

# Shih-Feng Tsai



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## Education

Ph.D. Division of Human Genetics, Mt. Sinai School of Medicine, City  
University of New York, USA (1987)

M.D. Taipei Medical College, Taiwan (1981)

## Professional Experiences

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|---------------|---|
| 2017- present | Director, Department of Research Planning and Development, National Health Research Institutes, Taiwan  |
| 2017-2020     | Principle Investigator, Flagship Program of Precision Medicine for AsiaPacific Biomedical Silicon Valley  |
| 2010- present | Distinguished Investigator, Institute of Molecular and Genomic Medicine (Formerly Institute of f Molecular and Genomic Medicine), National Health Research Institutes, Taiwan |
| 2000-2010     | Investigator, Division of Molecular and Genomic Medicine, National Health Research Institutes, Taiwan   |
| 2000-2007     | Director, Division of Molecular and Genomic Medicine, National Health Research Institutes, Taiwan   |
| 1997- present | Professor, Department of Life Sciences and Institute of Genomic Sciences (Formerly Institute of Genetics), National Yang-Ming University, Taiwan                              |
| 1991-1997     | Associate Professor, Institute of Genetics, National Yang-Ming University, Taiwan   |

1988-1990	Fellow, Department of Pediatrics, Harvard Medical School, U.S.A
1988-1990	Fellow, Division of Hematology/Oncology, Children's Hospital, U.S.A.
1987-1988	Fellow, Division of Medical Genetics, Mt. Sinai Medical Center, U.S.A.

### **Honors & Awards**

2006	The Outstanding Research Award, NSC
2009	NHRI Research Achievement Award

### **Research Interests**

Research areas include human genetic disorders, cancers, and microbial genomics. My laboratory has applied genetic mapping and DNA sequencing to identify genes/alleles associated with human diseases. Using high-throughput genomic methods, my laboratory has investigated the genetic basis of liver cancer and lung cancer, and we have conducted whole-genome sequencing projects on bacterial pathogens, including *Vibrio vulnificus* and *Klebsiella pneumoniae*. The sequence information can help understand the evolution of microbial organisms and the molecular basis of bacterial virulence and antimicrobial resistance.