

## **Principal Investigator**

**Name :** Dr. Wei, Chia Lin  
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## **Employment History**

2002-date Sr. Group Leader Clone Production & Management, Genome Institute of Singapore.  
Genome wide transcriptome cloning and sequencing

2002 Group Leader, Molecular Biology, Odyssey Pharmaceuticals. R&D, HTP clone production platform. Mammalian Protein Complementation Assays.  
Worked with Dr. Anthony Carrano V.P. of Research

1998-2002 Group Leader, Senior Scientist, Genomics, Large Scale Biology Corp. R&D, cDNA library technology development & target gene discovery.  
Worked with Dr. Yijun Ruan, Director.

1990-1994 Research Assistant, University of California at Davis.  
Cloning of eukaryotic translational initiation factor eIF-1A from Homo sapiens and S cerevisiae. Analysis of its role in protein synthesis and cell growth using biochemical and genetic approaches.  
Worked with Dr. John W. B. Hershey

1988-1989 Research Assistant, Natl. Acad. Sci., Taiwan R. O. C.  
Studied the interaction between the promoter region of the large surface protein gene of human hepatitis B virus and a liver specific nuclear factor by site-directed mutagenesis.  
Worked with Dr. Ling-Pai Ting.

## **Research Interests**

My research interest is to apply new genomic technologies and high throughput automation/sequencing platform to characterize gene expression in complex biological systems. Within the cloning and sequencing group, as part of overall goals to understand the transcriptome dynamics and complexity, my focus is to integrate our highly sophisticated library production capability and high throughput clone processing and sequencing operation to characterize transcriptomes in stem cells, cancer biology and model organisms. In addition to all the coding transcripts, we also heavily engage in the mapping of all the regulatory elements on human genome such as transcription factor binding sites in cancer and stem cells . I am also actively involving in the transcriptome data analysis, database design and data mining. With the automation platform and efficient gene discovery pipeline, we expect to extend from the transcriptome study to the high throughput functional genomic program in the near future.

## **Academic Qualifications**

1989-1994 Ph.D. Microbiology, University of California at Davis.  
Dissertation: Cloning and characterization of eukaryotic translational initiation

factor eIF-1A: Analysis of its role in protein synthesis.

Advisor: Dr. John W.B. Hershey

1984-1994 B.S. Medical Technology, National Yang-Ming University, Taiwan, R. O. C.

### **Selected Publications**

1. Wei Chia Lin, Takumi Miura, Robson Paul, Lim Sai Kiang, Xiu-qin Xu, Mathia Yu-Chuan Lee, Gupta Sanjay, Stanton, Lawrence W, Yongquan Luo, Jacqui Schmitt, Scott Thies, Wei Wang, Irina Khrebtukova, Daixing Zhou, Liu Tak Bun, Edison, Ruan Yijun, Mahendra Rao, Lim Bing, (2005) "Transcriptome Profiling of Murine and Human ES Cells reveals Divergent Paths Required to Maintain the Stem Cell State" . *Stem Cells*. 23 . 166-185
2. Ng, Patrick Wei Pern, Wei Chia Lin, Sung, Wing Kin Ken, Chiu, Kuo Ping, Lipovich Leonard, Ang Chin Chin, Gupta Sanjay, Shahab Atif, Wong Chee Hong, Ridwan Azmi, Liu Tak-Bun Edison, Ruan Yijun, (2005) "Gene identification signature (GIS) analysis for transcriptome characterization and genome annotation" . *Nature Method*. 2 . 105-111
3. Wei Chia Lin, Ng, Patrick Wei Pern, Chiu, Kuo Ping, Chee Hong Wong, Chin Chin Ang, Lipovich Leonard, Liu Tak Bun, Edison, Ruan Yijun, (2004) "5' Long serial analysis of gene expression (LongSAGE) and 3' LongSAGE for transcriptome characterization and genome annotation" . *Proc Natl Acad Sci USA*. 101 (32) . 11701-6
4. Vinsensius, B Vega S, Ruan Yijun, Liu Jianjun, Lee W.H., Wei Chia Lin, Su Yun S.T., Tang K.F., Zhang Tao, Lin S., Kolatkar, Prasanna R, Eong O.E., Ling A.E., Stanton, Lawrence W, Long P.M., Liu Tak Bun, Edison, (2004) "Mutational dynamics of the SARS corona virus in cell culture and human population." . *BMC Infectious Diseases* 4(1):32-40
5. Ruan Yijun, Wei Chia Lin, Thoreau Herve, Chia Jer-Ming, Lim Landri, Ng, Patrick Wei Pern, Zhang Tao, Chiu, Kuo Ping , Vinsensius, B Vega S, Liu Tak Bun, Edison, (2003) "Genome Sequence Analysis of Coronavirus Isolated from Singapore SARS Patients" . WHO SARS Aetiology Site
6. Ruan Yijun, Wei Chia Lin, Ling Ai Ee, Vinsensius, B Vega S, Thoreau Herve, Su Yun Se Thoe, Chia Jer-Ming, Ng, Patrick Wei Pern, Chiu, Kuo Ping, Lim Landri, Zhang Tao, Chan Kwai Peng, Lynette Oon Lin Ean, Ng Mah Lee, Leo Yee Sin, Ng, Lisa Fong-Poh, Ren Ee Chee, Stanton, Lawrence W, Long M. Philip, Liu Tak Bun, Edison, (2003) "Comparative full-length genome sequence analysis of 14 SARS coronavirus isolates and common mutations associated with putative origins of infection" . *Lancet*. 361 (9371) . 1779-85
7. Wei Chia Lin, (2002) "From Genome to Transcriptome to Proteome." . *Minireview. OMICS*. 6 (1): 131-134.

8. Wei Chia Lin, Carboy-Newcomb C., Steller H., (1999) "The pro-apoptotic function of Drosophila Hid is conserved in mammalian cells" . Proc. Natl. Acad. Sci. 96 (9): 4936-4941
9. Wei Chia Lin, John W. B. Hershey, (1995) "Characterization of yeast translation factor 1A and cloning of its essential gene." . J. Biol. Chem. 270 (39): 22788- 227

**Honors And Awards**

1994 Cabot Award, MIT

1995 1995 Lucille P. Markey Fellowship, MIT