

Xianghong Jasmine Zhou

Current Position

Professor
Department of Pathology & Laboratory Medicine
Institute for Quantitative and Computational Bioscience
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Education

1991-1995	Diplom in Biochemistry University of Tuebingen, Germany
1997-2000	Nach-Diplom in Computer Science Swiss Federal Institute of Technology (ETH)
1997-2000	PhD in Bioinformatics Swiss Federal Institute of Technology (ETH)
2001-2003	Post-doctoral Fellow in Biostatistics Department of Biostatistics Harvard University

Professional Experience

6.2016-present	Professor Department of Pathology and Laboratory Medicine University of California at Los Angeles
7.2015-6. 2016	Head, Computational Biology and Bioinformatics Program University of Southern California
2012-2016	Professor Departments of Biological Science and Computer Sciences University of Southern California
2011-2016	Member The USC Norris Comprehensive Cancer Center

2008-2012 **Associate Professor**
Department of Biological Science and Computer Science
University of Southern California

2003-2008 **Assistant Professor**
Department of Biological Science
University of Southern California

Professional Activities

Editorial

- Associate editor, PLOS Computational Biology (2014-2017)
- Associate Editor, BMC Genomics, (2010-2013)
- Special issue editor, Journal of Computational Biology (2012)
- Ad hoc editor, PLoS Computational Biology (2011, 2013)
- Ad hoc editor, PNAS (2013)
- Editorial Advisory Board for the “*Handbook of Research on Computational and Systems Biology: Interdisciplinary Applications.*” (2010)

Grant Review

- Panelist, NIH SBIR/STTR review panel, 2021
- Panelist, NIH Imaging/Biomarker Special Emphasis Panel, 2020
- Grant reviewer, Health Research Charities Ireland, 2020
- Grant Reviewer, Israel Science Foundation, 2020
- Grant Reviewers, DGSOM Seed Grant, 2020
- Grant Reviewer, UCLA Innovation Fund, 2019
- NIH Cancer Biomarker Special Emphasis Panel, 2018
- NIH SBIR/STTR review panel, 2016
- NIH CEGS Center Grant review panel, 2014
- NIH Study section member (Regular), Biological Data Management and Analysis, 2010-2016
- NIH Study section member (ad hoc), Special Emphasis Panel, 3/2009
- NSF Panelist, grant review panel, DBI, 5/2004, 10/2006
- NSF Panelist, grant review panel, IIS, 3/2008
- NSF electronic proposal review, 1/2006
- NIH Study section member (ad hoc), Bioinformatics Software and Maintenance, 9/2005
- External reviewer, Dutch National Science Foundation (NWO), 2/2008

Conference Organizing:

- Program Committee, International Conference on Intelligent Biology and Medicine, June 2018
- Program Committee, Annual Harvard Quantitative Genomics Symposium, 2017
- Session organizer, Integrative Analysis of High-throughput Sequencing Data, WNAR, 2013
- Program Committee, Pacific Symposium of Biocomputing (Cancer Panomics), 2013
- Organization Committee Member, Symposium of 30 Years of Computational Biology at USC, 3/2012
- Program Committee, IEEE International Conference on Systems Biology, 2012
- Chair of the Organization Committee, Cancer Genomics Workshop, 10/2011
- Chair, Functional Genomics Reunion Conference, Los Angeles, 7/2004

- Program Committee, the 18th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), 2010
- Program Committee, the 8th International Bioinformatics Workshop, 2010
- Program Committee, the 1st International Workshop on Graph Techniques for Biological Networks, 2009
- Program Committee, the 7th International Bioinformatics Workshop, 2009
- Program Committee, the 7th Annual International Conference on Computational Systems Biology Conference (CSB), 2008
- Program Committee, the 6th Annual International Conference on Computational Systems Biology Conference (CSB), 2007
- Program Committee, the 14th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), 2006
- Program Committee, the 4th Asia and Pacific Bioinformatics Conference (APBC), 2005

University and Department Services:

- Organizing Committee of Dept Research and Clinical Excellence Day, 2021-present
- Bioinformatics IDP Executive Committee, 2020-present
- Academic Personnel Committee of Dept Pathology, 2020-present
- Faculty Search Committee for the Director for the Molecular Diagnostics, UCLA, 2019
- Member, Curriculum Committee for the Bioinformatics PhD program, UCLA, 2018-present
- Member, the UCLA High Performance Computing Committee, Institute of Digital Research and Education (IDRE), 2017-present
- Member, Search Committee for Director of the Bioinformatics Program, April 2018
- Member, QCBio Retreat Planning committee, 2017
- Member, Admission Committee for the Bioinformatics PhD program, UCLA, 2016-present
- Head, USC Computational Biology and Bioinformatics program, 2015-2016
- Chair, USC BISC Reputation/Statue Committee, 2015
- Chair, Computational Biology PhD Admission Committee (2007-2015), USC
- Member, USC College Tenure and Promotion Committee, 2012-present
- Member, the Chair Search Committee for the Biological Sciences Department, 2012
- Member, the USC Women in Science and Engineering (WiSE) Program Committee, 2009,2010
- Member, Faculty Search Committee on Molecular and Evolutionary Biology, 2010
- Diversity Liaison, Faculty Search Committee on Computational Biology, 2013
- Diversity Liaison, Faculty Search Committee on Computational Structural Biology, 2010
- Diversity Liaison, Faculty Search Committee on Computational Structural Biology, 2009
- Undergraduate Admission, interview the Provost fellowship candidates, 2009
- Member, the James Zumberg Award review panel, 2008
- Member, the USC Strategic Planning Subcommittee, 2005
- Member of the Graduate Admission Committee (2003, 2004, 2005, 2006), Department of Biological Science, USC
- Member, Senior Hire Faculty Search Committee in Computational Biology (2008, 2009)
- Member, the RRI Building Planning Committee, 2005
- Coordinator, Computational Biology Seminar series, USC, 2004, 2005, 2006, 2007 Fall, 2009 Fall

Professional Societies

- Member, International Society of Computational Biology (ISCB)
- Member, American Association for the Advancement of Science (AAAS)
- Member, American Society of Clinical Oncology (ASCO)

Review for Scientific Journal

- Reviewer for *Cell*, *Nature Biotechnology*, *Nature Methods*, *Nature Protocol*, *Nature Communications*, *Science Advances*, *PNAS*, *Clinical Chemistry*, *British Journal of Cancer*, *Genome Research*, *Genome Biology*, *PLoS Computational Biology*, *Genetics*, *Biometrics*, *Bioinformatics*, *Journal of Computational Biology*, *Physiological Genomics*, *Genomics*, *BMC Bioinformatics*, *BMC Genomics*, *BMC Systems Biology*, *Human Genetics*, *Nucleic Acid Research*, *Journal of Theoretical Biology*, the *RECOMB proceeding*, *Journal Of Royal Society Interface*, *PLoS One*, *Pacific Symposium of Biocomputing*, *Genomics*, *Proteomics*, and *Bioinformatics (GPB)*, and *IEEE/ACM Transactions on Computational Biology and Bioinformatics*

Tenure and Promotion Dossier Review

- Harvard University, Brandeis University, U. Minnesota, Nanyang Technological University, Chinese Academy of Science, Case Western Reserve University, University of Iowa, Vanderbilt University, Academia Sinica, UCLA, U Texas, Indiana U, Scripps Institute, UC Irvine, UC Riverside, Tsinghua University, Chinese Academy of Sciences, Carnegie Mellon University, University of Pennsylvania, Children's Hospital Los Angeles/USC
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Other Services

- Judger, California Science Fair (2015)

Awards and Honors

- James Zumberg Research Innovation Award, USC (2004)
- Alfred Sloan Research Fellowship (2006)
- Selected as one of the "Microarray Innovators 2006" by *Genome Technology Magazine* (2006)
- NSF CAREER Award (2008)
- The Young Computational Biologist Award, by the International Conference of Computational Systems Biology (2009)
- Keynote speaker, The International Conference on Intelligent Biology and Medicine (ICIBM), Texas (2014)

Grants Received

Current:

- **The UCLA Center for the Early Detection of Liver Cancer**
NIH U01
Role: Contact PI
Duration: 10/2018-09/2023
Total cost: 4,296,384
- **Novel Computational Methods for the Analysis of Cell-Free DNA Sequencing Data**
NCI R01
Role: Contact PI
Duration: 07/2019-06/2023
Total cost: \$ 1,920,000
- **Informatics resources for liquid biopsy research**

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|------------|--------------------------|
| NCI U01 | Duration 09/2019-08/2022 |
| Role: Co-I | Total cost: 1,250,000 |
- Center for Mapping the 3D Genome Landscape**
 NIH U54
 Role: Co-I (PI: Alber)
 Duration: 10/2015-9/2021
 Total cost: \$4,000,000
 - Prioritization of Splicing Altering Genetic Variants in Alzheimer's Disease**
 NIH 1R01AG056476
 Role: Co-I (PI: X. Xiao)
 Duration 08/01/2017-04/30/2022
 Total cost: \$1,250,000

Completed:

- MAPGen Knowledge Base (MAPGenKB) and Coordination Center**
 NIH U01HL108634
 Role: PI (contact)
 Duration 08/2011 - 06/2018
 Total cost: \$5,500,000
- Integrative Analysis of Public RNA-seq Repositories**
 NIH R01
 Role: PI
 Duration: 4/2013-12/2017
 Total cost: \$1,362,680
- NSF CAREER: Integrated Approaches to Mapping Genome to Phenome**
 NSF (Grant #0747475)
 Role: PI
 Duration: 4/2008-3/2014
 Total cost: \$666,120
- Integrative Analysis of Cross-Platform Microarray Data**
 Grant type: NIH R01GM074163
 Role: PI
 Duration 1/2006-12/2011
 Total cost: \$1,029,000
- A web platform for integrative genomic analysis in aging**
 Grant type: NIH R21
 Role: PI
 Duration 3/2008-2/2011
 Total cost: \$358,600
- Integration of Oncogenic Networks in Cancer Phenotypes (Center Grant)**
 Grant type: NIH U54CA112952 (PI : Nevins/Duke)
 Role: PI of the USC subcontract
 Duration 10/2004-9/2009
 Total cost: \$335,780
- Collaborative Research: Endowing Biological Databases with Analytical Power: Indexing, Querying, and Mining of Complex Biological Structures**
 Grant type: NSF (Grant # 0515936)
 Role: PI
 Duration 10/2005-9/2008
 Total cost: \$228,616
- Statistical and Computational Studies of Multiple Networks**
 Grant type: NIH R21
 Role: Co-I (PI: Fengzhu Sun)
 Duration 6/2008-5/2012
 Total cost: \$358,600
- Gene Aging Nexus: web platform for integrated data mining**
 Grant type: Seaver Foundation
 Role: PI
 Duration: 08/2005-06/2008
 Total cost: \$480,000

- **Sloan Research fellowship**
Grant type: Sloan Foundation
Role: PI
Duration: 09/2006-08/2008
Total cost: \$45,000
- **Integrative Genomic Analysis of Aging**
Grant type: Zumberg Foundation
Role: PI
Duration: 07/2005-06/2006
Total cost: \$48,000
- **Genome Functional Annotation**
Grant type: Zumberg Foundation
Role: PI
Duration: 07/2005-06/2006
Total cost: \$24,000

Lectures & Presentations (since July 2016)

- *Cancer Detection, Monitoring, and Therapy Prognosis Using Cell-Free DNA*, Computational Bioscience Program Seminar Series, University of Pennsylvania and Children Hospital of Philadelphia, June 2021
- *Cancer Detection, Monitoring, and Therapy Prognosis Using Cell-Free DNA*, Computational Bioscience Program Seminar Series, Broad Institute, June 2021
- *Cancer Detection, Monitoring, and Therapy Prognosis Using Cell-Free DNA*, JCCC seminar series, UCLA, May 2021
- *Cancer Detection, Monitoring, and Therapy Prognosis Using Cell-Free DNA*, Computational Bioscience Program Seminar Series, University of Colorado at Denver, May 2021
- *Multi-feature Ensemble Learning of Cell-free DNA for Accurately Detecting and Locating Cancer*, AACR, April 2021
- *Cancer Detection and Monitoring Using Cell-free DNA*. California Precision Medicine Summit, Feb 2020
- *Ultrasensitive Detection of Cancer Using cfDNA Methylation Sequencing*, Liquid Biopsy Summit, June 17-19 2019, San Francisco, CA
- *Ultrasensitive Detection of Cancer Using cfDNA Methylation Sequencing*, NIH Workshop "Liver Fibrosis to Cancer", April 2019, Bethesda
- *Ultrasensitive Detection of Cancer Using cfDNA Methylation Sequencing*, Liquid Biopsies 2019, March 27-29, 2019, San Diego, CA
- *Liquid biopsy and applications in neuropathology*, 16th Annual World Congress of Society for Brain Mapping and Therapeutics, March 15-17, 2019, Los Angeles, CA.
- *Ultrasensitive Detection of Cancer Using cfDNA Methylation Sequencing*, 26th International Molecular Med TRI-CON, March 1-4, 2019, San Francisco, CA.
- *Computational methods for the non-invasive blood-based cancer detection*, UCLA Center for Domain Specific Computing Project Annual Review Meeting, February 28-March 1, 2019, Los Angeles, CA.
- *CancerLocator: Harnessing the diagnostic potential of cell-free DNA methylation*, *the Annual Chinese Clinical Oncology Conference*, Xiamen, 09/2018

- *CancerLocator: Harnessing the diagnostic potential of cell-free DNA methylation*, AACR conference, Chicago, 04/2018
- *CancerLocator: Harnessing the diagnostic potential of cell-free DNA methylation*, China IVD annual conference, Shanghai, 03/2018
- *CancerLocator: Non-Invasive Cancer Diagnosis and Tissue-of-Origin Prediction Using Methylation Profiles of Cell-Free DNA*, Molecular Medicine Tri-Conference, San Francisco, 02/2018
- *Cancer Detection using Cell-Free DNA*, Invited Seminar, Shanghai Ruijing Hospital, 07/2018
- *Harnessing the diagnostic potential of cell-free DNA-seq*, UCLA QCBio Symposium on Exploring the Frontiers of Biomedical Big Data, Los Angeles, 04/2017
- *Structure-Function Mapping of 3D Human Genome*, Molecular Medicine Tri-Conference, San Francisco, 02/2017
- *Integrative Analysis of Multi-dimensional Genomics Data*, Invited Seminar, School of Computing, CMU University, 10/2016
- *Searching for Meaningful Signals in the 3D Genome Universe and in the Blood of Cancer Patients*, Invited Seminar, Beijing University, 08/2016
- *Structure-Function Mapping of 3D Human Genome*, Plenary Talk at the International Conference of Systems Biology, Shangdong, China, 07/2016

Teaching & Supervision

- **Courses co-taught:**
Statistics for Biologists(BISC305)
Computational Molecular Biology (Algorithms) (Math578a)
Computational Molecular Biology Lab a (Math577a)
Computational Molecular Biology Lab b (Math577b)
Seminar in Computational Biology (BISC542)
Molecular Genetics and Biochemistry (BISC505)
Genomics and Molecular Genetics a & b (BISC502a & BISC502b)
Computational Genome Analysis (BISC478)
Practical Bioinformatics (BISC599)
Current Topics in Computational Biology (BISC577)
Ethics and Accountability in Biomedical Research (C234)
Bioinformatics Interdisciplinary Research Seminar(M202)
Directed Indiv Study (BIOINFO596)
Research in Bioinformatics (BIOINFO 599)
- **Current PhD students**
 - Ran Hu
 - Ye Wang
- **Previous PhD student**
 - Haiyan Hu (current position: Associate Professor, Department of Computer Science, University of Central Florida).

- Kangyu Zhang (current position: Senior Director, Bioinformatics and Biomarker Discovery, CStone Pharmaceuticals)
 - Juan Nunez-Iglesias (current position: Research Scientist at Life Sciences Computation Centre, University of Melbourne, Australia)
 - Min Xu (current position: Assistant Professor, Carnegie Mellon University)
 - Chao Dai (current position: Senior Scientist, Predicine)
 - Qingjiao Li (current position: Associate Professor, Sun Yat-sen University Hospital)
 - Hanjun Shin (current position: Senior Bioinformatics/Software Engineer, Agilent Technologies)
 - Mary Stackpole (current position: VP of Bioinformatics, EarlyDiagnostics)
 - Shuo Li (current position: Assistant Project Scientist, UCLA)
- **Previous Post-doc**
 - Yi Shi (current position: Associate Professor, Shanghai Jiaotong University)
 - Jianjun Hu (current position: Associate Professor, Computer Science, University of South Carolina)
 - Fei Pan (current position: Senior Research Associate, USC medical school)
 - Haifeng Li (current position: Principle Engineer, Amazon)
 - Chun-Chi Liu (current position: Chief Computing Officer, EarlyDiagnostics)
 - Shihua Zhang (current position: Professor, Chinese Academy of Science)
 - Quan Chen (current position: Data Scientist, Sema4)
 - Shuli Kang (current position: Senior Bioinformatics Scientist, Novartis Gene Therapy)
 - Shanshan He (current position: Senior Scientist, NanoString)
 - Zuyang Yuan (current position: Thoracic Surgeon at National Cancer Center, China)
- **Previous undergraduate research student**
 - Molly Rashid (current position: M.D. student at USC medical school)
 - Yichi Niu (current position: Ph.D student at Baylor College of Medicine)
 - Xinpei Lv
 - Margaret Li
- **PhD Dissertation Committee:**

(USC) Hyun-ju Lee, Lingqi Zhou, Li Wang, Michael Mehan, James Baurley, Zachry Fraser, Quan Chen

(UCLA) Kikuye Koyano, Zhanhao Peng, Kofi Amoah
- **PhD Qualify Exam Committee:**

(USC) Hyun-ju Lee, Lijuan Mo, Diana Abdueva, Dmitriy Skvortsov, Zhidong Tu, Chao Cheng, Matt Lebo, Lingqi Zhou, Xiting Yan, Li Wang, Huanying Ge, Xiaoming Wang, Yang-Ho Chen, James Baurley, Xiaoming Wang, Kjong Lehmann, Zachry Fraser, Ke Gong, Hanjiang Qu, Pei Long

(UCLA) Kikuye Koyano, Zhanhao Peng, Kofi Amoah, Favoor Esedebe

Publication/Bibliography

BOOK

1. Tseng GC, Ghosh D, and **Zhou XJ** (2015)
Integrating Omics Data: Statistical and Computational Methods.
Cambridge University Press. ASIN: B012GS1UC0.

RESEARCH PAPERS

2. Cannarozzi G, Hallett M, Norberg J, **Zhou X**. (2000)
A Cross-Comparison of a Large Dataset of Genes.
Bioinformatics. 16(7): 654-655.
3. **Zhou X**, Alber F, Folkers G, Gonnet GH, Chelvanayagam G. (2000)
An Analysis of the Helix-to-Strand Transition between Peptides with Identical Sequence.
Proteins. 41: 248-256.
4. **Zhou X**, Gonnet GH, Hallett M, Chelvanayagam G, Folkers G. (2001)
Identifying the Most Influential Residues for α -Helix Formation: The Subset Selection Problem Using Least Squares Optimization.
Proceedings of the 16th ACM Symposium on Applied Computing (SAC01): 51-55.
5. **Zhou X**, Gonnet GH, Hallett M, Munchbach M, Folkers G, James P. (2001)
Cell Fingerprinting: An approach to classify cells using their protein extracts with mass spectrometric analysis.
Proteomics. 1: 675-682.
6. Block-Alper L, Webster P, **Zhou X**, Superkova L, Wong WH, Schultz P and Meyer DI. (2002)
INO2, a Positive Regulator of Lipid Biosynthesis, is Essential for the Formation of Inducible Membranes in Yeast.
Mol Biol Cell. 2002, 13(1): 40-51.
7. **Zhou X**, Kao MJ, Wong WH. (2002)
From the Cover: Transitive Functional Annotation By Shortest Path Analysis of Gene Expression Data.
Proc Natl Acad Sci U S A. 99(20):12783-12788.
**This paper was highlighted in PNAS and Faculty of 1000*
8. **Zhou X**, Krueger JG, Kao MJ, Lee E, Du F, Menter A, Wong WH, Bowcock AM (2003)
Novel Mechanisms of T-cell and dendritic cell activation revealed by profiling of psoriasis on the 63,100-element oligonucleotide array.
Physiological Genomics 13:69-78.
9. Huang H, Kao MJ, **Zhou X**, Liu JS, Wong WH (2004)
Determination of local statistical significance of patterns in Markov sequences with application to promoter element identification.
Journal of Computational Biology 11(1):1-14.

10. **Zhou XJ**, Gibson G. (2004)
Cross-species Comparison of Genome-wide Expression Patterns.
Genome Biology 5(7):232.
11. Yan X, **Zhou XJ**, Han J (2005)
Mining Closed Relational Graphs with Connectivity Constraints.
Proceeding of the 11th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining, p324-333.
12. **Zhou XJ**, Kao MJ, Huang H, Wong A, Nunez-Iglesias J, Primig M, Aparicio OM, Finch CE, Morgan TE, Wong WH (2005)
Functional annotation and network reconstruction through cross-platform integration of microarray data.
Nature Biotechnology. 23(2):238-43.
**This paper was highlighted in Nature Review Genetics 6, 164(2005).*
13. Hu H, Yan X, Huang Y, Han J, **Zhou XJ** (2005)
Mining coherent dense subgraphs across massive biological networks for functional discovery.
Bioinformatics. 21 suppl 1: 213-221.(ISMB 2005)
14. Tu Z, Wang L, Xu M, **Zhou XJ**, Chen T, Yang Y, Sun F (2006)
Classification of the human genome into essential, disease and other genes by feature comparison.
BMC Genomics 7:31.
15. Fei P, Kamath K, Han J, Yan X, Zhang K, Huang Y, Hu H, Xu M, **Zhou XJ** (2006)
Integrative Array Analyzer: A software package for integrative analysis of cross-platform and cross-species microarray data.
Bioinformatics. 2006 Jul 1;22(13):1665-7.
16. Hu J, Li H, Waterman MS, **Zhou XJ** (2006)
Integrative Missing Value Estimation for Microarray Data.
BMC Bioinformatics. 7(1):449
17. Pan F, Chiu C, Pulapura S, Zhang K, Waterman MS, Finch CE, **Zhou XJ** (2006)
Gene Aging Nexus: A Web Database and Data Mining Platform for Microarray Data on Aging.
Nucleic Acid Research. 2007 Jan;35:D756-9.
18. Yan X, Mehan M, Huang Y, Waterman MS, Yu PS, **Zhou XJ** (2007)
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Bioinformatics, 23(13):i577-i586. (ISMB 2007)
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Bioinformatics, 23(13): i222-i229. (ISMB 2007)
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An Integrative network approach to map the transcriptome to the phenome.
Journal of Computational Biology. 16(8):1023-34 (RECOMB 2008)
22. Liu CC, Hu J, Kalakrishnan M, Huang H, **Zhou XJ** (2008)
Integrative Disease Classification Based on Cross-platform Microarray Data.
BMC Bioinformatics. 10 Suppl 1:S25.
23. Jin R, Macallen S, Liu CC, Xiang Y, Almaas E, **Zhou XJ** (2008)
Identifying Dynamic Network Modules with Temporal And Spatial Constraints.
Pacific Symposium of Biocomputing 2009, 203-214
24. Mulkar-Mehta R, Hobbs J, Liu CC, **Zhou XJ** (2009)
Discovering Causal and Temporal Relations in Biomedical Texts.
Proceeding of the AAAI Spring Symposium on Learning by Reading and Learning to Read, 74-80.
25. Mehan M, Nunez-Iglesias J, Dai C, Waterman MS, **Zhou XJ**. (2009)
An integrative modular approach to systematically predict gene-phenotype associations.
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Repressing the Polycomb Group Protein EZH2.
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27. Xu M, Li W, James G, Mehan MR, **Zhou XJ** (2009)
Automated Multi-dimensional Phenotypic Profiling Using Large Public Microarray
Repositories.
Proc Natl Acad Sci USA. vol. 106 no. 30 12323-12328.
**This paper was highlighted in Nature Methods, 6, 632 (2009), and selected by 2010
International Medical Informatics Association Yearbook of Medical Informatics.*
28. Li W, Xu M, **Zhou XJ** (2010).
Unraveling complex temporal associations in cellular systems across multiple time-series
microarray datasets.
Journal of Biomedical Informatics. 2010 Jan.
29. Nunez-Iglesias J, Liu CC, Morgan TE, Finch CE, **Zhou XJ** (2010).
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reveals altered miRNA regulation.
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30. Mehan MR, Nunez-Iglesias J, Dai C, Waterman MS, **Zhou XJ** (2010). An integrative modular
approach to systematically predict gene-phenotype associations. *BMC Bioinformatics*. 2010
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31. Huang H, Liu CC, **Zhou XJ** (2010).

Bayesian Probabilistic Approach Toward Transforming Public Microarray Repositories Into Disease Diagnosis Databases.

Proc Natl Acad Sci USA:107(15):6823-8

**This paper was highlighted in PNAS, GenomeWebNews, NatureSciBx, and FacultyOf1000*

32. Xu B, Chen C, Chen H, Zheng SG, Bringas P, Xu M, **Zhou X**, Chen D, Umans L, Zwijssen A, and Shi W. (2010)
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33. Li W, Liu CC, Zhang T, Li H, Waterman MS, **Zhou XJ** (2010).
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35. Li W, Hu H, Huang Y, Li H, Mehan MR, Nunez-Iglesias J, Xu M, Yan X, and **Zhou XJ** (2011).
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36. Taberlay PC, Kelly TK, Liu CC, You JS, de Carvalho DD, Miranda TB, **Zhou XJ**, Gangning Liang G, and Jones PA (2011)
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37. Li W, Dai C, Liu CC, and **Zhou XJ** (2012).
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38. Dai C, Li W, Liu J, and **Zhou XJ** (2012).
Systematic reconstruction of splicing regulatory modules by integrating many RNA-seq datasets.
BMC Systems Biology, 6(Suppl 1):S17.
39. Li W, Zhang S, Liu CC, **Zhou XJ** (2012).
Identify multi-layer gene regulatory modules from multi-dimensional genomic data.
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41. Zhang S, Liu CC, Li W, Shen H, Laird P, **Zhou XJ** (2012).
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Nucleic Acid Research, 2012 Aug 8.
42. **Zhou XJ**, Alber F (2012).
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Nucleic Acid Research, 2013 Feb p. 1-13.
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Nucleic Acid Research, 43(2):1268-82.

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Comparative 3D genome structure analysis of the fission and the budding yeast.
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