

# JULIA ZEITLINGER

## CURRICULUM VITAE

### PERSONAL DETAILS

*Stowers Institute for Medical Research  
1000 East 50th Street  
Kansas City, MO 64110  
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### AREAS OF RESEARCH

*Genomics technology  
Deep learning  
Cis-regulatory code  
Enhancer regulation  
Paused RNA polymerase II  
Drosophila and mouse development*

### PERSONAL SUMMARY

*In the era of high-throughput sequencing, an important goal is to understand how cis-regulatory DNA sequence information regulates gene expression in any cell type during development and disease. Our goal is to predict gene regulation from DNA sequence and to identify the predictive rules and molecular mechanisms that underlie the cis-regulatory code. We develop cutting-edge genomics technologies such as ChIP-nexus to map transcription factor binding at base-resolution and analyze cooperative binding interactions with interpretable deep learning models such as BPNet.*

### EDUCATION

#### 1995-2000

*Ph.D. work with Dirk Bohmann  
“The role of the transcription factor Fos in Drosophila”  
European Molecular Biology Laboratory, Germany  
Ph.D. degree awarded by the University of London, U.K.*

#### 1991-1995

*B.Sc. in Human Biology, First Class Honours  
King’s College London, U.K.  
Undergraduate project with Malcolm Maden and Nigel Holder  
“The role of retinoic acid in zebrafish development”*

### POSITIONS

#### 2018-present

*Investigator (equivalent of Full Professor)  
Stowers Institute for Medical Research (SIMR)*

#### 2023-present

*Professor  
Department of Pathology and Laboratory Medicine  
University of Kansas Medical Center (KUMC)*

#### 2015-2023

*Associate Professor  
Department of Pathology and Laboratory Medicine  
University of Kansas Medical Center (KUMC)*

#### 2013-2018

*Associate Investigator (equivalent of Associate Professor)  
Stowers Institute for Medical Research*

#### 2008-2015

*Assistant Professor  
Department of Pathology and Laboratory Medicine  
University of Kansas Medical Center*

#### 2007-2013

*Assistant Investigator (equivalent of Assistant Professor)  
Stowers Institute for Medical Research*

#### 2000-2007

*Postdoctoral studies with Richard Young  
Whitehead Institute for Biomedical Research  
“Transcriptional regulatory networks in yeast and Drosophila”*

## HONORS AND AWARDS

2015	<i>Neaves Award, Stowers Institute for Medical Research</i>
2012	<i>Hudson Prize by the M.R. and Evelyn Hudson Foundation</i>
2008-2013	<i>2008 NIH Director's New Innovator Award, National Institutes of Health</i>
2008-2012	<i>2008 Pew Scholar in Biomedical Sciences, Pew Charitable Trusts</i>
2000-2003	<i>Human Frontiers Science Program Long-Term Fellow</i>
1995-1999	<i>EMBL Ph.D. Student</i>
1992-1995	<i>German Academic Scholarship Foundation ("Studienstiftung")</i>

## GRANTS

Since 2018	<i>"A transposase system for integrative ChIP-exo and ATAC-seq analysis at single-cell resolution," National Institutes of Health, National Human Genome Research Institute (NHGRI), total cost &gt; \$2,700,000</i>
2008-2013	<i>"Investigating developmental potential based on a genome-wide chromatin status," National Institutes of Health, 2008 NIH Director's New Innovator Award, total cost \$2,385,000</i>
2008-2012	<i>"The role of RNA polymerase stalling in cellular memory during Drosophila development," Pew Charitable Trusts, 2008 Pew Scholar in Biomedical Sciences</i>
Since 2007	<i>"Transcriptional regulatory networks during Drosophila and mouse development", Core funding by the Stowers Institute for Medical Research Current budget ~ \$1,000,000 per year</i>

## PATENT

Effective 2019	<i>Patent on ChIP-nexus technology: United States Patent and Trademark: "Methods and Kits for Identifying Polypeptide Binding Sites in a Genome" Patent Number:10287628, Confirmation Number: 1684, Julia Zeitlinger, Qiye He, Jeffrey Johnston</i>
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## SUPERVISION OF PH.D. STUDENTS

*GSSIMR: Graduate School of the Stowers Institute for Medical Research, KUMC: Kansas University Medical Center, IGPBS: Interdisciplinary Graduate Program in Biomedical Sciences*

2008-2013	<i>Kai Chen (Ph.D. from Open University, U.K., Professor, Kunming University, China)</i>
2008-2013	<i>Björn Gärtner (Ph.D. from U Würzburg, Germany, Fate Therapeutics Inc, US)</i>
2010-2015	<i>Nina Koenecke (Ph.D. from Open University, U.K., EUROIMMUN, Germany)</i>
2013-2018	<i>Wanqing Shao (Ph.D. from GSSIMR, Genomic Scientist, Boston Children's Hospital, US)</i>
2013-2019	<i>Vivekanandan Ramalingam (Ph.D. with Honors from the IGPBS Program at KUMC, now postdoc at Anshul Kundaje's lab at Stanford, US)</i>
2016-2021	<i>Sergio Garcia-Moreno Alcantara (Ph.D. from Open University, U.K.)</i>
Since 2018	<i>Khyati Dalal (registered with the IGPBS Program at KUMC)</i>
Since 2019	<i>Kaelan Brennan (registered with GSSIMR)</i>
Since 2019	<i>Yue Liang (registered with GSSIMR)</i>

Since 2020	<i>Tatiana Gaitan (registered with GSSIMR)</i>
Since 2020	<i>Kim Escobar (registered with the IGPBS Program at KUMC)</i>
Since 2021	<i>Haining Jiang (registered with GSSIMR)</i>

## SUPERVISION OF POSTDOCS

2008-2014	<i>Qiye He (now Director, R&amp;D at Singlera Genomics, La Jolla, USA and Shanghai, China)</i>
2009-2011	<i>Sangeeta Bafna (now Manager-Patent &amp; Licensing, New Jersey Institute of Technology)</i>
2011-2016	<i>Malini Natarajan (now Senior Scientist at Moderna, Wakefield, Rhode Island, USA)</i>
2015-2017	<i>Robin Fropf (now Senior Scientist at Adaptive Biotechnologies Corp., Seattle, USA)</i>
2019-2022	<i>Nilay Shah (now Genomics Scientist and Manager at NCGM Global, India)</i>
2020-2022	<i>Curtis Bacon (now Research Scientist III, Eurofins Viracor, USA)</i>
2018-2023	<i>Sabrina Krueger (now Scientific Training Officer, EMBL)</i>
Since 2019	<i>Simon Bourdareau</i>
Since 2019	<i>Charles McAnany</i>

## SUPERVISION OF UNDERGRADUATES

Since 2009	<i>Hosted and supervised 23 summer scholars</i>
Since 2009	<i>Hosted and supervised 2 practicum students</i>
Since 2011	<i>Hosted and supervised 5 students for their master thesis</i>

## TEACHING

Since 2012	<i>Two-week course in the fall “Genomic and Computational Approaches to Understanding Gene Expression BIO 702” for GSSIMR Ph.D. students</i>
Since 2021	<i>Two-week course in the fall on Gene Expression for GSSIMR Ph.D. students</i>
Since 2008	<i>Talks or informal lectures at University of Kansas Medical Center (~1 per year)</i>

## PROFESSIONAL SOCIETIES

Since 2014	<i>American Society for Biochemistry and Molecular Biology (ASBMB)</i>
Since 2015	<i>International Society for Computational Biology (ISCB)</i>

## CONTINUING EDUCATION

2018	<i>EMBO leadership course</i>
2021-22	<i>Fellow in the Executive Leadership in Academic Technology, Engineering and Science (ELATES) Program</i>

## SCIENTIFIC LEADERSHIP

Since 2014	<i>Co-organizer of ASBMB’s biannual “Evolution and Core Processes in Gene Regulation”</i>
2015-2020	<i>Co-organizer of ISCB’s “Intelligent Systems for Molecular Biology”</i>
2016-2020	<i>Co-organizer of CSHL’s “Systems Biology: Global regulation of Gene Expression”</i>

## PEER REVIEW

- Since 2008** *Reviewer for Cell, Science, Nature, Nature Genetics, Genome Res, Genome Biol, Genes Dev, Mol Sys Biol, Dev Cell, Molecular Cell, Cell Systems, Cell Reports, Cell Host & Microbe, eLife, Nature Communications, Nature Protocols, PNAS, NAR, JBC, EMBO J., EMBO Reports, BioEssays, Development, PLOS Genetics, PLOS One, The FEBS Journal, Open Biology, BMC Genomics, BMC Biology, Methods, jove, Science Advances*
- Since 2015** *Ad-hoc reviewer at the NIH study sections Genetic Variation and Evolution (GVE), Genomics, Computational Biology and Technology (GCAT) and for the NIH Director's New Innovator Award, NIH Human BioMolecular Atlas Program (HubMAP, Special Review Panel Gene Regulatory Network (NIH/NHGRI)*
- Since 2016** *Reviewer of international grants: European Research Council (ERC), Wellcome Trust, US-Israel Binational Science Foundation (BSF), Swiss National Science Foundation (SNSF), Deutsche Forschungsgemeinschaft (DFG)*

## GOVERNING

- 2011-2014** *GSSIMR Admission Committee*
- Since 2016** *Member of the GSSIMR Assessment Committee, Chair since 2018*
- Since 2019** *Dean's Council of GSSIMR*
- Since 2016** *Faculty Governing Committee of GSSIMR*
- 2016-2021** *Strategic Planning Committee of GSSIMR*
- Since 2013** *Faculty Search Committee for SIMR (responsible for computational applicants)*
- Since 2022** *Committee member for creating the Computational Fellow Program and the Bioinformatics Postbaccalaureate Program*
- Since 2022** *Committee member for the computational infrastructure at SIMR*

## Selected invited talks

1. **Invited departmental seminar.** "Global analysis of Pol II pausing during *Drosophila* development," University of California, San Diego, CA, January 9, 2013.
2. **Invited conference speaker.** "A global change in Pol II pausing during the *Drosophila* midblastula transition," EMBL Meeting in Heidelberg, Germany, May 9, 2013.
3. **Invited conference speaker.** "Enhancer regulation during development," The Banbury Center of Cold Spring Harbor Laboratory in New York, October 29, 2013.
4. **Invited departmental seminar.** "Using genomics approaches to understand gene regulation during development," University of California, Santa Cruz, January 7, 2014.
5. **Invited departmental seminar.** "Genome-wide approaches to understand gene regulation during development," Carnegie Mellon University, Pittsburgh, PA, February 7, 2014.
6. **Invited departmental seminar.** "Using genomics approaches to understand gene regulation during development," University of Mexico, April 7, 2014.
7. **Invited departmental seminar.** "Using genomics approaches to understand gene regulation during development," National Institute of Health, October 23, 2014.
8. **Invited departmental seminar.** "Using genomics approaches to gene regulation during development," University of Chicago, November 13, 2014.
9. **Invited conference speaker.** "Enhancer priming and patterning in the early *Drosophila* embryo", Lorne Genome Conference, Lorne, Australia, February 16, 2015.
10. **Invited conference speaker.** "Enhancer priming and patterning in the early *Drosophila* embryo", ASBMB Meeting, St. Louis, Missouri, June 26, 2015
11. **Invited conference speaker.** "Repressed enhancers poised for silencing and other stories", Chromatin & Epigenetic Regulation of Transcription, Pennsylvania State University Summer Symposium, July 22, 2015
12. **Invited conference speaker.** "Repressed enhancers during *Drosophila* pattern formation are poised for silencing", European *Drosophila* Research Conference, Heidelberg, Germany, September 10, 2015
13. **Invited keynote speaker.** "Combinatorial Regulation of Enhancers during *Drosophila* Development", RECOMB/ISCB, Philadelphia, November 18, 2015
14. **Invited conference speaker.** "Pol II initiation and pausing: a relay race?", Epigenomics Meeting, Puerto Rico, February 1, 2016
15. **Invited departmental seminar.** "A genomics approach to understanding gene regulation in development", Columbia University, April 7, 2016
16. **Invited departmental seminar.** "Peeking into transcription using high-resolution genomics techniques", University of Southern California, December 1, 2016
17. **Invited departmental seminar.** "Peeking into transcription in vivo using high-resolution genomics techniques", Stanford University, January 25, 2017
18. **Invited conference speaker.** "Paused Pol II inhibits new initiation", Cold Spring Harbor Laboratory Systems Biology: Global Regulation of Gene Expression, February 26, 2017
19. **Invited keynote speaker.** "Why the pause? Catching RNA Polymerase II in vivo", Annual *Drosophila* Research Conference, April 2, 2017
20. **Invited conference speaker.** "Why the pause? Catching RNA Polymerase II in vivo", EMBL Chromatin and Epigenetics conference, May 4, 2017
21. **Invited departmental seminar.** "Peeking into transcription in vivo using high-resolution genomics techniques", Max Planck Institute for Molecular Genetics, May 8, 2017

22. **Invited departmental seminar.** "Analyzing RNA polymerase II with genomics approaches: an old dog with new tricks?", University of California, Berkeley, November 7, 2017
23. **Invited departmental seminar.** "Discovering transcription mechanisms using high-resolution genomics approaches", Duke University, February 6, 2018
24. **Invited conference speaker.** "Lola-PI is a promoter pioneer factor that primes promoters for tissue-specific activation", Cold Spring Harbor Laboratory, Systems Biology Meeting, March 21, 2018
25. **Invited conference speaker.** "Deep learning reveals nuanced organizational features of the cis-regulatory code in mouse ES cells", CSHL Transcription Meeting, August 29, 2018
26. **Invited departmental seminar.** "Using high-resolution genomics approaches to decode transcription: from maps to mechanisms", Yale University, September 11, 2018
27. **Invited conference speaker.** "Using deep learning to understand the cis-regulatory code in mouse embryonic stem cells", Genomics in Action, University of Oregon, February 1, 2019
28. **Invited conference speaker.** "Looking inside the black box: using deep learning to discover cis-regulatory code", Fly Cell Atlas Meeting at Janelia Farm, March 26, 2019
29. **Invited departmental seminar.** "Looking inside the black box: using deep learning to discover cis-regulatory code", University of California Irvine, April 25, 2019
30. **Invited conference speaker.** "A transpose system for integrative ChIP-exo and ATAC-seq analysis", Advanced Genomic Technology Development Grantee Meeting, Boston, MA, May 30, 2019
31. **Invited speaker.** "Deep learning reveals nuanced organizational features of cis-regulatory elements in mouse embryonic stem cells", KUCC Cancer Biology retreat, June 4, 2019
32. **Invited departmental seminar.** "From biology to computation and back: deep learning of cis-regulatory code", LMU Munich, July 19, 2019
33. **Invited conference speaker.** "BPNet: base-resolution deep learning of transcription factor binding reveals nuanced organizational features of the cis-regulatory code in mouse ES cells", ISMB Basel, Switzerland, July 23, 2019
34. **Invited departmental seminar.** "Using deep learning to discover cis-regulatory syntax", Stanford University, November 7, 2019
35. **Invited conference speaker.** "Deep learning of ChIP-nexus data reveals cis-regulatory motif syntax", CHSL Systems Biology: Global Regulation of Gene Expression (Virtual), March 20, 2020
36. **Invited conference speaker.** "A transpose system for integrative ChIP-exo and ATAC-seq analysis (ChIP-next)", NHGRI virtual AGTD Grantee Meeting, May 29, 2020
37. **Invited departmental seminar.** "Out of the black box: a high-resolution genomics view on how genes are regulated", University of Southern California, February 9, 2021
38. **Invited conference speaker.** "High-resolution in vivo binding footprints suggest a common TFIID structure with promoter-specific TBP dynamics", Cold Spring Harbor Laboratory: Mechanisms for Eukaryotic Transcription, September 1, 2021
39. **Invited departmental seminar.** "Elucidating cis-regulatory code for development using high-resolution deep genomics", New York University, April 4, 2022
40. **Invited theory lunch seminar.** "The inverted learning paradigm of decoding genome information", Harvard University (virtual), April 22, 2022
41. **Invited departmental seminar.** "Elucidating cis-regulatory code for development using high-resolution deep genomics", Memorial Sloan Kettering Cancer Center, May 5, 2022
42. **Invited conference speaker.** "The cis-regulatory code of chromatin accessibility in the early Drosophila embryo" at the ASBMB conference "Evolution and core processes in gene expression" July 21-24, 2022
43. **Invited conference speaker.** "Deciphering the genome's second code by interpretable deep learning" at the Symposium "Programmable Life, the Inaugural Symposium of the Barcelona Collaboratorium" October 4-5, 2022



# Publications

## PREPRINTS

- Alexandari AM, Horton CA, Shrikumar A, Shah N, Li E, Weilert M, Pufall MA, **Zeitlinger J**, Fordyce PM and Kundaje A. (2023). bioRxiv 2023.05.11.540401. doi: <https://doi.org/10.1101/2023.05.11.540401>
- Ramalingam V, Yu X, Slaughter BD, Unruh JR, Brennan KJ, Onyshchenko A, Lange JL, Natarajan M, Michael Buck M and **Zeitlinger J**. (2022) Lola-I is a developmentally regulated promoter pioneer factor. bioRxiv 2022.04.25.489272; doi: <https://doi.org/10.1101/2022.04.25.489272>
- Horton CA, Alexandari AM, Hayes MGB, Marklund E, Schaepe JM, Aditham AK, Shah N, Shrikumar A, Afek A, Greenleaf WJ, Gordân R, **Zeitlinger J**, Kundaje A and Fordyce PM. (2022) Short tandem repeats bind transcription factors to tune eukaryotic gene expression. bioRxiv 2022.05.24.493321; doi: <https://doi.org/10.1101/2022.05.24.493321>

## PEER-REVIEWED ARTICLES

- Ramalingam V, Yu X, Slaughter BD, Unruh JR, Brennan KJ, Onyshchenko A, Lange JJ, Natarajan M, Buck M and **Zeitlinger J**. (2023) Lola-I is a promoter pioneer factor that establishes de novo Pol II pausing during development. *Nat Commun*. Sept 21;14(1):5862.
- Brennan KJ, Weilert M, Krueger S, Pampari A, Liu HY, Yang AWH, Hughes TR, Rushlow CA, Kundaje A and **Zeitlinger J**. (2023) Chromatin accessibility is a two-tier process regulated by transcription factor pioneering and enhancer activation. *Dev Cell*. Aug 3:S1534-5807(23)00347-7.
- Soffers JHM, Alcantara SG, Li X, Shao W, Seidel CW, Li H, **Zeitlinger J**, Abmayr SM and Workman JL. (2021) The SAGA core module is critical during Drosophila oogenesis and is broadly recruited to promoters. *PLoS Genet*. Nov 22;17(11):e1009668.
- Avsec Ž, Weilert M, Shrikumar A, Krueger S, Alexandari A, Dalal K, Fropf R, McAnany C, Gagneur J, Kundaje A,\* and **Zeitlinger J**.\* (2021) Base-resolution models of transcription factor binding reveal soft motif syntax. *Nat Genet*. Mar; 53(3): 354-366. \* co-corresponding authors
- Ramalingam V, Natarajan M, Johnston J and **Zeitlinger J**. (2021) TATA and paused promoters active in differentiated tissues have distinct expression characteristics. *Mol Sys Biol*. Feb 17; (2):e9866.
- Tao F, Soffers J, Hu D, Chen S, Gao X, Zhang Y, Zhao C, Smith SE, Unruh JR, Zhang D, Tsuchiya D, Venkatraman A, Zhao M, Li Z, Qian P, Parmely T, He XC, Washburn M, Florens L, Perry JM, **Zeitlinger J**, Workman J and Li L. (2020)  $\beta$ -Catenin and Associated Proteins Regulate Lineage Differentiation in Ground State Mouse Embryonic Stem Cells. *Stem Cell Reports*. Aug 7; S2213-6711(20)30295-2.
- Vincent BJ, Rice GR, Wong GM, Glassford WJ, Downs KI, Shastay JL, Charles-Obi K, Natarajan M, Gogol M, **Zeitlinger J** and Rebeiz M. (2019) An Atlas of Transcription Factors Expressed in Male Pupal Terminalia of *Drosophila melanogaster*. *G3*. Dec 3; 9(12):3961-3972.
- Tettey TT, Gao X, Shao W, Li H, Story BA, Chitsazan, AD, Glaser RL, Goode ZH, Seidel CW, Conaway RC, **Zeitlinger J**, Blanchette M and Conaway JW. (2019) A Role for FACT in RNA Polymerase II Promoter-Proximal Pausing. *Cell Reports*. June 25; 27(13):3770-3779.e7.

- Shao W, Alcantara SG and Zeitlinger J. (2019) Reporter-ChIP-nexus reveals strong contribution of the *Drosophila* initiator sequence to RNA polymerase pausing. *Elife*. April 25; 8:e41461.
- Miller DE, Staber C, Zeitlinger J and Hawley RS. (2018) GENOME REPORT: Highly Contiguous Genome Assemblies of 15 *Drosophila* Species Generated Using Nanopore Sequencing. *G3*. Oct 3;8(10):3131-3141.
- Li Z, Qian P, Shao W, Shi H, He XC, Gogol M, Yu Z, Wang Y, Qi M, Zhu Y, Perry JM, Zhang K, Tao F, Zhou K, Hu D, Han Y, Zhao C, Alexander R, Xu H, Chen S, Peak A, Hall K, Peterson M, Perera A, Haug JS, Parmely T, Li H, Shen B, Zeitlinger J, He C and Li L. (2018) Suppression of m<sup>6</sup>A reader Ythdf2 promotes hematopoietic stem cell expansion. *Cell Research*. Sep;28(9):904-917.
- Papagianni A, Fores M, Shao W, He S, Koenecke N, Andreu MJ, Samper N, Paroush Z, Gonzalez-Crespo S, Zeitlinger J and Jimenez, G. (2018) Capicua controls Toll/IL-1 signaling targets independently of RTK regulation. *Proceedings of the National Academy of Sciences*. Feb 20;115(8):1807-1812.
- De Kumar B, Parker HJ, Paulson A, Parrish ME, Zeitlinger J and Krumlauf R. (2017) Hoxa1 targets signaling pathways during neural differentiation of ES cells and mouse embryogenesis. *Developmental Biology*, Dec 1;432(1):151-164.
- De Kumar B, Parker HJ, Paulson A, Parrish ME, Pushel I, Singh NP, Zhang Y, Slaughter BD, Unruh JR, Florens L, Zeitlinger J and Krumlauf R. (2017) HOXA1 and TALE proteins display cross-regulatory interactions and form a combinatorial binding code on HOXA1 targets. *Genome Research*, Sept;27(9):1501-1512.
- Pascual J, Jacobs J, Sansores-Garcia L, Natarajan M, Zeitlinger J, Aerts S, Halder G and Hamaratoglu F. (2017) Hippo Reprograms the Transcriptional Response to Ras Signaling. *Developmental Cell*, Sep 25;42(6):667-680.e4.
- Shao W and Zeitlinger J. (2017) Paused RNA polymerase II inhibits new transcriptional initiation. *Nature Genetics*, July;49(7):1045-1051.
- Koenecke N, Johnston J, He Q, Meier S and Zeitlinger J. (2017) *Drosophila* poised enhancers are generated during tissue patterning with the help of repression. *Genome Research*, Jan;27(1):64-74.
- Koenecke N, Johnston J, Gaertner B, Natarajan M and Zeitlinger J. (2016) Genome-wide identification of *Drosophila* dorso-ventral enhancers by differential histone acetylation analysis. *Genome Biology*, Sept 27;17(1):196.
- Sun Y, Nien CY, Chen K, Liu HY, Johnston J and Zeitlinger J.\* Rushlow C.\* (2015) Zelda overcomes the high intrinsic nucleosome barrier at enhancers during *Drosophila* zygotic genome activation. *Genome Research*, Nov;25(11):1703-1714. \* co-corresponding authors
- He Q, Johnston J and Zeitlinger J. (2015) ChIP-nexus enables improved detection of *in vivo* transcription factor binding footprints. *Nature Biotechnology*, Apr;33(4):395-401.
- Wang YL, Duttke SH, Chen K, Johnston J, Kassavetis GA, Zeitlinger J and Kadonaga JT. (2014) TRF2, but not TBP, mediates the transcription of ribosomal protein genes. *Genes & Development*, Jul 15; 28(14):1550-1555.
- Ikmi A, Gaertner B, Seidel C, Srivastava M, Zeitlinger J and Gibson MC. (2014) Molecular evolution of the yap/yorkie proto-oncogene and elucidation of its core transcriptional program. *Molecular Biology and Evolution*, Jun;31(6):1375-1390.
- Bardet AF, Steinmann J, Bafna S, Knoblich JA, Zeitlinger J and Stark A. (2013) Identification of transcription factor binding sites from ChIP-seq data at high-resolution. *Bioinformatics*, Nov; 29(21):2705-2713.



- Chen K, Johnston J, Wanqing S, Meier S, Staber C and Zeitlinger J. (2013) A global change in RNA Polymerase II pausing during the *Drosophila* mid blastula transition. *eLife*, Aug 13;2:e00861.
- Lagha M, Bothma JP, Esposito E, Ng S, Stefanik L, Tsui C, Johnston J, Chen K, Gilmour DS, Zeitlinger J and Levine MS. (2013) Paused Pol II coordinates tissue morphogenesis in the *Drosophila* embryo. *Cell*, May 23;153(5):976-987.
- Gaertner B,\* Johnston J,\* Chen K, Wallaschek N, Paulson A, Garruss AS, Gaudenz K, De Kumar B, Krumlauf R and Zeitlinger J. (2012) Poised RNA Polymerase II changes over developmental time and prepares genes for future expression. *Cell Reports*, Dec 27;2(6):1670-1683. \*equal contribution
- Bardet AF, He Q, Zeitlinger J and Stark A. (2011) A computational pipeline for comparative ChIP-seq analyses. *Nature Protocols*, Dec15;7(1):45-61.
- He Q, Bardet A, Patton B, Purvis J, Johnston J, Paulson A, Gogol M, Stark AI,\* and Zeitlinger J.\* (2011) High conservation of transcription factor binding and evidence for combinatorial regulation across six *Drosophila* species. *Nature Genetics*, May;43(5):414-421. \*co-corresponding authors
- Hendrix D, Hong JW, Zeitlinger J, Rokhsar DS and Levine M. (2008) Promoter elements associated with RNA Pol II stalling in the *Drosophila* embryo. *Proceedings of the National Academy of Sciences*, Jun 3;105(22):7762-7767.
- Zeitlinger J, Stark A, Kellis M, Hong JW, Nechaev S, Adelman K, Levine M and Young RA. (2007) RNA polymerase stalling at developmental control genes in the *Drosophila melanogaster* embryo. *Nature Genetics*, Dec;39(12):1512-1516.
- Muse GW, Gilchrist DA, Nechaev S, Shah R, Parker JS, Grissom SF, Zeitlinger J, Adelman K. (2007) RNA polymerase is poised for activation across the genome. *Nature Genetics*, Dec;39(12):1507-1511.
- Zeitlinger J, Zinzen R, Stark A, Kellis M, Zhang H, Young RA and Levine M. (2007) Whole-genome ChIP-chip analysis of Dorsal, Twist and Snail suggests integration of diverse patterning processes in the *Drosophila* embryo. *Genes & Development*, Feb 15;21(4):385-390.
- Qi Y, Rolfe A, MacIsaac KD, Gerber GK, Pokholok D, Zeitlinger J, Danford T, Dowell RD, Fraenkel E, Jaakkola TS, Young RA and Gifford DK. (2006) High-resolution computational models of genome binding events. *Nature Biotechnology*, Aug;24(8):963-970.
- Pokholok DK,\* Zeitlinger J,\* Hannett NM, Reynolds DB and Young RA. (2006) Activated signal transduction kinases frequently occupy target genes. *Science*, July 28;313(5786):533-536. \*equal contribution
- Boyer LA, Plath K, Zeitlinger J, Brambrink T, Medeiros LA, Lee TI, Levine SS, Wernig M, Tajonar A, Ray MK, Bell GW, Otte, AP, Vidal M, Gifford DK, Young RA. and Jaenisch R. (2006) Polycomb complexes repress developmental regulators in murine embryonic stem cells. *Nature*, May 18;441(7091):349-53.
- Pokholok DK, Harbison CT, Levine S, Cole M, Hannett NH, Lee TI, Walker K, Lewitter F, Rolfe PA, Herbolzheimer E, Bell GW, Zeitlinger J, Gifford DK and Young RA. (2005) Genome-wide map of nucleosome acetylation and methylation in yeast. *Cell*, Aug 26;122(4):517-527.
- Harbison CT, Gordon DB, Lee TI, Rinaldi NJ, MacIsaac KD, Danford TW, Hannett NM, Tagne J-B, Reynolds DB, Yoo J, Jennings EG, Zeitlinger J, Pokholok DK, Kellis M, Rolfe A, Takusagawa KT, Lander ES, Gifford DK, Fraenkel E and Young RA. (2004) Transcriptional regulatory code of a eukaryotic genome. *Nature*, Sept 2;431(7004):99-104.

- Zeitlinger J, Simon I, Harbison CT, Hannett NM, Volkert TL, Fink GF and Young RA. (2003) Program-specific distribution of a transcription factor dependent on partner transcription factor and MAPK signaling. *Cell*, May 2;113(3):395-404.
- Lee TI, Rinaldi NJ, Robert F, Odom DT, Bar-Joseph Z, Gerber GK, Hannett NM, Harbison CT, Thompson CM, Simon I, Zeitlinger J, Jennings EG, Murray HL, Gordon DB, Ren B, Wyrick JJ, Tagne JB, Volkert TL, Fraenkel E, Gifford DK and Young RA. (2002) Transcriptional regulatory networks in *Saccharomyces cerevisiae*. *Science*, Oct 25;298(5594):799-804.
- Simon I, Barnett J, Hannett N, Harbison CT, Rinaldi NJ, Volkert TL, Wyrick JJ, Zeitlinger J, Gifford DK, Jaakkola TS and Young RA. (2001) Serial regulation of transcriptional regulators in the yeast cell cycle. *Cell*, Sept 21;106(6):697-708.
- Ren B,\* Robert F,\* Wyrick JJ,\* Aparicio O, Jennings EG, Simon I, Zeitlinger J, Schreiber J, Hannett N, Kanin E, Volkert TL, Wilson CJ, Bell SP and Young RA. (2000) Genome-wide location and function of DNA binding proteins. *Science*, Dec 22;290(5500):2306-2309. \*equal contribution
- Zeitlinger J and Bohmann D. (1999) Thorax closure in *Drosophila*: involvement of Fos and the JNK pathway. *Development*, 126, 3947-3956.
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