

Tingyou Wang

Feinberg School of Medicine
Northwestern University
420 E Superior St
Chicago, IL 60611
☎ phone +1 3125036580
✉ tywang@northwestern.edu

Current Position

2022–present **Research Associate**, Northwestern University Feinberg School of Medicine, USA

Education

- 2018–2021 **Postdoctoral Research Fellow**, The Hormel Institute, University of Minnesota, USA
2013–2017 **PhD. Bioinformatics and Genomics**, The University of Hong Kong, Hong Kong
2008–2011 **MSc. Bioinformatics**, China Agricultural University, Beijing, China
2003–2007 **BEng. Mechanical Design, Manufacturing and Automation**, China Agricultural University, Beijing, China

Research Interests

Data analysis and algorithm design on sequencing data
Genetic basis of systemic lupus erythematosus
Cancer genomics and immuogenomics
Gene regulation and systems biology
Machine learning, deep learning and large-scale data mining
Applications of large language models in biomedical research

Publications

- 2026 "Tumor-specific lncRNA IGF1R-AS1 trans-regulates chromatin interactions associated with oncogenic MYC signaling", Yongyong Yang[#], **Ting-You Wang[#]**, Joshua Fry[#], Yingming Li[#], Qingshu Meng[#], Qingxiang Guo, Nathan E. Patchen, Abhirami Ramakrishnan, et al. *Nature Communications*, 2026, 17(1) ([#]These authors contribute equally to this work.)
- 2026 "A genomic language model for chimera artifact detection in Nanopore direct RNA sequencing", Yangyang Li[#], **Ting-You Wang[#]**, Qingxiang Guo, Yanan Ren, Xiaotong Lu, Qi Cao, Rendong Yang. *Nature Communications*, 2026, 17(1), 1864 ([#]These authors contribute equally to this work.)
- 2025 "OctopusSV and TentacleSV: a one-stop toolkit for multi-sample, cross-platform structural variant comparison and analysis", Qingxiang Guo, Yangyang Li, **Ting-You Wang**, Abhi Ramakrishnan, Rendong Yang. *Bioinformatics*, 2025, 41(11)
- 2025 "Ketone drink enhances therapeutic efficacy in prostate cancer by targeting EZH2", Chae-hyun Yum, Richard Schaefer, Rui Wang, **Ting-You Wang**, Xiaotong Lu, Qi Liu, et al. *Oncogenesis*, 2025, 14(1), 24
- 2025 "Androgen receptor-regulated lncRNA PRCAT71 promotes AR signaling through the interaction with KHSRP in prostate cancer", Yongyong Yang, **Ting-You Wang**, Qianru Li, Jiawen Lu, Yanan Ren, Adam B. Weiner, Joshua Fry, et al. *Science Advances*, 2025, 11(15)

- 2024 "EZH2 directly methylates PARP1 and regulates its activity in cancer", Qingshu Meng, Jiangchuan Shen, Yanan Ren, Qi Liu, Rui Wang, Qiaqia Li, Weihua Jiang, Quan Wang, Yixiang Zhang, Jonathan Trinidad, Xiaotong Lu, **Tingyou Wang**, Yanqiang Li, et al. *Science Advances*, 2024, 10(48)
- 2024 "Comparative analyses of gene networks mediating cancer metastatic potentials across lineage types", Sheng Wang, Emily K Stroup, **Ting-You Wang**, Rendong Yang, Zhe Ji, *Briefings in Bioinformatics*, 2024, 25(4)
- 2022 "Chapter 5: Detecting Medium and Large Insertions and Deletions with transIndel", **Ting-You Wang** and Rendong Yang, *Variant Calling - Methods and Protocols, Humana, New York, NY, 2022, vol 2493*
- 2021 "Opposing transcriptional programs of KLF5 and AR emerge during therapy for advanced prostate cancer", Meixia Che, Aashi Chaturvedi, Sarah Munro, Samuel Pitzen, Alexander Ling, Weijie Zhang, Joshua Mentzer, Sheng-Yu Ku, Loredana Puca, Yanyun Zhu, Andries Bergman, Tesa Severson, Colleen Forster, Yuzhen Liu, Jacob Hildebrand, Mark Daniel, **Ting-You Wang** et al. *Nature Communications*, 2021, 12, 6377
- 2021 "A pan-cancer transcriptome analysis of exon splicing identifies novel cancer driver genes and neoepitopes", **Ting-You Wang**, Qi Liu, Yanan Ren, Sk. Kayum Alam, Li Wang, Zhu Zhu, Luke H. Hoepfner, Scott M. Dehm, Qi Cao, Rendong Yang, *Molecular Cell*, 2021, 81:2246-2260 e2212
Highlighted in Cancer Immunology Research, June 1, 2021
- 2021 "Integrated protocol for exon and exon-derived neoantigen identification using human RNA-seq data with ScanExon and ScanNeo", **Ting-You Wang** and Rendong Yang, *STAR Protocols*, 2021, 2, 100788
- 2021 "LncGSEA: a versatile tool to infer lncRNA associated pathways from large-scale cancer transcriptome sequencing data", Yanan Ren, **Ting-You Wang**, Leah Anderton, Qi Cao, Rendong Yang, *BMC Genomics*, 2021, 22(1):574
- 2021 "Identification of 38 novel loci for systemic lupus erythematosus and genetic heterogeneity between ancestral groups", Yong-Fei Wang, Yan Zhang, Zhiming Lin, Huoru Zhang, **Ting-You Wang**, Yujie Cao, David L Morris, et al. *Nature Communications*, 2021, 12, 772
- 2020 "ScanITD: Detecting internal tandem duplication with robust variant allele frequency estimation", **Ting-You Wang**, Rendong Yang, *GigaScience*, 2020, 9
- 2020 "RAS internal tandem duplication disrupts GTPase-activating protein (GAP) binding to activate oncogenic signaling", Andrew C Nelson, Thomas J Turbyville, Srisathyanarayanan Dharmaiah, Megan Rigby, Rendong Yang, **Ting-You Wang**, John Columbus, et al., *Journal of Biological Chemistry*, 2020, 295, 9335-9348
- 2020 "Identification of regulatory modules that stratify lupus disease mechanism through integrating multi-omics data", **Ting-You Wang**, Yong-Fei Wang, Yan Zhang, Jiangshan Jane Shen, Mengbiao Guo, Jing Yang, et al. *Molecular Therapy - Nucleic Acids*, 2020, 19, 318-329
- 2019 "ScanNeo: identifying indel derived neoantigens using RNA-Seq data", **Ting-You Wang**, Li Wang, Sk. Kayum Alam, Luke H. Hoepfner, Rendong Yang, *Bioinformatics*, 2019, 35(20), 4159-4161
- 2018 "HLA-IMPUTER: an easy to use web application for HLA imputation and association analysis using population-specific reference panels", Jiangshan Shen, Chao Yang, Yong-Fei Wang, **Ting-You Wang**, Mengbiao Guo, et al. *Bioinformatics*, 2018, 35(7), 1244-1246

- 2018 "Identification of ST3AGL4, MFHAS1, CSNK2A2 and CD226 as loci associated with systemic lupus erythematosus (SLE) and evaluation of SLE genetics in drug repositioning", Yong-Fei Wang, Yan Zhang, Zhengwei Zhu, **Ting-You Wang**, David L Morris, Jiangshan Jane Shen, et al. *Annals of the Rheumatic Diseases*, 2018, 77(7):1078-1084
- 2017 "Regulatory and evolutionary signatures of sex-biased genes on both the X chromosome and the autosomes", Jiangshan Shen, **Ting-You Wang**, Wanling Yang. *Biology of Sex Differences*, 2017, 8(1):35
- 2016 "Genome-wide association meta-analysis in Chinese and European individuals identifies ten new loci associated with systemic lupus erythematosus", David L Morris, Yujun Sheng, Yan Zhang, Yong-Fei Wang, Zhengwei Zhu, Philip Tomblason, Lingyan Chen, Deborah S Cunninghame Graham, James Bentham, Amy L Roberts, Ruoyan Chen, Xianbo Zuo, **Tingyou Wang**, Leilei Wen, Chao Yang, Lu Liu, Lulu Yang, Feng Li, Yuanbo Huang, Xianyong Yin, Sen Yang, Lars Rönnblom, Barbara G Fürtrohr, Reinhard E Voll, Georg Schett et al. *Nature Genetics*, 2016, 48, 940-946
- 2015 "Meta-analysis of GWAS on two Chinese populations followed by replication identifies novel genetic variants on the X chromosome associated with systemic lupus erythematosus", Yan Zhang, Jing Zhang, Jing Yang, Yongfei Wang, Lu Zhang, Xianbao Zuo, Liangdan Sun, Hai-Feng Pan, Nattiya Hirankarn, **Tingyou Wang**, Ruoyan Chen, Dingge Ying, et al. *Human Molecular Genetics*, 2015, 24(1), 274-284
- 2014 "Chromosome-8-Coded Proteome of Chinese Chromosome Proteome Data Set (CCPD) 2.0 with Partial Immunohistochemical Verifications", Yang Liu, Wantao Ying, Zhe Ren, Wei Gu, Yang Zhang, Guoquan Yan, Pengyuan Yang, Yinkun Liu, Xuefei Yin, Cheng Chang, Jing Jiang, Fengxu Fan, Chengpu Zhang, Ping Xu, Quanhui Wang, Bo Wen, Liang Lin, **Tingyou Wang**, Chaoqin Du et al., *Journal of Proteome Research*, 2014, 13(1), 126-136.
- 2013 "Qualitative and quantitative expression status of the human chromosome 20 genes in cancer tissues and the representative cell lines", Quanhui Wang[#], Bo Wen[#], Guangrong Yan[#], Junying Wei[#], Liqi Xie[#], Shaohang Xu, Dahai Jiang, **Tingyou Wang**, Ruo Zhou, Haiyi Zhao et al., *Journal of Proteome Research*, 2013, 12(1), 151-161. ([#]These authors contribute equally to this work.)
- 2011 "A predicted protein-protein interaction network of the filamentous fungus *Neurospora crassa*", **Ting-You Wang**, Fei He, Qi-Wen Hu, Ziding Zhang, *Molecular BioSystems*, 2011, 7, 2278-2285.

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- 2019 "Comprehensive analysis of exon splicing in human cancer", Poster presentation at the Cold Spring Harbor Laboratory meeting on Genome Informatics 2019, Cold Spring Harbor, USA
- 2018 "Indel detection from DNA and RNA sequencing of primary and advanced prostate cancer", Poster presentation at the Cold Spring Harbor Laboratory meeting on biological data science 2018, Cold Spring Harbor, USA
- 2017 "Integrative analysis of transcriptional regulation unveils regulatory modules that stratify SLE transcriptome", Poster presentation at the American Society of Human Genetics 2017 Annual Meeting, Orlando, USA
- 2016 "Hierarchical relationships among susceptibility genes, transcription factors and differentially expressed genes for systemic lupus erythematosus and signaling modules revealed by a systems approach", Poster presentation at the American Society of Human Genetics 2016 Annual Meeting, Vancouver, Canada

- 2016 "Understanding gene expression changes in Systemic Lupus Erythematosus through a systems approach", Poster presentation at the 13th International Congress of Human Genetics, Kyoto, Japan

Work experience

- 2021–2022 **Staff Researcher**, *The Hormel Institute, University of Minnesota, USA*
2017–2018 **Research Assistant I**, *The University of Hong Kong, Hong Kong*
2011–2013 **Bioinformatics engineer**, *BGI Genomics, Shenzhen, China*

Teaching experience

- 2009 Teacher Assistant for undergraduate students in the course of Bioinformatics.

Awards and scholarships

- 2020 The Eagles Telethon Post Doctoral Fellowship Award
2019 Minnesota Supercomputing Institute 2019 Annual Research Exhibition Travel Award
2018 Faculty Outstanding Research Output Award
2013-2017 Postgraduate Scholarship
2008-2009 Outstanding graduate student leader award (vice-president of CAU Graduate Student Union)
2008-2009 Outstanding academic performance scholarship

Conferences attended

- 2019 Cold Spring Harbor Laboratory meeting on genome informatics 2019, Cold Spring Harbor, USA
2018 Cold Spring Harbor Laboratory meeting on biological data science 2018, Cold Spring Harbor, USA
2017 American Society of Human Genetics 2017 Annual Meeting, Orlando, USA
2017 Genome Variation in Precision Medicine 2017, Guangzhou, China
2016 American Society of Human Genetics 2016 Annual Meeting, Vancouver, Canada
2016 The 13th International Congress of Human Genetics, Kyoto, Japan
2014 2014 East-West Alliance Global Symposia, Hong Kong
2013 Frontiers in Biomedical Research HKU 2013, Hong Kong
2012 ICG-7 & Bio-IT APAC 2012, Hong Kong SAR, China
2011 The 6th International Conference on Genomics (ICG-6), Shenzhen, China

Software developed

- ScanNeo A pipeline for identifying insertion and deletion (indel) introduced neoantigens from RNA sequencing data. <https://github.com/ylab-hi/ScanNeo>
ScanITD It performs a stepwise seed-and-realignment procedure for internal tandem duplication (ITD) detection with accurate variant allele fraction prediction. <https://github.com/ylab-hi/ScanITD>
ScanExitron A computational workflow for exon splicing identification. <https://github.com/ylab-hi/ScanExitron>

Professional Activities

Reviewer

Bioinformatics, BMC Bioinformatics, BMC Genomics, Briefings in Bioinformatics, Bioinformatics Advances, Biomolecules, Cancers, Cells, Cell Proliferation, Communications Medicine, Current Protocols, Frontiers in Artificial Intelligence, Frontiers in Genetics, Frontiers in Immunology, Gene, Genes, Genomics, Human Gene, International Journal of Molecular Sciences, Medical Microbiology and Immunology, Nucleic Acids Research, PLOS Computational Biology, PLOS ONE, PeerJ, Scientific Reports, STAR Protocols

News coverage

ACIR Making the cut: exons as a new source of neoantigens. <https://acir.org/weekly-digests/2021/april/making-the-cut-exons-as-a-new-source-of-neoantigens>

ScitoVation Discovery of a new mechanism for genetic change: exon splicing implications for carcinogenesis. <https://scitovation.com/discovery-of-a-new-mechanism-for-genetic-change-exon-splicing-implications-for-carcinogenesis/>

About me

Nationality: Chinese

Languages spoken: Chinese (native), English (fluent)

Programming languages: Python, Perl, PHP, R

Technical experience with: Git, Vim, L^AT_EX, PyTorch