

## Curriculum Vitae

**Chia-Lin WEI, PhD**

**CONTACT INFORMATION**

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**PRESENT POSITION**

Professor and Director, Genome Technologies, The Jackson Laboratory

**EDUCATION**

1984-1989 B.S. Medical Technology, National Yang-Ming University, Taiwan  
1989-1994 Ph.D. Microbiology University of California, Davis

**EMPLOYMENT**

2016 – The Jackson Laboratory  
2010 - 2016 Senior Staff Scientist, Genomics Division, LBNL  
Head, Production Sequencing,  
Group Lead, Sequencing Technology,  
Member of Strategic Management Team,  
2009 - 2010 Associate Professor, Department of Biological Sciences  
National University of Singapore  
2003 – 2010 Senior Group Leader, Genome Technology and Biology  
Genome Institute of Singapore  
2002 – 2003 Group Leader, Cloning and Sequencing, Genome Institute of  
Singapore  
2002 Group Leader, Molecular Biology, Odyssey Pharmaceuticals  
1998 – 2002 Scientist, then Group Leader, Genomics, Large Scale Biology Corp.  
1994 – 1997 Postdoctoral Fellow, Department of Biology  
Massachusetts Institute of Technology

**AWARD AND RELATED PROFESSIONAL EXPERIENCES**

<b>Organizer and Chair</b>	Annual international long-read sequencing workshop (longread.jax.org) and conferences related to sequencing, epigenomics, genome technology, JGI annual Genome Technology workshop
<b>Grant Reviewer</b>	Netherlands National Grant for Gene Regulation Consortium WellcomeTrust application for investigator awards
<b>Reviewer</b>	Genome Research, PLoS Biology, Nature, Cell, PLoS Genetics, Nucleic Acid Research, Nature Genetics, Nature Method, Scientific Reports, Genome Biology ... etc
<b>Editorial Board</b>	Frontiers, Translational Cancer Research. Stem Cells International ( <a href="http://www.hindawi.com/journals/sci/">http://www.hindawi.com/journals/sci/</a> )

## **Scientific Advisory Board** eGenesis, Inc.

- 2006 Singapore National Science Award
- 2014 Thomson Reuters Highly Cited Researcher (world's most influential scientific minds 2014)
- 2015 Distinguished chair professor Research Center for Tumor Medical Science, China Medical University (CMU), Taiwan.
- 2015 Emerging leader nomination, Leadership development program at LBNL
- 2016 International Talent Acceleration Program Award from Education Ministry Taiwan.
- 2019 Highly Cited Researchers by the Clarivate Analytics Web of Science Group

## **PATENTS AND INVENTION DISCLOSURE**

1. Method for generating full-length coding sequence cDNA libraries. Patent application No. 00801.0206.
2. Colony array-based cDNA library normalization by hybridizations of complex RNA probes and gene specific probes. Patent application No. 00801.0197.
3. Method 5' and 3' SAGE: Patent P015405GB. Awarded European, Japan, United States of America
4. Detection of severe acute respiratory syndrome by the polymerase chain reaction. Patent application No. 60/464,965.
5. Identification of genetic variations among SARS-CoV isolates. Patent application No. 60/466056 and 60/468062.
6. Method for Gene Identification Signature (GIS) Analysis. Patent Awarded. US Patent application No. 10/664,234. China, Taiwan, Canada, Japan, United States of America, and Europe
7. Method of diagnosing SARS corona virus infection. PCT/SG2004/000174.
8. Invention disclosure: Natural fusion genes and proteins created by trans-splicing events in embryonic stem cells and their utilities in studying and manipulating stem cell properties.
9. Invention disclosure: The use of PMMV and other abundant fecal-borne viruses as indicators to monitor sewage contamination.
10. Method of processing and genome mapping of ditag sequences. US Patent 8,428,882
11. Nucleic Acid Interaction Analysis: United States of America, Singapore, Indian, European, Japan.
12. Agents for enhancement of production of biofuel precursors in microalgae. U.S Patent application US Patent App. 15/243,896 Patent Number 10155954 (issue date 12/18/2018), Patent number 10,472,643 (issue date 11/12/2019)
13. Methods for high resolution detection of structural variation in a genome U.S. Provisional Application. Ref No.: 10543/006168-US0. US20190080045A1
14. Methods for multiplex chromatin interaction analysis by droplet sequencing with single molecule precision. US Patent App. 16/233,860. US20190214106A1
15. Extrachromosomal DNA identification and methods of use. US Patent Provisional.
16. Methods for detecting regulatory elements in the genomes: gene transcription enhancers and repressors. US Provisional Application No. 62/980,342

17. Subgenomic RNAs as indicators of disease severity of SARS-CoV-2 infection. US Provisional Application.

**PUBLICATIONS (2016-2020)** ORCID identifier is 0000-0001-6820-0461

Complete list of published work at Google Scholar:

<https://scholar.google.com/citations?hl=en&user=ijaotPYAAAJ>

(Total citation: 28,781, hi-index: 55 and i10-index: 92)

1. Sayadi A, Jeyakani J, Seet SH, Wei CL, Bourque G, Bard FA, Jenkins NA, Copeland NG, Bard-Chapeau EA. Functional features of EVI1 and EVI1Δ324 isoforms of MECOM gene in genome-wide transcription regulation and oncogenicity. **Oncogene**. 2016 May 5;35(18):2311-21.
2. Marijke J. van Baren, Charles Bachy, Emily Nahas Reistetter, Samuel O. Purvine, Jane Grimwood, Sebastian Sudek, Hang Yu, Camille Poirier, Thomas J. Deerinck, Alan Kuo, Igor V. Grigoriev, Chee-Hong Wong, Richard D. Smith, Stephen J. Callister, **Chia-Lin Wei**, Jeremy Schmutz and Alexandra Z. Worden. Evidence-based green algal genomics reveals marine diversity and ancestral characteristics of land plants. **BMC Genomics**. 2016;17:267.
3. Waltman PH, Guo J, Reistetter EN, Purvine S, Ansong CK, van Baren MJ, Wong CH, **Wei CL**, Smith RD, Callister SJ, Stuart JM, Worden AZ. Identifying aspects of the post-transcriptional program governing the proteome of the green alga *Micromonas pusilla* **PLoS One**. 2016 11(7):e0155839.
4. Gina Turco, Kaisa Kajala, Govindarajan Ramamoorthy, Chew-Yee Ngan, Andrew Olson, Shweta Deshpande, Barbara Waring, Scott Stelpflug, Patricia Klein, Shawn Kaeppler, Doreen Ware, **Chia-Lin Wei**, Peter Etchells, and Siobhan Brady. DNA Methylation and Gene Expression Regulation Associated with Vascularization in *Sorghum bicolor*. **New Phytol**. 2017 214(3):1213-1229.
5. Liang Gong, Yao-Ting Huang, Chee-Hong Wong, **Chia-Lin Wei** and Po-Yu Liu; co-corresponding author. Culture-independent analysis of liver abscess using nanopore sequencing. **PLoS One**. 2018 9;13(1):e0190853.
6. Liang Gong, Chee-Hong Wong, Wei-Chung Cheng, Harianto Tjong, Francesca Menghi, Chew Yee Ngan, Edison T. Liu, **Chia-Lin Wei**. Picky Comprehensively Detects High Resolution Structural Variants in Nanopore Long Reads. **Nature Methods** 2018 15 (6), 455-460. doi: 10.1038/s41592-018-0002-6
7. Valentina Cerrato, Sara Mercurio, Ketty Leto, Elisa Fucà, Eriola Hoxha, Sara Bottes, Miriam Pagin, Marco Milanese, Giulia Concina, Sergio Ottolenghi, **Chia-Lin Wei**, Giambattista Bonanno, Giulio Pavesi, Filippo Tempia, Annalisa Buffo and Silvia K. Nicolis. Sox2 conditional mutation in mouse causes ataxic symptoms, cerebellar vermis hypoplasia, and postnatal defects of Bergmann glia. **Glia** May 6 2018. <https://doi.org/10.1002/glia.23448>
8. Jian Guo, Susanne Wilken, Valeria Jimenez, Lisa Sudek, Chang Jae Choi, Charles Bachy, Emily Reistetter, Denis Klimov, Charles Ansong, Richard Dannebaum, David Milner, Virginia Elrod, Samuel Purvine, **Chia-Lin Wei**, Govindarajan Kunde-Ramamoorthy, Thomas Richards, Ursula Goodenough, Richard Smith, Stephen Callister, and Alexandra Worden. Specialized proteomic responses and an ancient photoprotection mechanism sustain marine green algal growth during phosphate limitation. 2018 **Nature Microbiology** 3:781 <https://doi.org/10.1038/s41564-018-0178-7>
9. Charles Bachy, Christina J. Charlesworth, Amy M. Chan, Jan F. Finke, Chee-Hong Wong, Chia-Lin Wei, Sebastian Sudek, Maureen L. Coleman, Curtis A. Suttle and Alexandra Z. Worden. Transcriptional responses of the marine green alga *Micromonas pusilla* and an infecting prasinovirus under different phosphate conditions. **Environmental Microbiology** (2018) May 11 <https://doi:10.1111/emi.14273>
10. Gong L., Wong C-H., Idol J., Ngan CY, **Wei CL**. Ultra-long Read Sequencing for Whole Genomic DNA Analysis. **J. Vis. Exp**, 2019 Mar 15;(145).

11. Roberts DS., Maurya R., Takemon Y., Vitte J., Gong L., Zhao J., Wong C-H., Slattery W., Peng K.A., Lekovic G., Schwartz M S., Bulsara K., Ngan CY, Giovannini M., and **Wei CL**. Linked-read Sequencing Analysis Reveals Tumor-specific Genome Variation Landscapes in Neurofibromatosis Type-2 (NF2) Patients. **Otol Neurotol**. 2019 Feb;40(2):e150-e159.
12. Meizhen Zheng, Simon Zhongyuan Tian, Daniel Capurso, Minji Kim, Rahul Maurya, Byoungkoo Lee, Emaly Piecuch, Liang Gong, Jacqueline Jufen Zhu, Chee Hong Wong, Chew Yee Ngan, Ping Wang, Xiaolan Ruan, Chia-Lin Wei, Yijun Ruan. Multiplex Chromatin Interaction Analysis by Droplet Sequencing with Single Molecule Precision. **Nature**. 2019 Feb;566(7745):558-562. doi: 10.1038/s41586-019-0949-1
13. Bertolini J, Favaro R, Wong C-H, Pagin M, Ngan CY, Vermunt M, Martynoga B, Barone C, Mariani J, Cardozo MJ, Tabanera N, Zambelli F, Mercurio S, Ottolenghi S, Robson P, Creighton M, Bovolenta P, Pavesi G, Guillemot F, Nicolis SK, **Wei CL**. Mapping the Global Chromatin Connectivity Network for Sox2 Function in Neural Stem Cell Maintenance. **Cell Stem Cell** 2019 24(3):462-476.
14. Jyun-Hoing Lin, Zong-Yen Wu, Liang Gong, Chee-Hong Wong, Wen-Cheng Chao, Chun-Ming Yen, Ching-Ping Wang, Chia-Lin Wei \*, Yao-Ting Huang \*, Po-Yu Liu \* Complex microbiome in brain abscess revealed by whole-genome culture-independent and culture-based sequencing. **J Clin Med**. 2019 Mar 12;8(3). pii: E351. doi: 10.3390/jcm8030351.
15. Wei CL, Nicolis SK, Zhu Y, Pagin M. Sox2-Dependent 3D Chromatin Interactomes in Transcription, Neural Stem Cell Proliferation and Neurodevelopmental Diseases. **J Exp Neurosci**. 2019 Aug 7;13:1179069519868224
16. Ngan CY, Wong CH, Tjong H, Wang W, Goldfeder R, Choi C, He H, Gong L, Lin J, Urban B, Chow J, Li M, Lim J, VPhilip V, Murray SA, Wang H, **Wei CL**. Chromatin interaction analyses elucidate the roles of PRC2-bound silencers in mouse development. **Nat Genet**. 2020 Mar;52(3):264-272.
17. Byoungkoo Lee, Jiahui Wang, Liuyang Cai, Minji Kim, Sandeep Namburi, Harianto Tjong, Yuliang Feng, Ping Wang, Zhonghui Tang, Ahmed Abbas, Chia-Lin Wei, Yijun Ruan, Sheng Li. ChIA-PIPE: A fully automated pipeline for comprehensive ChIA-PET data analysis and visualization. **Sci. Adv**. 2020 Jul 10;6(28): eaay2078.
18. Ping Wang, Zhonghui Tang, Byoungkoo Lee, Jacqueline Jufen Zhu, Liuyang Cai, Przemyslaw Szalaj, Simon Zhongyuan Tian, Meizhen Zheng, Dariusz Plewczynski, Xiaolan Ruan, Edison T. Liu, Chia-Lin Wei and Yijun Ruan. Chromatin topology reorganization and transcription repression by PML-RAR $\alpha$  in acute promyeloid leukemia. **Genome Biol**. 2020 May 11;21(1):110.
19. Miriam Pagin<sup>1</sup>, Mattias Pernebrink<sup>2</sup>, Simone Giubolini<sup>1</sup>, Cristiana Barone<sup>1</sup>, Gaia Sambruni<sup>1</sup>, Yanfen Zhu<sup>3</sup>, Matteo Chiara<sup>4</sup>, Sergio Ottolenghi<sup>1</sup>, Giulio Pavesi<sup>4</sup>, Chia-Lin Wei<sup>3</sup>, Claudio Cantù<sup>2</sup> and Silvia K. Nicolis<sup>1\*</sup>. Sox2 controls neural stem cell self-renewal through a Fos-centered gene regulatory network. **Stem Cells**. 2021 Mar 19. doi: 10.1002/stem.3373
20. Yanfen Zhu, Amit D. Gujar, Chee-Hong Wong, Harianto Tjong, Chew Yee Ngan, Liang Gong, Yi-An Chen, Hoon Kim, Jihe Liu, Meihong Li, Adam Mil-Homens, Rahul Maurya, Chris Kuhlberg, Fanyue Sun, Eunhee Yi, Ana C. deCarvalho, Yijun Ruan, Roel G.W. Verhaak and Chia-Lin Wei. Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. *Cancer Cell* (2021) 39, 1–14 May 10, doi: 10.1016/j.ccell.2021.03.006.

## **ONGOING RESEARCH SUPPORT**

1 R33 CA236681-01A1      Wei (PI)  
NIH/NCI

07/16/2020-06/30/2023

Advancing Ultra Long-read Sequencing and Chromatin Interaction Analyses for Chromosomal and Extrachromosomal Structural Variation Characterization in Cancer

Role: Principal Investigator

1 R25 HG010611-01 Wei (PI) 8/12/2019 - 5/31/2022

NIH/NHGRI

The Jackson Laboratory's Workshop on Long-Read Genomic Technologies

The goal of this project is to host an annual 4-day workshop on long-read sequencing technologies at The Jackson Laboratory for Genomic Medicine.

Role: Principal Investigator

1 R01 GM127531-01A1 Wei (PI) 2/1/2019 - 1/31/2023

NIH/NIGMS

Development of Single Molecule Chromatin Interaction Assays (smChIA) in Single Nuclei

The goal of this project is to develop a completely new system of next-generation technology for chromatin interaction assays based on the SeqLL single-molecule protein detection and DNA-sequencing platform.

Role: Principal Investigator

1 R01 CA237208-01A1 Verhaak (PI) 12/1/2019 - 1/30/2024

NIH/NCI

Extrachromosomal DNA as a Targetable Mechanism in Glioblastoma

The goal of this project is to determine the influence of extrachromosomal DNA (ecDNA) on tumor evolution and resistance and to validate a potential therapeutic strategy based on ecDNA inhibition.

Role: Co-Investigator

5 U54 DK107967-05 Ruan (PI) 9/30/2015 - 7/31/2020

NIH/NIDDK

Nucleome Positioning System for Spatiotemporal Genome Organization and Regulation

The goal of this project is the development of a Nucleome Positioning System that will provide a powerful platform for studying genomic structure in space (3D) and time (4D).

Role: Co-Investigator

5 UM1 HG009409-03 Ruan (PI) 2/1/2017 - 1/31/2021

NIH/NHGRI

Comprehensive Mapping of Long-Range Chromatin Interactions in Human and Mouse Genomes

Our major goal is to produce high quality, high resolution and comprehensive maps of long-range chromatin interactions between the structural and functional elements in human and mouse genomes.

Role: Co-Investigator

JAX-CUBE-FY19-GAC Churchill (PI) 7/15/2019 - 7/14/2021

The Jackson Laboratory Competitive Internal Awards

Cube Proof of Concept Aim 2.1. Complete transcriptome profiling of non-islet metabolic tissues in ~500 HFHS-treated DO mice

The goal of this project is to perform RNA-seq with existing frozen mouse DO tissues from the Keller et al. (Genetics, 2018) experiments, in which ~500 DO mice were sensitized on a HFHS diet.

Role: Co-Investigator