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
Enhancer regulation
Paused RNA polymerase II
Drosophila and mouse development
Computational models
Deep learning

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 high-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
Stowers Institute for Medical Research

2015-present
Associate Professor
Department of Pathology and Laboratory Medicine
University of Kansas Medical Center (KUMC)

2013-2018
Associate Investigator
Stowers Institute for Medical Research

2008-2015
Assistant Professor
Department of Pathology and Laboratory Medicine
University of Kansas Medical Center (KUMC)

2007-2013
Assistant Investigator
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

Since 2018	*“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 > $1,200,000 per year*

SUPERVISION OF PH.D. STUDENTS

2008-2013	*Kai Chen (Ph.D. from Open University, U.K., now Professor, Kunming University, China)*
2008-2013	*Björn Gärtner (Ph.D. from U Würzburg, Germany, now at Fate Therapeutics Inc, US)*
2010-2015	*Nina Koenecke (Ph.D. from Open University, U.K., now at EUROIMMUN, Germany)*
2013-2018	*Wanqing Shao (Ph.D. from Graduate School of the Stowers Institute, now postdoc in Ting Wang’s lab, Wash U, US)*
2013-2019	*Vivekanandan Ramalingam (Ph.D. with Honors from the IGPBS Program at KUMC, now postdoc at Anshul Kundaje’s lab at Stanford, US)*
2016-2021	*Sergio Garcia-Moreno Alcantara (Ph.D. from Open University, U.K.)*
Since 2018	*Khyati Dalal (registered with the IGPBS Program at KUMC)*
Since 2019	*Kaelan Brennan (registered with the Graduate School of the Stowers Institute)*
Since 2019	*Yue Liang (registered with the Graduate School of the Stowers Institute)*
Since 2020	*Tatiana Gaitan (registered with the Graduate School of the Stowers Institute)*
Since 2020	*Kim Escobar (registered with the IGPBS Program at KUMC)*

SUPERVISION OF POSTDOCS

2008-2014	*Qiye He (now Director, R&D at Singlera Genomics, La Jolla, USA and Shanghai, China)*

2009-2011	*Sangeeta Bafna (now Manager-Patent & Licensing, New Jersey Institute of Technology)*
2011-2016	*Malini Natarajan (now Senior Scientist at Moderna, Wakefield, Rhode Island, USA)*
2015-2017	*Robin Fropf (now Senior Scientist at Adaptive Biotechnologies Corp., Seattle, USA)*
Since 2018	*Sabrina Krueger*
Since 2019	*Simon Bourdareau*
Since 2019	*Nilay Shah*
Since 2019	*Charles McAnany*
Since 2020	*Curtis Bacon*

TEACHING

Since 2008	*Talks or informal lectures at University of Kansas Medical Center (~1 per year)*
Since 2012	*Two-week course in the fall "Genomic and Computational Approaches to Understanding Gene Expression BIO 702" for Ph.D. students of the Stowers Graduate School of the Stowers Institute*

LEADERSHIP TRAINING

2018	*EMBO leadership course*
2019	*Workshop on how to be an effective leader by David Renz, PhD*
2021-22	*Fellow in the Executive Leadership in Academic Technology, Engineering and Science (ELATES) Program*

SCIENTIFIC LEADERSHIP

Since 2014	*Co-organizer of the bi-annual ASBMB meeting "Evolution and Core Processes in Gene Regulation", next to be held in 2022*
Since 2015	*Co-organizer of the annual ISMB meeting of the International Society for Computational Biology (ISCB)*
2016-2020	*Co-organizer of the CSHL meeting "Systems Biology: Global regulation of Gene Expression"*

PEER REVIEW

Since 2015	*Ad-hoc reviewer for NIH study section Genetic Variation and Evolution (GVE), NIH study section Genomics, Computational Biology and Technology (GCAT), NIH Director's New Innovator Award, NIH Human BioMolecular Atlas Program (HubMAP), ERC*
Since 2008	*Reviewer for Cell, Science, Nature, Nature Genetics, Nature Methods, Genome Res, Genome Biol, PLoS Genetics, Mol Sys Biol, Dev Cell, Molecular Cell, Cell Systems, eLife, PNAS, NAR and others*

PUBLICATIONS

PEER-REVIEWED ARTICLES

Soffers, J.H.M., Alcantara, S.G., Li, X., Shao, W., Seidel, C.W., Li, H., Zeitlinger, J., Abmayr, S.M., Workman, J.L. (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.*, 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., Zeitlinger, J. (2021) TATA and paused promoters active in differentiated tissues have distinct expression characteristics. *Mol Sys Biol*. Feb 17; (2):e9866.

Zeitlinger, J. (2020) Seven myths of how transcription factors read cis-regulatory code. *Curr Opin Syst Biol.* Oct 23; 22-31.

Tao, F., Soffers, J., Hu, D., Chen, S., Gao, X., Zhang, Y., Zhao, C., Smith, S.E., Unruh, J.R., Zhang, D., Tsuchiya, D., Venkatraman, A., Zhao, M., Li, Z., Qian, P., Parmely, T., He, X.C., Washburn, M., Florens, L., Perry, J.M., Zeitlinger, J., Workman, J., 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, B.J., Rice, G.R., Wong, G.M., Glassford, W.J., Downs, K.I., Shastay, J.L., 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, T.T., Gao, X., Shao, W., Li, H., Story, B.A., Chitsazan, A.D., Glaser, R.L., Goode, Z.H., Seidel, C.W., Conaway, R.C., Zeitlinger, J., Blanchette, M., and Conaway, J.W. (2019) A Role for FACT in RNA Polymerase II Promoter-Proximal Pausing. *Cell Reports*. June 25; 27(13):3770-3779.e7.

Shao, W., Alcantara, S.G., 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, D.E., Staber, C., Zeitlinger, J., and Hawley, R.S. (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, X.C., Gogol, M., Yu, Z., Wang, Y., Qi, M., Zhu, Y., Perry, J.M., 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, J.S., 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, M.J., 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, H.J., Paulson, A., Parrish M.E., 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, H.J., Paulson, A., Parrish M.E., Pushel, I., Singh, N.P., Zhang, Y., Slaughter, B.D., Unruh, J.R., 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, C.Y., Chen, K., Liu, H.Y., 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, Y.L., Duttke, S.H., Chen, K., Johnston, J., Kassavetis, G.A., Zeitlinger, J. and Kadonaga, J.T. (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, M.C. (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, A.F., Steinmann, J., Bafna, S., Knoblich, J.A., 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 bastula transition. *eLife,* Aug 13;2:e00861.

Lagha, M., Bothma, J.P., Esposito, E., Ng, S., Stefanik, L., Tsui, C., Johnston, J., Chen, K., Gilmour, D.S., Zeitlinger, J. and Levine, M.S., (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, A.S., 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, A.F., 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.l.* 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, J.W., Zeitlinger, J., Rokhsar, D.S. 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, J.W., Nechaev, S., Adelman, K., Levine, M. and Young, R.A. (2007) RNA polymerase stalling at developmental control genes in the *Drosophila melanogaster* embryo. *Nature Genetics*, Dec;39(12):1512-1516.

Muse, G.W., Gilchrist, D.A., Nechaev, S., Shah, R., Parker, J.S., Grissom, S.F., 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, R.A. 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, K.D., Gerber, G.K., Pokholok, D., Zeitlinger, J., Danford, T., Dowell, R.D., Fraenkel, E., Jaakkola, T.S., Young, R.A. and Gifford, D.K. (2006) High-resolution computational models of genome binding events. *Nature Biotechnology*, Aug;24(8):963-970.

Pokholok, D.K.*, Zeitlinger, J.*, Hannett, N.M., Reynolds, D.B. and Young, R.A. (2006) Activated signal transduction kinases frequently occupy target genes. *Science*, July 28;313(5786):533-536. *equal contribution

Boyer, L.A., Plath, K., Zeitlinger, J., Brambrink, T., Medeiros, L.A., Lee, T.I., Levine, S.S., Wernig, M., Tajonar, A., Ray, M.K., Bell, G.W., Otte, A.P., Vidal, M., Gifford, D.K., Young, R.A. and Jaenisch, R. (2006) Polycomb complexes repress developmental regulators in murine embryonic stem cells. *Nature*, May 18;441(7091):349-53.

Pokholok, D.K., Harbison, C.T., Levine, S., Cole, M., Hannett, N.H., Lee, T.I., Walker, K., Lewitter, F., Rolfe, P.A., Herbolsheimer, E., Bell, G.W., Zeitlinger, J., Gifford, D.K. and Young, R.A. (2005) Genome-wide map of nucleosome acetylation and methylation in yeast. *Cell*, Aug 26;122(4):517-527.

Harbison, C.T., Gordon, D.B., Lee, T.I., Rinaldi, N.J., Macisaac, K.D., Danford, T.W., Hannett, N.M., Tagne, J.-B., Reynolds, D.B., Yoo, J., Jennings, E.G., Zeitlinger, J., Pokholok, D.K., Kellis, M., Rolfe, A., Takusagawa, K.T., Lander, E.S., Gifford, D.K., Fraenkel, E. and Young, R.A. (2004) Transcriptional regulatory code of a eukaryotic genome. *Nature*, Sept 2;431(7004):99-104.

Zeitlinger, J., Simon, I., Harbison, C.T., Hannett, N.M., Volkert, T.L., Fink, G.F. and Young, R.A. (2003) Program-specific distribution of a transcription factor dependent on partner transcription factor and MAPK signaling. *Cell*, May 2;113(3):395-404.

Lee, T.I., Rinaldi, N.J., Robert, F., Odom, D.T., Bar-Joseph, Z., Gerber, G.K., Hannett, N.M., Harbison, C.T., Thompson, C.M., Simon, I., Zeitlinger, J., Jennings, E.G., Murray, H.L., Gordon, D.B., Ren, B., Wyrick, J.J., Tagne, J.B., Volkert, T.L., Fraenkel, E., Gifford, D.K. and Young, R.A. (2002) Transcriptional regulatory networks in *Saccharomyces cerevisiae*. *Science*, Oct 25;298(5594):799-804.

Simon, I., Barnett, J., Hannett, N., Harbison, C.T., Rinaldi, N.J., Volkert, T.L., Wyrick, J.J., Zeitlinger, J., Gifford, D.K., Jaakkola, T.S. and Young, R.A. (2001) Serial regulation of transcriptional regulators in the yeast cell cycle. *Cell*, Sept 21;106(6):697-708.

Ren, B.*, Robert, F.*, Wyrick, J.J.*, Aparicio, O., Jennings, E.G., Simon, I., Zeitlinger, J., Schreiber, J., Hannett, N., Kanin, E., Volkert, T.L., Wilson, C.J., Bell, S.P. and Young, R.A. (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, F.A., Jackson, D.B., 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, L.M., 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

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, D.N., Fay, J.C., 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.

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