

## Cole Trapnell, Ph.D.

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	Department of Genome Sciences	
	University of Washington	
	Seattle, WA, 98105, USA	

APPOINTMENT	<b>University of Washington</b>
	Assistant Professor of Genome Sciences, July 2014 - present

TRAINING	<b>Harvard University</b>
	Postdoctoral Training, 2010 - 2014
	Department of Stem Cell and Regenerative Biology
	<b>Mentor:</b> John L. Rinn

	<b>University of Maryland, College Park</b>
	Ph.D. Computer Science, 2010
	<b>Advisors:</b> Steven Salzberg, Lior Pachter

	<b>University of Maryland, College Park</b>
	B.S. Computer Science, 2005
	B.S. Mathematics, 2005

PROFESSIONAL	<b>University of Washington</b>	<b>2014 - pres.</b>
EXPERIENCE	Assistant Professor, Department of Genome Sciences	
	<b>Harvard University</b>	<b>2010 - 2014</b>
	Postdoctoral Fellow, Department of Stem Cell and Regenerative Biology	
	<b>The Broad Institute of MIT and Harvard</b>	<b>2010 - 2014</b>
	Visiting Postdoctoral Fellow	
	<b>University of California, Berkeley</b>	<b>2008 - 2010</b>
	Visiting Student Researcher, Department of Mathematics	
	<b>University of Maryland, College Park</b>	<b>2006 - 2010</b>
	Graduate Research Assistant, Department of Computer Science	
	<b>Actuate Corporation</b>	<b>2005 - 2006</b>
	Software Engineer	
	<b>TopGun Software/LeverageFX</b>	<b>2002 - 2005</b>
	Co-founder and Software Engineer	
	<b>U.S. Army Research Laboratory</b>	<b>1999 - 2002</b>
	Student Engineer	

HONORS AND AWARDS	<p>ISCB Overton Prize, 2018</p> <p>NIH Director's New Innovator Award, 2015</p> <p>Alfred P. Sloan Foundation Research Fellowship, 2015</p> <p>Damon Runyon Dale F. Frey Award for Breakthrough Scientists, 2014</p> <p>Damon Runyon Postdoctoral Fellowship, 2011-2014</p> <p>Finalist, Burroughs-Wellcome Career Award at the Scientific Interface, 2013</p> <p>Genome Biology Award, <i>BioMed Central</i>, 2010. (Bowtie, with Langmead, <i>et al</i>)</p> <p>Next-Generation Sequencing Paper of the Year, 2009. <i>Bioinformatics</i> (TopHat)</p> <p>Teaching Excellence Award, 2007, University of Maryland Computer Science Department</p>
SOFTWARE	<p><b>Monocle:</b> Time-series and differential expression analysis for single-cell RNA-Seq.</p> <p><b>Cufflinks:</b> Transcriptome assembly and differential expression with RNA-Seq.  Citations for related article<sup>†</sup> Trapnell <i>et al</i>, 2010: 4,402  Highlighted as a notable breakthrough in Computational Biology, 2010.  See: H. Craig Mak, <i>Nature Biotechnology</i> Vol. 29, 45 (2011)</p> <p><b>TopHat:</b> Spliced short read alignment for RNA-Seq.  Citations for related article<sup>†</sup> Trapnell <i>et al</i>, 2009: 4,933</p> <p><b>Bowtie:</b> Ultrafast short read mapping (with Ben Langmead)  Citations for related article<sup>†</sup> Langmead <i>et al</i>, 2009: 8,578</p> <p><b>Spats:</b> RNA structure with SHAPE-Seq (with Sharon Aviran)</p> <p><b>MUMmerGPU:</b> Fast sequence alignment on the GPU (with Michael Schatz)</p>
TEACHING	UW GENOME 551: Gene Regulation
PATENTS	High-throughput methodology for identifying RNA-Protein interactions transcriptome-wide. (issued: 13/911,429)
PUBLICATIONS	<p><u><i>Journal Articles:</i></u></p> <ol style="list-style-type: none"> <li>1. Darren A. Cusanovich*, Andrew J. Hill*, Delasa Aghamirzaie, Riza M. Daza, Hannah A. Pliner, Joel B. Berletch, Galina N. Filippova, Xingfan Huang, Lena Christiansen, William S. DeWitt, Choli Lee, Samuel G. Regalado, David F. Read, Frank J. Steemers, Christine M. Disteche, <b>Cole Trapnell</b><sup>†</sup>, Jay Shendure<sup>†</sup>, A first generation atlas of <i>in vivo</i> mammalian chromatin accessibility at single cell resolution. (in press at <i>Cell</i>)</li> <li>2. Hannah A. Pliner, Jonathan Packer, Jos L. McFaline-Figueroa, Darren Cusanovich, Riza Daza, Sanjay Srivatsan, Xiaojie Qiu, Dana Jackson, Anna Minkina, Andrew Adey, Frank Steemers, Jay Shendure<sup>†</sup>, <b>Cole Trapnell</b><sup>†</sup>, Chromatin accessibility dynamics of myogenesis at single cell resolution. (in press at <i>Molecular Cell</i>)</li> </ol>

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<sup>†</sup>Google Scholar, as of 11/18/2016

\*Equal contribution

<sup>†</sup>Co-corresponding author

3. Davide Cacchiarelli<sup>†</sup>, Xiaojie Qiu, Sanjay Srivatsan, Michael J. Ziller, Eliah Overbey, Jonna Grimsby, Prapti Pokharel, Ken Livak, Shuqiang Li, Alex Meissner, Tarjei Mikkelsen, John Rinn, **Cole Trapnell**<sup>†</sup>, Aligning single-cell developmental and reprogramming trajectories identifies molecular determinants of reprogramming outcome. (in press at *Cell Systems*)
4. Ryan M. Mulqueen, Dmitry Pokholok, Steve Norberg, Andrew J. Fields, Duanchen Sun, Kristof A. Torkenczy, Jay Shendure, **Cole Trapnell**, Brian J. O’Roak, Zheng Xia, Frank J. Steemers, Andrew C. Adey, Scalable and efficient single-cell DNA methylation sequencing by combinatorial indexing. *Nature Biotechnology* 36, pages 428-431 (2018)
5. Darren Cusanovich\*, James Reddington\*, David Garfield\*, Riza Daza, Raquel Marco-Ferreres, Lena Christiansen, Xiaojie Qiu, Frank Steemers, **Cole Trapnell**, Jay Shendure<sup>†</sup>, Eileen Furlong<sup>†</sup>, The cis-regulatory dynamics of embryonic development at single cell resolution. *Nature* 555, 538-542 (2018)
6. Alistair B. Russell, **Cole Trapnell**, Jesse D. Bloom, Extreme heterogeneity of influenza virus infection in single cells. *eLife* 7:e32303 (2018)
7. Andrew Hill\*, Jose L. McFaline-Figueroa\*, Jay Shendure<sup>†</sup>, **Cole Trapnell**<sup>†</sup>, On the design of CRISPR-based single cell molecular screens. *Nature Methods* 15, pages 271274 (2018).
8. Junyue Cao, Jonathan S. Packer, Vijay Ramani, Darren A. Cusanovich, Chau Huynh, Riza Daza, Xiaojie Qiu, Choli Lee, Scott N. Furlan, Frank J. Steemers, Andrew Adey, Robert H. Waterston<sup>†</sup>, **Cole Trapnell**<sup>†</sup>, Jay Shendure<sup>†</sup>, Comprehensive single cell transcriptional profiling of a multicellular organism by combinatorial indexing. *Science* 357: 6352 661-667. (2017)
9. Xiaojie Qiu, Qi Mao, Ying Tang, Li Wang, Raghav Chawla, Hannah Pliner, **Cole Trapnell**, Reversed graph embedding resolves complex single-cell developmental trajectories. *Nature Methods*, 14, 979982. (2017)
10. Jin Zhang, Sutheera Ratanasirintrawoot, Sriram Chandrasekaran, Zhaoting Wu, Scott B Ficarro, Chunxiao Yu, Christian A Ross, Davide Cacchiarelli, Qing Xia, Marc Seligson, Gen Shinoda, Wen Xie, Patrick Cahan, Longfei Wang, Shyh-Chang Ng, Supisara Tintara, **Cole Trapnell**, Tamer Onder, Yui-Han Loh, Tarjei Mikkelsen, Piotr Sliz, Michael A Teitell, John M Asara, Jarrod A Marto, Hu Li, James J Collins, George Q Daley, LIN28 regulates stem cell metabolism and conversion to primed pluripotency. *Cell Stem Cell* 19:1 66-80. (2017)
11. Xiaojie Qiu, Andrew Hill, Jonathan Packer, Dejun Lin, Yian Ma, **Cole Trapnell**, Census enables lineage-, isoform-, and allele-resolution mRNA quantification in single cells. *Nature Methods* 14 (3), 309-315. (2017)
12. Serena Liu and **Cole Trapnell**. Single-cell transcriptome sequencing: recent advances and remaining challenges. *F1000 Faculty Reviews*. (2016) *Invited paper*.

13. **Cole Trapnell**, Defining cell types and states with single-cell genomics.  
*Genome Research*, 25:1491-1498. (2015) *Invited paper*.
14. Naresh K. Hanchate, Kunio Kondoh, Zhonghua Lu, Donghui Kuang, Xiaolan Ye, Xiaojie Qiu, Lior Pachter, **Cole Trapnell**<sup>†</sup>, Linda B. Buck<sup>†</sup>, Single-cell transcriptomics reveals receptor transformations during olfactory neurogenesis,  
*Science*, 350:62-65. (2015)
15. Davide Cacchiarelli\*, **Cole Trapnell**\*, Michael J. Ziller\*, Magali Soumillon, Marcella Cesana, Rahul Karnik, Zachary D. Smith, Sutheera Ratanasirintrao, Xiaolan Zhang, Shannan Ho Sui, Zhaoting Wu, Veronika Akopian, Casey A. Gifford, John Doench, John L. Rinn, George Q. Daley, Alexander Meissner, Eric S. Lander, Tarjei S. Mikkelsen, Integrative analyses of human reprogramming reveal dynamic nature of induced pluripotency.  
*Cell*, 16:2 412-424 (2015)
16. Darren A. Cusanovich, Riza Daza, Andrew Adey, Hannah Pliner, Lena Christiansen, Kevin L. Gunderson, Frank J. Steemers, **Cole Trapnell**, Jay Shendure, Multiplex single cell profiling of chromatin accessibility by combinatorial cellular indexing.  
*Science*, 348: 6237 910-914. (2015)
17. Takuji Suzuki, Paritha Arumugam, Takuro Sakagami, Nico Lachmann, Claudia Chalk, Anthony Sallese, Shuichi Abe, **Cole Trapnell**, Brenna Carey, Thomas Moritz, Punam Malik, Carolyn Lutzko, Robert E. Wood, and Bruce C. Trapnell, Pulmonary Macrophage Transplantation Therapy.  
*Nature*, 514: 450-453. (2014)
18. **Cole Trapnell**\*, Davide Cacchiarelli\*, Jonna Grimsby, Prapti Pokharel, Shuqiang Li, Michael Morse, Niall J. Lennon, Kenneth J. Livak, Tarjei S. Mikkelsen, John L. Rinn, The dynamics and regulators of cell fate decisions are revealed by pseudotemporal ordering of single cells.  
*Nature Biotechnology*, 32: 381-386. (2014)
19. Ezgi Hacisuleyman\*, Loyal A. Goff\*, **Cole Trapnell**, Adam Williams, Jorge Henao-Mejia, Lei Sun, Patrick McClanahan, David G. Hendrickson, Martin Sauvageau, David R. Kelley, Michael Morse, Jesse Engreitz, Eric S. Lander, Mitch Guttman, Harvey F. Lodish, Richard Flavell, Arjun Raj, John L. Rinn. Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre  
*Nature Structural & Molecular Biology*, 21: 198-206. (2014)
20. Ian M. Silverman, Fan Li, Anissa Alexander, Loyal Goff, **Cole Trapnell**, John L. Rinn, Brian D. Gregory, RNase-mediated protein footprint sequencing reveals protein-binding sites throughout the human transcriptome.  
*Genome Biology* 15:R3 (2014)
21. Stephen Altschul, Barry Demchak, Richard Durbin, Robert Gentleman, Martin Krzywinski, Heng Li, Anton Nekrutenko, James Robinson, Wayne Rasband, James Taylor, **Cole Trapnell**, The anatomy of successful computational biology software.  
*Nature Biotechnology*, 31, 894-897. (2013)
22. Casey A Gifford\*, Michael J Ziller\*, Hongcang Gu, **Cole Trapnell**, Julie Donaghey, Alexander Tsankov, Alex K Shalek, David R Kelley, Alexander A Shishkin, Robbyn Issner, Xiaolan Zhang, Michael Coyne, Jennifer L Fostel, Laurie Holmes, Jim Meldrim, Mitchell Guttman, Charles Epstein, Hongkun Park, Oliver Kohlbacher, John Rinn,

- Andreas Gnirke, Eric S Lander, Bradley E Bernstein, Alexander Meissner, Transcriptional and epigenetic dynamics during specification of human embryonic stem cells. *Cell*, 153, 5, 1149-1163. (2013)
23. Daehwan Kim, Geo Pertea, **Cole Trapnell**, Harold Pimentel, Ryan Kelley, Steven L Salzberg, TopHat2: Accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome Biology*, 14:R36. (2013)
24. Stefanie A Mortimer, **Cole Trapnell\***, Sharon Aviran\*, Lior Pachter, Julius B Lucks, SHAPE-Seq: High-Throughput RNA Structure Analysis. *Current Protocols in Chemical Biology* DOI: 10.1002/9780470559277.ch120019. (2013)
25. Lei Sun\*, Loyal A Goff\*, **Cole Trapnell\***, Ryan Alexander, Kinyui Alice Lo, Ezgi Hacisuleyman, Martin Sauvageau, Barbara Tazon-Vega, David R Kelley, David G Hendrickson, Bingbing Yuan, Manolis Kellis, Harvey F Lodish, John L Rinn, Long noncoding RNAs regulate adipogenesis. *Proc. of the National Academy of Sciences* 110, 9, 3387-3392. (2013)
26. **Cole Trapnell\***, David Hendrickson\*, Martin Sauvageau, Loyal Goff, John Rinn, Lior Pachter, Differential analysis of gene regulation at transcript resolution with RNA-seq. *Nature Biotechnology*, 31, 4653. (2013)
27. **Cole Trapnell**, Adam Roberts, Loyal Goff, Geo Pertea, Daehwan Kim, David R. Kelley, Harold Pimentel, Steven L. Salzberg, John L. Rinn, Lior Pachter, Differential gene and transcript expression analysis of RNA-Seq experiments with TopHat and Cufflinks. *Nature Protocols*, 7, 562578. (2012)
28. Tim R. Mercer, Daniel J. Gerhardt, Marcel E. Dinger, Joanna Crawford, **Cole Trapnell**, Jeffrey A. Jeddloh, John S. Mattick, and John L. Rinn, Targeted RNA sequencing reveals the deep complexity of the human transcriptome. *Nature Biotechnology*, 30: 99-104. (2012)
29. Moran N. Cabili, **Cole Trapnell**, Loyal Goff, Magdalena Koziol, Barbara Tazon-Vega, Aviv Regev and John L. Rinn, Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. *Genes and Development*, 2011.25. (2011)
30. Adam Roberts, Harold Pimentel, **Cole Trapnell<sup>†</sup>**, and Lior Pachter<sup>†</sup>, Identification of novel transcripts in annotated genomes using RNA-Seq. *Bioinformatics*, 27 (17): 2325-2329. (2011)
31. Julius B. Lucks, Stefanie A. Mortimer, **Cole Trapnell**, Shujun Luo, Sharon Aviron, Lior Pachter, Jennifer A. Doudna, and Adam P. Arkin, SHAPE-Seq: Multiplexed RNA Secondary and Tertiary Structure Determination. *Proc. of the National Academy of Sciences* 108, 27. (2011)
32. Sharon Aviran, **Cole Trapnell**, Julius B. Lucks, Stefanie A. Mortimer, Jennifer A. Doudna, Adam P. Arkin, and Lior Pachter, Modeling and automation of SHAPE-Seq analysis. *Proc. of the National Academy of Sciences*, 108, 27. (2011)

33. Manuel Garber, Manfred Grabherr, Mitchell Guttman, and **Cole Trapnell**, Computational Methods for Transcriptome Annotation and Quantification. *Nature Methods*, 8, 469-477. (2011)
34. Adam Roberts, **Cole Trapnell**, Julie Donaghey, John L. Rinn, and Lior Pachter, Improving RNA-Seq expression estimates by correcting for fragment bias. *Genome Biology* 12:R22. (2011)
35. **Cole Trapnell**, Brian Williams, Geo Pertea, Ali Mortazavi, Gordon Kwan, Marijke J. van Baren, Steven L. Salzberg, Barbara Wold, and Lior Pachter, Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. *Nature Biotechnology*, 28, 511-515. (2010)
36. Robert K. Bradley\*, Xiao-Yong Li\*, **Cole Trapnell**, Stuart Davidson, Lior Pachter, Hou Cheng Chu, Mark D. Biggin, and Michael B. Eisen, Binding site turnover produces pervasive quantitative changes in transcription factor binding between closely related *Drosophila* species. *PLoS Biology*, 8(3): e1000343. (2010)
37. **Cole Trapnell** and Steven L. Salzberg, How to map billions of short reads onto genomes. *Nature Biotechnology*, 27, 455-457. (2009)
38. **Cole Trapnell\***, Michael C. Schatz\*, Optimizing Data Intensive GPGPU Computations for DNA Sequence Alignment. *Parallel Computing*, 35:8-9. (2009)
39. **Cole Trapnell**, Lior Pachter, and Steven L. Salzberg, TopHat: discovering splice junctions with RNA-Seq. *Bioinformatics* 25(9):1105-1111. (2009)
40. Ben Langmead, **Cole Trapnell**, Mihai Pop, and Steven L. Salzberg, Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biology*, 10:R25. (2009)
41. Steven L. Salzberg *et al*, Genome sequence and rapid evolution of the rice pathogen *Xanthomonas oryzae* pv. *oryzae* PXO99. *BMC Genomics* 9:204. (2008)
42. Michael C. Schatz\*, **Cole Trapnell\***, Arthur L. Delcher, and Amitabh Varshney, High-throughput sequence alignment using Graphics Processing Units. *BMC Bioinformatics*, 8:474. (2007)

#### Conference Papers:

- Bruce C. Trapnell, Jr**, A Peer-to-Peer Blacklisting Strategy Inspired by Leukocyte-Endothelial Interaction. *Proceedings of the Fourth International Conference on Artificial Immune Systems* (2005)

#### Book Chapters:

- Mark Neal and **Bruce C. Trapnell, Jr**, Go Dutch: Exploit Interactions and Environments with Artificial Immune Systems. *In Silico Immunology*, Springer (2007)