JULIA ZEITLINGER

CURRICULUM VITAE

PERSONAL DETAILS

Stowers Institute for Medical Research
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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

Our long-term goal is to understand the cis-regulatory code, a complex and fundamentally unresolved problem in biology. A comprehensive understanding would allow us to read gene regulatory information in the human genome, including cellular instructions regulating development and disease. To predict gene regulation from DNA sequence, we develop cutting-edge genomics technologies (e.g. ChIP-nexus), apply them to a variety of cell types in different model organisms, and use interpretable deep learning (BPNet) to extract the sequence rules that instruct the biology. We validate the rules experimentally and link them to the molecular mechanisms that underlie the cis-regulatory code.

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

2019-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)

2014-2018
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	*Neaves Award, Stowers Institute for Medical Research*
2012	*Hudson Prize by the M.R. and Evelyn Hudson Foundation*
2008-2013	*2008 NIH Director's New Innovator Award, National Institutes of Health*
2008-2012	*2008 Pew Scholar in Biomedical Sciences, Pew Charitable Trusts*
2000-2003	*Human Frontiers Science Program Long-Term Fellow*
1995-1999	*EMBL Ph.D. Student*
1992-1995	*German Academic Scholarship Foundation ("Studienstiftung")*

GRANTS

2018-2023	*"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 > $2,700,000*
2008-2013	*"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*
2008-2012	*"The role of RNA polymerase stalling in cellular memory during Drosophila development," Pew Charitable Trusts, 2008 Pew Scholar in Biomedical Sciences*
Since 2007	*"Transcriptional regulatory networks during Drosophila and mouse development", Core funding by the Stowers Institute for Medical Research Current budget ~ $1,000,000 per year*

PATENT

Effective 2019	*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*

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

Since 2021	*Haining Jiang (registered with GSSIMR)*
Since 2020	*Kim Escobar (registered with the IGPBS Program at KUMC)*
Since 2020	*Tatiana Gaitan (registered with GSSIMR)*
Since 2019	*Yue Liang (registered with GSSIMR)*
Since 2019	*Kaelan Brennan (registered with GSSIMR)*
2018-2023	*Khyati Dalal (Ph.D. from KUMC, Postgraduate Researcher in the lab)*
2016-2021	*Sergio Garcia-Moreno Alcantara (Ph.D. from Open University, U.K, Novogene Europe)*
2013-2019	*Vivekanandan Ramalingam (Ph.D. with Honors from the IGPBS Program at KUMC, now postdoc at Anshul Kundaje's lab at Stanford, US)*
2013-2018	*Wanqing Shao (Ph.D. from GSSIMR, Genomic Scientist, Boston Children's Hospital, US)*

2008-2013	*Björn Gärtner (Ph.D. from U Würzburg, Germany, Fate Therapeutics Inc, US)*
2010-2015	*Nina Koenecke (Ph.D. from Open University, U.K., Roche Diagnostics, Germany)*
2008-2013	*Kai Chen (Ph.D. from Open University, U.K., Professor, Kunming University, China)*

SUPERVISION OF POSTDOCS

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

SUPERVISION OF UNDERGRADUATES

Since 2011	*Hosted and supervised 6 students for their master thesis*
Since 2009	*Hosted and supervised 2 practicum students*
Since 2009	*Hosted and supervised 23 summer scholars*

TEACHING

Since 2021	*Two-week course in the fall on Gene Expression for GSSIMR predoctoral students*
Since 2012	*Two-week course in the fall "Genomic and Computational Approaches to Understanding Gene Expression BIO 702" for GSSIMR predoctoral students*
Since 2008	*Talks or informal lectures at University of Kansas Medical Center (~1 per year)*

PROFESSIONAL SOCIETIES

| Since 2015 | *International Society for Computational Biology (ISCB)* |
| Since 2014 | *American Society for Biochemistry and Molecular Biology (ASBMB)* |

CONTINUING EDUCATION

| 2021-22 | *Fellow in the Executive Leadership in Academic Technology, Engineering and Science (ELATES) Program* |
| 2018 | *EMBO leadership course* |

SCIENTIFIC LEADERSHIP

2016-2020	*Co-organizer of CSHL's "Systems Biology: Global regulation of Gene Expression"*
2015-2020	*Co-organizer of ISCB's "Intelligent Systems for Molecular Biology"*
Since 2014	*Co-organizer of ASBMB's biannual "Evolution and Core Processes in Gene Regulation"*

PEER REVIEW

Since 2023   *Standing member of the NIH study section Genomics, Computational Biology and Technology (GCAT)*

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)*

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 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*

GOVERNING

Since 2023   *Chair of the Steering Committee for Computational Biology*

Since 2022   *Committee member for the computational infrastructure at SIMR*

Since 2022   *Committee member for creating the Computational Fellow Program and the Bioinformatics Postbaccalaureate Program*

Since 2019   *Dean's Council of GSSIMR*

Since 2016   *Member of the GSSIMR Assessment Committee, Chair since 2018*

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)*

2011-2014   *GSSIMR Admission Committee*

SELECTED INVITED TALKS

1. **Invited conference speaker.** *"Deciphering the cis-regulatory code that guides development using interpretable deep learning", MBSJ Symposium in Kobe, Japan, December 6, 2023*
2. **Invited departmental seminar.** *"Understanding the sequence rules of gene regulation during development using interpretable deep learning", Princeton University, October 23, 2023*
3. **Invited conference speaker.** *"Deciphering sequence rules of transcription factor binding in vivo with interpretable deep learning" Rules of protein-DNA recognition, Cancun, Mexico, October 10, 2023*
4. **Invited lecturer.** *"Deciphering the cis-regulatory code by interpretable deep learning" CSHL Gene Expression course, August 11, 2023*
5. **Invited conference speaker.** *"Deciphering the cis-regulatory code of development using interpretable deep learning" Penn State Summer Symposium, August 8, 2023*
6. **Invited seminar.** *"How to interpret the cis-regulatory sequence rules learned by a deep learning model" Barcelona Collaboratorium, July 6, 2023*

7. ***Invited symposium speaker. "****Deciphering cis-regulatory code for development using interpretable deep learning", Symposium organized by students, University of Colorado, Boulder, May 19, 2023*

8. ***Invited departmental seminar "****Deciphering cis-regulatory code for development using interpretable deep learning", Michigan State University, April 26, 2023*

9. ***Invited departmental seminar. "****Deciphering cis-regulatory code for development using interpretable deep learning", University of Wisconsin, Madison, April 6, 2023*

10. ***Invited conference speaker. "****Deciphering the genome's second code by interpretable deep learning", Inaugural Symposium of the Barcelona Collaboratorium, October 4-5, 2022*

11. ***Invited seminar speaker****. "Using neural networks to understand how transcription factors read out the cis-regulatory code", DeepMind, London, UK, August 17, 2022*

12. ***Invited seminar speaker. "****Using neural networks to decipher the cis-regulatory code", Max Planck Institute for Multidisciplinary Sciences, Göttingen, Germany, August 15, 2022*

13. ***Invited conference speaker. "****The cis-regulatory code of chromatin accessibility in the early Drosophila embryo", ASBMB's "Evolution and core processes in gene expression" July 21-24, 2022*

14. ***Invited departmental seminar. "****Elucidating cis-regulatory code for development using high-resolution deep genomics", Memorial Sloan Kettering Cancer Center, May 5, 2022*

15. ***Invited theory lunch seminar. "****The inverted learning paradigm of decoding genome information", Harvard University (virtual), April 22, 2022*

16. ***Invited departmental seminar. "****Elucidating cis-regulatory code for development using high-resolution deep genomics", New York University, April 4, 2022*

17. ***Invited departmental seminar. "****Using high-resolution genomics to predict cell-type-specific gene regulation from DNA sequence", Frontiers in Biology seminar at Stanford, November 10, 2021*

18. ***Invited seminar speaker. "****Predicting gene regulation and development from DNA sequence", Wash U, November 5, 2021*

19. ***Invited conference speaker. "****High-resolution in vivo binding footprints suggest a common TFIID structure with promoter-specific TBP dynamics", CSHL Transcription Meeting (virtual), Sept 1, 2021*

20. ***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*

21. ***Invited departmental seminar. "****Using deep learning to discover cis-regulatory syntax", Frontiers in Biology seminar at Stanford University, November 7, 2019*

22. ***Invited conference speaker. "****Deep learning reveals nuanced organizational features of the cis-regulatory code in mouse ES cells", CSHL Transcription Meeting, August 29, 2019*

23. ***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*

24. ***Invited departmental seminar. "****From biology to computation and back: deep learning of cis-regulatory code", LMU Munich, Germany, July 19, 2019*

25. ***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*

26. ***Invited departmental seminar. "****Looking inside the black box: using deep learning to discover cis-regulatory code", University of California Irvine, April 25, 2019*

27. ***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*

28. ***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*

29. ***Invited departmental seminar. "****Using high-resolution genomics approaches to decode transcription: from maps to mechanisms", Yale University, September 11, 2018*

PUBLICATIONS

PREPRINTS

Dalal K, McAnany C, Weilert M, McKinney MC, Krueger S, and Zeitlinger J (2024) Interpretable deep learning reveals the sequence rules of Hippo signaling. *BioRxiv*. 10.1101/2024.02.22.580842

Alexandari AM, Horton CA, Shrikumar A, Shah N., Li E, Weilert M., Pufall MA, Zeitlinger J, Fordyce PM, and Kundaje A (2023) De novo distillation of thermodynamic affinity from deep learning regulatory sequence models of in vivo protein-DNA binding. *BioRxiv*. 10.1101/2023.05.11.540401

PEER-REVIEWED ARTICLES

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. (2023) Short tandem repeats bind transcription factors to tune eukaryotic gene expression. *Science.* Sept 22;381(6664):eadd1250.

Maven BEJ, Gifford CA, Weilert M, Gonzalez-Teran B, Hüttenhain R, Pelonero A, Ivey KN. Samse-Knapp K, Kwong W, Gordon D, McGrego M, Nishion T, Okorie E, Rossman S, Costa MW, Frogan NJ, Zeitlinger J and Srivastava D. (2023) The multi-lineage transcription factor ISL1 controls cardiomyocyte cell fate through interactions with NKX2.5. *Stem Cell Reports*. Nov 14;18(11):2138-2153.

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. *Nature Communications*. 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 in the Drosophila embryo is determined by transcription factor pioneering and enhancer activation. *Developmental 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 Genetics*. 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. *Nature Genetics.* 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. *Molecular Systems Biology*. 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) β-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^{6}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 ToII/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* midblastula 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 A* 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, Herbolsheimer 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.

Zeitlinger J, Kockel L, Peverali FA, Jackson DB, Mlodzik M and Bohmann D. (1997) Defective dorsal closure and loss of epidermal decapentaplegic expression in *Drosophila* fos mutants. *EMBO Journal*, Dec 15;16(24):7393-7401.

Kockel L, Zeitlinger J, Staszewski LM, Mlodzik M and Bohmann D. (1997) Jun in *Drosophila* development: redundant and nonredundant functions and regulation by two MAPK signal transduction pathways. *Genes & Development*, July 1;11(13):1748-1758.

Costaridis P, Horton C, Zeitlinger J, Holder N and Maden M. (1996) Endogenous retinoids in the zebrafish embryo and adult. *Developmental Dynamics*, Jan;205(1):41-51.

REVIEW ARTICLES

Nora EP, Aerts S, Wittkopp PJ, Bussemaker HJ, Bulyk M, Sinha S, Zeitlinger J, Crocker J, Fuxman Bass JI (2023) Emerging questions in transcriptional regulation. *Cell Systems* doi: 10.1016/j.cels.2023.03.005.

Raicu A-M, Fay JC, Rohner N, Zeitlinger J and Arnosti D. (2023) Off the deep end: What can deep learning do for the gene expression field? *JBC* doi: https://doi.org/10.1016/j.jbc.2022.102760

Zeitlinger J. (2020), Seven myths of how transcription factors read the cis-regulatory code. *Current Opinion in Systems Biology: https://authors.elsevier.com/sd/article/S2452-3100(20)30030-5*

Arnosti DN, Fay JC, Zeitlinger J. (2015) Cori meets Dobzhansky: Evolution and Gene Expression in St. Louis: A report on the "Evolution and Core Processes in Gene Regulation" meeting in St. Louis, June 25-28, *Bioessays*, Oct;37(10):1042-4.

Gaertner B and Zeitlinger J. (2014) RNA polymerase II pausing during development. *Development*, 141(6): doi: 1179-83. doi: 10.1242/dev.088492.

Zeitlinger J. (2011) Book review of Evolution, Development, and the Predictable Genome, by David L. Stern. *American Journal of Human Biology*, 23, 234-236. doi: 10.1002/ajhb.21162.

Zeitlinger J and Stark A. (2010) Developmental gene regulation in the era of genomics. *Developmental Biology*, 339(2), 230-239.