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## BIOGRAPHICAL SKETCH

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NAME in English <b>Tingwen Chen</b>	POSITION TITLE <b>Assistant Research Fellow</b>
NAME in Chinese <b>陳亭蚊</b>	

EDUCATION/TRAINING			
INSTITUTION AND LOCATION	DEGREE (if applicable)	MM/YY	FIELD OF STUDY
Department of Life Science, National Yang-Ming University, Taipei, Taiwan	B.S.	09/2014	Biology
Institute of BioMedical Informatics, National Yang-Ming University, Taipei, Taiwan	Ph.D.	05/2011	Bioinformatics

## A. Positions and Honors

### Positions and Employment

Summer intern in Vita Genomics (July. 2005 – Sep. 2005)

Post-doctoral Fellow, Head & Neck Surgery, The University of Texas MD Anderson Cancer Center (Apr. 2015 – Oct. 2015)

Post-doctoral Fellow, Molecular Medicine Research Center, Chang Gung University (Sep. 2011 – present)

## B. Selected Peer-reviewed Publications (2012-2017) (in chronological order)

### Referred papers (\*first/equal contribution or corresponding author)

1. **Chen TW\***, Gan RC, Fang YK, Chien KY, Liao WC, Chen CC, Wu TH, Chang IY, Yang C, Huang PJ et al (2017, Sep). FunctionAnnotator, a versatile and efficient web tool for non-model organism annotation. Scientific Reports.
2. **Chen TW\***, Lee CC, Liu H, Wu CS, Pickering CR, Huang PJ, Wang J, Chang IY, Yeh YM, Chen CD et al (2017, Sep). APOBEC3A is an oral cancer prognostic biomarker in Taiwanese carriers of an APOBEC deletion polymorphism. Nature Communications.
3. Sablok G, **Chen TW\***, Lee CC, Yang C, Gan RC, Wegrzyn JL, Porta NL, Nayak KC, Huang PJ, Varotto C et al (2017, Apr). ChloroMitoCU: Codon patterns across organelle genomes for functional genomics and evolutionary applications. DNA RESEARCH.
4. Gan RC, **Chen TW\***, Wu TH, Huang PJ, Lee CC, Yeh YM, Chiu CH, Huang HD, Tang P (2016, Dec). PARRoT- a homology-based strategy to quantify and compare RNA-sequencing from non-model organisms. BMC Bioinformatics, 17(Suppl 19):513.
5. Tsai KW, Leung CM, Lo YH, **Chen TW**, Chan WC, Yu SY, Tu YT, Lam HC, Li SC, Ger LP (2016, Jun). Arm Selection Preference of MicroRNA-193a Varies in Breast Cancer. Scientific Reports.
6. Chang PY, Chen CC, Chang YS, Tsai WS, You JF, Lin GP, **Chen TW**, Chen JS, and Chan EC (2016, Feb). MicroRNA-223 and microRNA-92a in stool and plasma samples act as complementary biomarkers to increase colorectal cancer detection. Oncotarget, 10.18632/oncotarget.7119.
7. Chen YC, **Chen TW**, Su MC, Chen CJ, Chen KD, Liou CW, Tang P, Wang TY, Chang JC, Wang CC, Lin HC, Chin CH, Huang KT, Lin MC, Hsiao CC. (2015, Dec). Whole Genome DNA Methylation Analysis

- of Obstructive Sleep Apnea: IL1R2/ NPR2/ AR/ SP140 Methylation and Clinical Phenotype. *SLEEP*, 8. **Chen TW**, Gan RC, Chang YF, Liao WC, Wu TH, Lee CC, Huang PJ, Lee CY, Chen YY, Chiu CH et al (2015, Aug). Is the whole greater than the sum of its parts? De novo assembly strategies for bacterial genomes based on paired-end sequencing.. *BMC Genomics*, 16:648.
9. Huang PJ, Lee CC, Tan BC, Yeh YM, Huang KY, Gan RC, **Chen TW**, Lee CY, Yang ST, Liao CS et al (2015, Feb). Vanno: a visualization-aided variant annotation tool. *Human mutation*, 36(2):167-74.
10. Huang PJ, Lee CC, Tan BC, Yeh YM, Julie Chu L, **Chen TW**, Chang KP, Lee CY, Gan RC, Liu H et al (2015, Jan). CMPD: cancer mutant proteome database. *Nucleic acids research*, 43 (D1): D849-D855..
11. Tsai KW, Hu LY, **Chen TW**, Li SC, Ho MR, Yu SY, Tu YT, Chen WS, Lam HC (2015, Jan). Emerging role of microRNAs in modulating endothelin-1 expression in gastric cancer.. *Oncology reports*, 33(1):485-93.
12. Chou LF, **Chen TW**, Ko YC, Pan MJ, Tian YC, Chiu CH, Tang P, Hung CC, Yang CW (2014, Nov). Potential Impact on Kidney Infection: Whole Genome Analysis for *Leptospira santarosai* serovar Shermani. *Emerg Microbes Infect*, 3(11):e82.
13. **Chen TW\***, Li HP, Lee CC, Gan RC, Huang PJ, Wu TH, Lee CY, Chang YF, Tang P (2014, Jun). ChIPseek, a web-based analysis tool for ChIP data.. *BMC Genomics*.
14. Leung CM, **Chen TW**, Li SC, Ho MR, Hu LY, Liu WS, Wu TT, Hsu PC, Chang HT, Tsai KW (2014, Mar). MicroRNA expression profiles in human breast cancer cells after multifraction and single-dose radiation treatment. *Oncology reports*, 31(5):2147-56.
15. Leung CM, Li SC, **Chen TW**, Ho MR, Hu LY, Liu WS, Wu TT, Hsu PC, Chang HT, Tsai KW (2014, Mar). Comprehensive microRNA profiling of prostate cancer cells after ionizing radiation treatment.. *Oncology reports*, 31(3):1067-78.
16. Chen WS, **Chen TW\***, Yang TH, Hu LY, Pan HW, Leung CM, Li SC, Ho MR, Shu CW, Liu PF et al (2013, Oct). Co-modulated behavior and effects of differentially expressed miRNA in colorectal cancer. *BMC Genomics*.
17. Huang PJ, Yeh YM, Gan RC, Lee CC, Chen TW, Lee CY, Liu H, Chen SJ, Tang P (2013, Aug). CPAP: Cancer Panel Analysis Pipeline. *Human mutation* , 34(10):1340-6.
18. **Chen TW\***, Gan RC, Wu TH, Huang PJ, Lee CY, Chen YY, Chen CC, Tang P (2012, Dec). FastAnnotator--an efficient transcript annotation web tool.. *BMC Genomics*.
19. **Chen TW\***, Gan RR, Wu TH, Lin WC, Tang P (2012, Jun). VIP DB--a viral protein domain usage and distribution database. *Genomics*, 100(3):149-56.
20. **Chen TW\***, Wu TH, Ng WV, Lin WC (2011, Nov). Interrogation of alternative splicing events in duplicated genes during evolution.. *BMC Genomics*.
21. **Chen TW\***, Wu TH, Ng WV, Lin WC (2010, Oct). DODO: an efficient orthologous genes assignment tool based on domain architectures. Domain based ortholog detection. *BMC bioinformatics*.

## C. Research Support

### Ongoing Research Support

MOST 106-2311-B-182-005, Ministry of Science and Technology 2017/7/1- 2018/6/30

### Completed Research Support (2006-2010)