dendritic cells in different physiological stages under *Cordyceps sinensis* treatment. *PLoS One*, 2012, JUL:7(7): e40824.
11. **Cheng WC**, Shu WY, Li CY, Tsai ML, Chang CW, Chen CR, Wang TH, Hsu IC. Inter- and intra-individual variance of gene expression in clinical studies. *PLoS One*, 2012, JUN:7(6):e38650.
12. Chen CR, Shu WY, Tsai ML, **Cheng WC**, Hsu IC. THEME: a web tool for loop-design microarray data analysis. *Computers in Biology and Medicine*, 2012, FEB:42(2): 228-234.
13. Chang CW, **Cheng WC**, Chen CR, Shu WY, Tsai ML, Huang CL, Hsu IC. Identification of Human Housekeeping Genes and Tissue-Selective Genes by Microarray Meta-Analysis. *PLoS One*, 2011, JUL:6(7): e22859.
14. **Cheng WC**, Chang CW, Chen CR, Tsai ML, Shu WY, Li CY, Hsu IC. Identification of Reference Genes across Physiological States for qRT-PCR through Microarray. *PLoS One*, 2011, FEB:6(2): e17347.
15. Li CY, Chao LP, Wang SC, Tsai ML, Chang HZ, Fang SH, Liao PC, Ho CL, Chen ST, **Cheng WC**, Chiang CS, Hua KF, Hsu IC. Honokiol Inhibits LPS-induced Maturation and Inflammatory Response on Human Monocyte-derived Dendritic Cells. *Journal of Cellular Physiology*. 2010, SEP:226(9): 2338-2349.
16. **Cheng WC**, Tsai ML, Chang CW, Huang CL, Chen CR, Shu WY, Lee YS, Wang TH, Hong JH, Li CY, Hsu IC. Microarray Meta-analysis Database (M2DB): A Uniformly Pre-processed, Quality Controlled, and Manually Curated Human Clinical Microarray Database. *BMC Bioinformatics*. 2010, AUG:10;11(1):421.