Chung-Yung Chen

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Associate Professor, Department of Bioscience
Epigenomics, SNP, Stem cells genomics, Bioinformatics

◆ Research Interests

- ◆ Chung-Yung is an associate professor in the genomic area of the Department of Bioscience Technology. Courses taught include Concept of Computer Science, Genetics, Perl for Bioinformatics, Bioinformatics, Database for Bioinformatics, Advance Genetics, Molecular Biology.

- ◆ Chung-Yung's research is related to human genome study and also linked to human stem cells. Research topics include epigenetic studies in human hematopoietic stem cell differentiation controlled by gene methylation, single nucleotide polymorphism study related toxin by anti-cancer drug, the RNA structure prediction by bioinformatics, and synthetic genomic using bacterial special mobile transfer system.

◆ Selected Publications

- ◆ Comparative Genome Analysis of *Vibrio vulnificus,* a Marine Pathogen. **Chung-Yung Chen**, Keh-Ming Wu, Yo-Cheng Chang, Chuan-Hsiung Chang, Hui-Chi Tsai, Tsai-Lien Liao, Yen-Ming Liu, Hsiang-Ju Chen, Arthur Bo-Ting Shen, Jian-Chiuan Li, Teh-Li Su, Chung-Ping Shao, Chung-Te Lee, Lien-I Hor, and Shih-Feng Tsai. Genome Research13, 2577-2587.2003.

- ◆ IRSS: a web-based tool for automatic layout and analysis of IRES secondary structure prediction and searching system in silico. Tzong-Yuan Wu, Chi-Chun Hsieh, Jun-Jie Hong, **Chung-Yung Chen** and Yuh-Show Tsai. BMC Bioinformatics 10, 2009.

- ◆ Human papillomavirus genotyping and characterization in North Taiwan. Chin-Hung Wang, Ronald Garingalao Garvilles, and **Chung-Yung Chen**. Journal of Medical Virology 82: 1416-1423, 2010.

- ◆ Biochemical and genetic insights into asukamycin biosynthesis. Zhe Rui, Kateřina Petříčková, František Škanta, Stanislav Pospíšil, Yanling Yang, **Chung-Yung Chen**, Shih-Feng Tsai, Heinz G. Floss, Miroslav Petříček, Tin-Wein Yu. J. Biol. Chem. 285: 24915-24924, 2010.

◆ Recent Applications of Research

- ◆ Epigenetics related to stem cell study, stem cell mechanism study, stem cell therapy, and bioinformatic tools for RNA and DNA patterns.