
Chien-Lin Lin, Ph.D.

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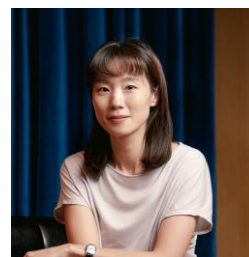
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**Education**

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| 1998-2002 | B.S., Zoology, National Taiwan University, Taiwan |
| 2002-2003 | M.S., Neuroscience, University College London, United Kingdom |
| 2005-2012 | Ph.D., Molecular Medicine, University of Massachusetts Medical School, USA |

Research and Professional Positions Held in Chronological Sequence

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| 2003-2005 | Research Associate, Institute of Biomedical Sciences, Academia Sinica, Taiwan |
| 2012-2016 | Postdoctoral Research Associate, Brown University, USA |
| 2017-present | Assistant Research Fellow, Institute of Molecular Biology, Academia Sinica, Taiwan |
| 2019-present | Jointly Appointed Assistant Professor, Genome & Systems Biology Degree Program, National Taiwan University, Taiwan |

Research Interests

The human coding sequences are encoded by 1% of the genome. My career aims to answer the question of how this tiny amount of genetic information is precisely expressed and regulated among the huge pool of material. Particularly, I long to know how pre-mRNA splicing and RNA destiny is controlled. My career started from studying translation regulation mediated by specific element in the mRNA 3' untranslated region (UTR) that is recognized by an RNA-binding protein CPEB1. Further, my research applied genomics and comparative genomics to understand conserved RNA splicing mechanism involving both sequence and structural cues. With the multidisciplinary training combining biochemistry, genomics and computational biology, I aim to decipher the rules of gene expression by systematic deduction from ample observations. Therefore, data mining and high throughput assays are essential for unbiased investigation. Massively parallel splicing minigenes are used to test the contribution of intronic and splice site sequences, and massively parallel reporter assays are to test various UTRs that determine mRNA stability and translation efficiency. Statistical learning is used to grab the meaningful factors making the biological decisions. I further extend the research to the disease-associated regulation, and use the underlying decisive rules to assess the deleterious effect of mutations. The predictive results are supported by the association with human diseases reported in genomic databases. My research goal is to identify the fundamental rule of gene regulation, and contribute to the genetic interpretation for precision medicine.

Major Honors and Awards

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| 1999 | National Taiwan University Presidential Award |
| 2001 | National Science Council College Student Research Scholarship |
| 2003 | Universities UK Overseas Research Students Awards |

2006	University of Massachusetts Medical School Dean's Award for Outstanding Achievement in the Core Curriculum
2007	The 22nd Joint Annual Conference of Biomedical Sciences Honorable Award of Poster Exhibit
2009	Ministry of Education Studying Abroad Scholarship
2014	Boston Taiwanese Biotechnology Symposium Oral Presentation Award
2015	Boston Taiwanese Biotechnology Symposium Oral Presentation Award
2015	Brown University BioMed Postdoc Travel Award
2016	Boston Taiwanese Biotechnology Symposium Oral Presentation Award
2017-2019	Academia Sinica Initial Employment Academic Research Grants
2017-2020	Ministry of Science and Technology Talented Scholar Fellowship
2020-2023	National Health Research Institutes Career Development Award
2020-2022	Ministry of Science and Technology Outstanding Young Scholar Research Grant
2020	The foundation for the Advancement of Outstanding Scholarship Young Scholars' Creativity Award