

## ***Curriculum Vitae***

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### **Positions held**

Jul. 2019 Founding Director, Center for Cancer Genomics  
Northwestern University Lurie Cancer Center  
Duane and Susan Burnham Professor of Molecular Medicine  
Associate Professor of Biochemistry and Molecular Genetics  
Northwestern University Feinberg School of Medicine

Mar. 2015 – Jun. 2019 Director, Bioinformatics Division  
Institute for Personalized Medicine  
Pennsylvania State University

Oct. 2013 – Jun. 2019 Assistant Professor  
Department of Biochemistry and Molecular Biology  
Penn State College of Medicine

### **Education and training**

Oct. 2013 Postdoctoral Functional Epigenomics/Genomics  
Dr. Bing Ren's laboratory, UC San Diego, School of Medicine

May 2008 Ph.D. *Computer Science*, University of South Carolina, USA

Jul. 2000 B.A. *English*, Peking University, China

### **Honors/Awards**

2016 Leukemia Research Foundation New Investigator

2015 ISMB travel fellowship

2014 Pharmaceutical Research and Manufacturers of America (PhRMA) Research Starter Grants recipient

2008 Outstanding Graduate Student, College of Engineering and Computing, University of South Carolina

### **Editorial**

Associate Editor, *Science Advances*, handling manuscripts on epigenomics/cancer genomics/single cell.

*Ad hoc* reviewer for Nature, Nature Genetics, Nature Method, Cancer Cell, Science Immunology, Nature Communications, Cell Systems, Genome Research, Genome Biology, PloS Genetics, Bioinformatics, Cancer Research, PloS Computational Biology, eLife, Molecular Cellular Biology, RNA.

### **Grant Reviewer**

11/08/2019 NCI Special Emphasis Panel, ZCA1-TCRB-D-J2, RFA-CA-19055, Next Gen. Technologies for Next Gen Cancer Models or New Technologies for Use with NGCMs in Experiments to Accelerate Our Understanding of Cancer, **The Beau Biden Cancer Moonshot Initiative.**

10/11/2019	Ad hoc member, NIH Genomics, Computational Biology and Technology Study Section (GCAT).
07/18/2019	NIDDK Special Emphasis Panel, ZDK1-GRB-7-O4, RFA-DK-18-017: Ancillary Studies to the NIDDK Inflammatory Bowel Disease Genetics Consortium.
04/18/2019	NIDDK Special Emphasis Panel, ZDK1 GRB-J M2, Contribution of T1D Disease-associated Variants.
07/19/2018	NIDDK Special Emphasis Panel, ZDK1-GRB-7-O4, RFA-DK-17-017: Ancillary Studies to the NIDDK Inflammatory Bowel Disease Genetics Consortium.

**Peer-reviewed publications** (total citations: 7,500 times, H-index 18, i10-index 21)

1. Yali Ding\*, Bo Zhang\*, Jonathon L. Payne, ... Kimberly J. Payne, **Feng Yue#**, Sinisa Dovatz# (2019). Ikaros tumor suppressor function includes induction of active enhancers and super-enhancers along with pioneering activity. **Leukemia**, 2019. (Co-corresponding author).
2. Galip Yardimci, Hakan Ozadam, Michael E.G. Sauria, ... , Mark Gerstein, Anshul Kundaje, Qunhua Li, James Taylor, **Feng Yue**, Job Dekker, William S Noble (2019). Measuring the reproducibility and quality of Hi-C data. **Genome Biology**, 20:57.
3. Jesse Dixon, Jie Xu, Vishnu Dileep, Ye Zhan, Fan Song, ..., William Stafford Noble, Job Dekker, David M. Gilbert, **Feng Yue** (2018). Integrative Detection and Analysis of Structural Variation in Cancer Genomes. **Nature Genetics** 50, 1388–1398.
4. Yanli Wang, Bo Zhang, Lijun Zhang, Lin An, Jie Xu, Daofeng Li, Mayank NK Choudhary, Yun Li, Ming Hu, Ross Hardison, Ting Wang#, **Feng Yue#** (2018). The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions. **Genome biology**, 19:151.
5. Yan Zhang, Lin An, Jie Xu, Bo Zhang, W. Jim Zheng, Ming Hu, Jijun Tang, and **Feng Yue** (2018). Enhancing Hi-C data resolution with deep convolutional neural network HiCPlus. **Nature Communications** 9, Article number: 750.
6. Taryn E. Mockus, Colleen S. Netherby, Tarik Salameh, Heather M. Schmitz, Matthew D. Lauver, Shwetank, Yuka Imamura, James R. Broach, **Feng Yue**, and Aron E. Lukacher (2018). "CD4 T cells control homeostasis of brain-resident CD8 T cells during persistent polyomavirus infection. **PLoS Pathogen**.14(10):e1007365.
7. Tao Yang, Feipeng Zhang, Galip Gurkan Yardimci, Ross C Hardison, William Stafford Noble, **Feng Yue#**, and Qunhua Li# (2017). HiCRep: assessing the reproducibility of Hi-C data using a stratum-adjusted correlation coefficient. **Genome Research**. 27(11), 1939-1949 (**co-corresponding author**).
8. Yu Zhang, Lin An, **Feng Yue**, and Ross Hardison (2016). Jointly characterizing epigenetic dynamics across multiple human cell types. **Nucleic Acids Research** 44(14), 6721-31.
9. Xu Z, Zhang G, Duan Q, Chai S, Zhang B, Wu C, Jin F, **Yue F**, Li Y, and Hu M (2016). HiView: an integrative genome browser to leverage Hi-C results for the interpretation of GWAS variants. **BMC Res. Notes** 9: 159.
10. Joshua I. Warrick, Vonn Walter, Hironobu Yamashita, ... , **Feng Yue**, Tejaswi Iyyanki, Yuka I. Kawasawa, Matthew Kaag, Wansong Guo, Jay D. Raman, Joo-Seop Park & David J. DeGraff (2016). FOXA1, GATA3 and PPAR $\gamma$  Cooperate to Drive Luminal Subtype in Bladder Cancer: A Molecular Analysis of Established Human Cell Lines. **Sci. Rep.** 6, Article number: 38531.

11. Allen Wang\*, **Feng Yue\***, Yan Li\*, Ruiyu Xie, Thomas Harper, Nisha A. Patel, *et al.* (2015). Epigenetic priming of enhancers predicts developmental competence of hESC-derived endodermal lineage intermediates. **Cell Stem Cell** 16, 386-99 (\* Co-first Author).
  12. Bing Ren and **Feng Yue** (2015). "Transcriptional Enhancers: Bridging the Genome and Phenome." **Cold Spring Harb Symp Quant Biol.** 80, 17-26.
  13. Danny Leung, Nisha Rajagopal, Inkyung Jung, ... , **Feng Yue**, Manoj Hariharan, Pradipta Ray, Samantha Kuan, Lee Edsall, Hongbo Yang, Neil C. Chi, Michael Q. Zhang, Joseph R. Ecker and Bing Ren (2015). Comprehensive profiling reveals dynamic chromatin signatures at cis-regulatory elements in human tissues. **Nature** 518, 350-354.
  14. **Feng Yue\***, Cheng Yong\*, Alessandra Breschi\*, Jeff Vierstra\*, Weisheng Wu\*, Tyrone Ryba\*, et al. & The Mouse ENCODE Consortium (2014). A comparative encyclopedia of DNA elements in the mouse genome." **Nature** 515, 355-365 (\* Co-first author).
  15. Cheng Y, Ma Z, Kim BH, ..., Mouse ENCODE Consortium, Kundaje A, Wang T, Pennacchio LA, Weng Z, Hardison RC, Snyder MP (2014). Principles of regulatory information conservation between mouse and human." **Nature** 515, 371-375.
  16. Benjamin D. Pope, Tyrone Ryba, Vishnu Dileep, **Feng Yue**, Weisheng Wu, Olgert Denas, et al. (2014). Topologically-associating domains are stable structural units of replication timing regulation. **Nature** 515, 402-405.
  17. Virginia Perez-Andreu, Kathryn G. Roberts, Heng Xu, Colton Smith, Hui Zhang, Wenjian Yang, ... , **Feng Yue**, ..., and Jun J. Yang (2014). A genome-wide association study of susceptibility to acute lymphoblastic leukemia in adolescents and young adults. **Blood** 125, 680-686.
  18. Virginia Perez-Andreu, Kathryn G Roberts, Richard C Harvey, Wenjian Yang, Cheng Cheng, Deqing Pei, ... , **Feng Yue**, ... , and Jun J Yang (2013). Inherited GATA3 variants are associated with Ph-like childhood acute lymphoblastic leukemia and risk of relapse. **Nature Genetics** 45(12):1494-8.
- Publications during Postdoctoral and Ph.D. training:**
19. Gary C. Hon, Nisha Rajagopal, Yin Shen, David McCleary, **Feng Yue**, MD Dang, and Bing Ren (2013). Epigenetic memory at embryonic enhancers identified in DNA methylation maps from adult mouse tissues. **Nature Genetics** 45, 1198-1206.
  20. Jesse R. Dixon, Siddarth Selvaraj, **Feng Yue**, Audrey Kim, Yan Li, Yin Shen, Ming Hu, Jun S. Liu & Bing Ren (2012). Topological domains in mammalian genomes identified by analysis of chromatin interactions. **Nature** 485, 376-380.
  21. Yin Shen\*, **Feng Yue\***, David F. McCleary, Zhen Ye, Lee Edsall, Ulrich Wagner, et al. (2012). A map of cis-regulatory sequences in the mouse genome. **Nature** 488, 116-20 (\* Co-first author).
  22. Wei Xie, Cathy L. Barr, Audrey Kim, **Feng Yue**, Ah Young Lee, James Eubanks, Emma L. Dempster, and Bing Ren (2012). Base-resolution analyses of sequence and parent-of-origin dependent DNA methylation in the mouse genome. **Cell** 148, 816-831.
  23. Mark Rebeiz, Brian Castro, Feng Liu, **Feng Yue**, and James W. Posakony (2012). "Ancestral and conserved cis-regulatory architectures in developmental control genes. **Developmental Biology** 362, 282–294.
  24. The Mouse ENCODE Consortium (2012). An encyclopedia of mouse DNA elements (Mouse ENCODE)." **Genome Biology** 13, 418.
  25. **Feng Yue**, Jian Shi, and Jijun Tang (2009). Simultaneous phylogeny reconstruction and multiple sequence alignment. **BMC Bioinformatics**, 10(Suppl. 1):S11.
  26. **Feng Yue** and Jijun Tang (2009). A space-efficient algorithm for three sequence alignment and ancestor inference. **Int'l Journal of Data Mining and Bioinformatics** 3, 192-204.

27. **Feng Yue**, Meng Zhang, and Jijun Tang (2009). Phylogenetic reconstruction from transposition. **BMC Genomics**, 9 (Suppl. 2):S15.
28. **Feng Yue**, Liying Cui, Claude W. dePamphilis, Bernard ME Moret, and Jijun Tang (2009). Gene rearrangement Analysis from Chloroplast Genomes with Inverted Repeat. **BMC Genomics**, 9(Suppl. 1):S25.

### **Invited Departmental Seminar**

- 01/09/2020 Penn Bioinformatics Forum seminar series, Institute for Biomedical informatics, University of Pennsylvania, Philadelphia, PA.
- 10/24/2019 Springer Nature: Sustainable Development Goals (SDG) speaker series, Shanghai, China.
- 09/27/2019 Dept. of Bioinformatics and Genomics, Department, UNC Charlotte.
- 03/04/2019 Cancer Center Seminar Series, City of Hope, Los Angeles, CA.
- 02/05/2019 Dept. of Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI.
- 11/26/2018 Memorial Sloan Kettering Cancer Center, New York, NY.
- 10/03/2018 Dept. of Genetics, MD Anderson Cancer Center, Houston, TX.
- 10/01/2018 Bioinformatics Interdepartmental Program, UCLA, Los Angeles, CA.
- 09/24/2018 Dept. of Genetics, Washington University, St. Louis, MO.
- 08/04/2018 Dept. of Biochemistry and Molecular Genetics, Northwestern University.
- 02/13/2018 Center for Metabolic Disease, Temple University School of Medicine, Philadelphia, PA.
- 01/19/2018 Dept. of Biomedical Informatics, Ohio State University, Columbus, OH.
- 12/06/2017 Research Postgraduate Symposium, HKU Medical Faculty, The University of Hong Kong.
- 10/24/2017 Dept. of Biomedical Sciences, Cornell University, Ithaca, NY.
- 10/17/2017 Dept. of Biomedical Engineering, Johns Hopkins University, Baltimore, MD.
- 12/15/2015 College of Medicine, Fudan University, Shanghai, China.
- 10/13/2015 Department of Biomedical Informatics, University of Pittsburg
- 05/11/2015 Department of Biology, Temple University, Philadelphia, PA.
- 03/09/2015 Center for Computational Biology and Bioinformatics, Indiana University-Purdue University Indianapolis, IN.
- 05/13/2014 School of Life Sciences, Tsinghua University, Beijing, China.

### **Conference Presentations**

- 12/05/2019 4D Nucleome (4DN) network and the American Society of Cell Biology (ASCB), Washington, D.C.
- 09/18/2019 Jackson Laboratory Workshop on Long-Read Sequencing, Farmington, CT.

08/04/2019 2019 Gordon Research Conference (GRC) on Genome Architecture, Hong Kong, China.

03/18/2019 Keystone Symposia on 3D Genome: Gene Regulation and Disease, Banff, Alberta Canada.

12/07/2018 4D Nucleome (4DN) network and the American Society of Cell Biology (ASCB), San Diego, CA.

10/26/2018 International human epigenome consortium Annual meeting (IHEC 2018), Hong Kong, China.

10/08/2018 Cold Spring Harbor Asia Conference, Systems Biology of Gene Regulation and Genome Editing, Suzhou, China.

09/14/2018 Nuclear Landscapes 2018 (NP2018), Warsaw, Poland.

07/07/2018 International Society for Computational Biology Annual Meeting (ISMB 2018), *3D Genomics: Computational approaches for analyzing the role of three-dimensional chromatin organization in gene regulation*, Chicago, IL.

04/25/2018 Jackson Laboratory Long-Read Sequencing Workshop, Farmington, CT.

04/18/2018 Cold Spring Harbor Asia Conference: Chromatin, Epigenetics & Transcription, Suzhou, China.

04/14/2018 American association for Cancer Research Annual meeting Annual Meeting (AACR 2018), *Emerging Methods for Quantitative Functional Genomic Analysis*, Chicago, IL.

03/20/2018 CSHL Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, NY.

11/08/2017 Workshop on 3D Genome Mapping Technology, Jackson Laboratory, The Jackson Laboratory for Genomic Medicine, Farmington, Connecticut.

11/03/2017 11th annual conference for the Program in Quantitative Genomics (PQG) Harvard University, Boston, MA.

10/10/2017 Second Annual MidAtlantic Bioinformatics Meeting, hosted by the Children's Hospital of Philadelphia and University of Pennsylvania, Philadelphia, PA.

09/19/2017 4D Nucleome Annual Meeting, Bethesda, MD.

05/17/2017 Great Lakes Bioinformatics Conference (GLBIO 2017), Chicago, IL

12/08/2016 International Conference on Intelligent Biology and Medicine (ICIBM 2016), Houston, TX.

11/21/2016 WashU Epigenome Day, Washington University, St. Louis, MO.

11/08/2016 Workshop on 3D Genome Mapping Technology, Jackson Laboratory, The Jackson Laboratory for Genomic Medicine, Farmington, Connecticut.

11/16/2016 American Society of Human Genetics Annual Meeting (ASHG 2016), Vancouver, Canada.

06/08/2016 ENCODE 2016: Research Applications and Users Meeting, Stanford, CA.

04/21/2016 Keystone Symposia on Epigenetics and Chromatin, Whistler, BC, Canada.

02/04/2016 EPIGENOMICS 2016 - a special international meeting sponsored by the NIH Common Fund.

10/11/2015 Workshop on 3D Genome Mapping Technology, Jackson Laboratory, The Jackson Laboratory for Genomic Medicine, Farmington, Connecticut.

07/14/2015 Highlight track, ISMB/ECCB 2015, Dublin, Ireland.

07/10/2015 Regulatory Genomics Special Interest Group (RegGenSIG), ISMB/ECCB 2015, Dublin, Ireland.

06/29/2015 Co-chair and presenter, ENCODE 2015: Research Applications and Users Meeting, Potomac, MD.

05/11/2015 Department of Biology, Temple University, Philadelphia, PA.

05/02/2015 Annual meeting for the Association for Research in Vision and Ophthalmology (ARVO), Denver, CO.

04/01/2015 Session chair and invited speaker, ENCODE workshop, Keystone Symposia Epigenomics, Keystone, CO.

03/17/2015 Co-chair, ENCODE outreach group discussion panel, ENCODE consortium annual meeting, CSHL, NY.

03/09/2015 Center for Computational Biology and Bioinformatics, Indiana University-Purdue University Indianapolis, IN.

01/31/2015 CSHL System Biology Conference (Puerto Rico).

01/23/2015 Xiangshan Conference (Beijing, China).

12/06/2014 International Conference on Intelligent Biology and Medicine (ICIBM 2014), San Antonio, TX.

### **Professional Services and Outreach Activities**

2017 - Co-chair, Joint Analysis workgroup, NIH 4D Nucleome Project

03/19/2019 Chair, ENCODE Consortium Workshop, Keystone Symposia on 3D Genome: Gene Regulation and Disease, Banff, Alberta Canada.

May 2017 - Co-chair, Integrative analysis working group, 4D Nucleome Consortium.

2015 – 2017 Co-chair, ENCODE consortium outreach group.

Oct. 2016 Chair, Joint ENCODE and 4DN workshop American Society of Human Genetics annual meeting (ASHG 2016), Vancouver, Canada

Jun. 2016 Co-organizer, ENCODE 2016: Research Applications and Users Meeting, Sanford, CA

Mar. 2016 Chair, ENCODE workshop, Annual Society of Toxicology Meeting (SOT 2016)

Oct. 2015 Chair, ENCODE workshop in ASHG (American Society of Human Genetics) annual meeting

Jul. 2015 Co-organizer, 2015 Penn State Chromatin Summer Symposium

Jun. 2015 Co-organizer, ENCODE 2015: Research Applications and Users Meeting

Apr. 2015 Chair, ENCODE workshop, Keystone Symposia Epigenomics

Oct. 2014 Co-organizer, ENCODE workshop in ASHG (American Society of Human Genetics) annual meeting

## **Ongoing External Research Support**

1R01HG009906 (Yue)      NIH/NHGRI      01/08/2018 – 12/31/2022  
Title: Visualization, modeling and validation of chromatin interaction data  
Goal: Create an online system for users to explore both published and their own chromatin interaction data, modeling chromatin interaction data, and perform functional validation experiment.  
Role: PI

R35GM124820 (Yue)      NIH/NIGMS      09/01/2017-07/31/2022  
Maximizing Investigators' Research Award (MIRA, R35)  
Title: Impact of Genetic Variants on Gene Regulation and 3D Genome Organization in Human Diseases;  
Goal: Looking for regulatory genetic variants and identify their functions in human disease  
Role: PI

R24DK106766 (Hardison)      NIH/NIDDK      07/18/2016-05/31/2021  
Title: VISION: Validated Systematic IntegratiON of epigenomic data  
Goal: identify the epigenomic landscapes in hematopoiesis.  
Role: Co-Investigator

U01CA176063 (Wang)      NIH/NCI      09/01/2015-/08/31/2020  
Title: The WashU 4DN network data coordination and integration center  
Goal: Building data center for the 4D Nucleome consortium and perform integrative data analysis to study the underlying mechanism of chromatin interactions.  
Role: Co-investigator