Joseph, Ta-Chien Tseng
Associated Professor
Institute of Bioinformatics, College of Bioscience and Biotechnology
National Cheng-Kung University.
Tel: 886-6-2757575 ext. 31206
Email: tctseng@mail.ncku.edu.tw

EDUCATION

1991-1998 **Ph.D**. Department of Life Science, Molecular and Cellular Biology Unit, National Tsing-Hua University, Taiwan.

1985-1989 **B.S**. Department of Electrical and Control Engineering
National Chiao -Tung University, Taiwan.

FIELDS OF SPECIALITY

Bioinformatics, Translatome sequencing, exome sequencing, transcriptome sequencing, microRNA profiling, translational regulation, Molecular Biology, System Biology.

EXPERIENCE

2012-Present **Deputy Director**, Center for Genomic Medicine, Nat'l Cheng-Kung University

2011-Present **Associated Professor**, Institute of Bioinformatics and Biosignal Transduction, College of Bioscience and Biotechnology, Nat'l Cheng-Kung University

2008-2011 **Assistant Professor**, Institute of Bioinformatics, College of Bioscience and Biotechnology, Nat'l Cheng-Kung University

2003-2008 **Research Assistant Professor**, Program for promoting academic excellence of university, Department of Pharmacology, Nat'l Cheng-Kung University

2000-2002 **R&D Associated Director**, AsiaGen Corporation

1999-2000 **Postdoctoral Fellow**, Department of Biomedical Research,
St. Elizabeth's Medical Center of Boston, Massachusetts, USA.
Advisor: Dr. Athar Chishti

1998-1999 **Postdoctoral Fellow**, Institution of Biomedical Sciences,
Academia Sinica, Taipei, Taiwan. Advisor: Dr. Tang K., Tang

PUBLICATIONS

Chang CW, Lee WB, Chen-Deng A, Liu T, **Tseng JT**, Chang D. (2015) Light-RCV: a lightweight read coverage viewer for next generation sequencing data. **BMC Bioinformatics.** 16 Suppl 18:S11.

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PATENT

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Application of Ribosome Profiling technology in identifying the actionable biomarker for clinical diagnosis

Joseph T. Tseng*
Center of Genomic Medicine, Institute of Bioinformatics and Biosignal Transduction, and Department of Biotechnology and Bioindustry Sciences, College of Bioscience and Biotechnology, Nat'l Cheng-Kung University, Tainan, Taiwan

It is become increasingly clear that not all biology questions can be answered just by looking at the transcriptome. It is rather the proteome, i.e. the complete set of proteins encoded by genome, which determines the cellular phenotype and the plasticity of cells in response to external signals. Besides, from the study of gene expression in yeast and mammalian cells, a striking lack of correlation between the steady-state levels of mRNAs, as determined using microarrays, and the proteins (i.e. proteomes) encoded by those mRNAs was reported. Therefore, to profiling the mRNAs engaged in the translation process, named as tanslatome analysis, may provide more detailed information about the cell physiology or fate.

Ribosome profiling or ribo-seq is a new technique that provide genome-wide information on protein synthesis in vivo, and filled the technological gap existing between our abilities to quantify the transcriptome and the proteome. The applications of ribosome profiling were used to identify the translation star sites, the distribution and the speed of translating ribosome, and to study the effects of microRNAs on translation. This technology already dramatically change our understanding of translational control. In my lab, we have successfully established and modified this technology to get a more high quality data with lower cost. And the translatome result of different kinds of colon polyps were analyzed. From the results, we identity several good biomarkers for further validation and highlight the importance of Ribo-Seq technology in biomarker discovery.