

Cole Trapnell, Ph.D.

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INFORMATION	Foege Building Room S333C	colettrap@uw.edu
	Department of Genome Sciences	
	University of Washington	
	Seattle, WA, 98105, USA	

APPOINTMENT	University of Washington
	Assistant Professor of Genome Sciences, July 2014 - present

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

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

	University of Maryland, College Park
	B.S. Computer Science, 2005
	B.S. Mathematics, 2005

PROFESSIONAL	University of Washington	2014 - pres.
EXPERIENCE	Assistant Professor, Department of Genome Sciences	
	Harvard University	2010 - 2014
	Postdoctoral Fellow, Department of Stem Cell and Regenerative Biology	
	The Broad Institute of MIT and Harvard	2010 - 2014
	Visiting Postdoctoral Fellow	
	University of California, Berkeley	2008 - 2010
	Visiting Student Researcher, Department of Mathematics	
	University of Maryland, College Park	2006 - 2010
	Graduate Research Assistant, Department of Computer Science	
	Actuate Corporation	2005 - 2006
	Software Engineer	
	TopGun Software/LeverageFX	2002 - 2005
	Co-founder and Software Engineer	
	U.S. Army Research Laboratory	1999 - 2002
	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>Monocle: Time-series and differential expression analysis for single-cell RNA-Seq.</p> <p>Cufflinks: Transcriptome assembly and differential expression with RNA-Seq. Citations for related article[†] 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>TopHat: Spliced short read alignment for RNA-Seq. Citations for related article[†] Trapnell <i>et al</i>, 2009: 4,933</p> <p>Bowtie: Ultrafast short read mapping (with Ben Langmead) Citations for related article[†] Langmead <i>et al</i>, 2009: 8,578</p> <p>Spats: RNA structure with SHAPE-Seq (with Sharon Aviran)</p> <p>MUMmerGPU: Fast sequence alignment on the GPU (with Michael Schatz)</p>
TEACHING	<p>Co-instructor for UW GENOME 551: Gene Regulation (with John Stam). Winter 2016</p> <p>Guest lecturer for MIT 6.047/6.878: Computational Biology: Genomes, Networks, Evolution. This is a graduate course that covers the fundamentals of computational biology.</p> <p>Guest lecturer for Harvard STAT 115: Introduction to computational biology and bioinformatics. This is a course for undergraduates and graduate students that provides a statistical introduction to computational biology.</p> <p>Recitation teaching assistant for University of Maryland CMSC 212: Intro to Hardware-level Programming, Fall 2006 and Spring 2007.</p>
OUTREACH	<p>RNA-Seq informatics workshops:</p> <p>Hanson-Wade RNA-Seq Summit (Boston) 2015</p> <p>Tufts Computational Biology Initiative Transcriptomics Symposium 2012</p> <p>Broad-E workshop series, Summer 2012 and 2013</p> <p>Functional Genomics Data Society (FGED) meeting, 2009.</p>

[†]Google Scholar, as of 11/18/2016

REVIEWER

Cell
Science
Nature
Nature Biotechnology
Nature Methods
eLife
Genome Research
Genome Biology
Bioinformatics
BMC Bioinformatics
PLoS Computational Biology
Human Molecular Genetics
Genomics

TRAINEES

Postdoctoral fellows:

Jose L. McFaline, Ph.D. 2015-present
 Raghav Chawla, M.D., Ph.D., 2016-present
 Dejun Lin, Ph.D. 2016-present (with Noble lab)
 Delasa Aghamirzaie, Ph.D. 2016-present

Graduate students:

Andria Ellis (Genome Sciences), 2017-present
 Lauren Saunders (Molecular and Cellular Biology; joint with Parichy lab, UVA), 2017-present
 Jonathan Packer (Genome Sciences; joint with Waterston lab), 2016-present
 Sanjay Srivatsan (MSTP Program), 2015-present
 Xiaojie Qiu (Molecular and Cellular Biology), 2014-present
 Hannah Pliner (Genome Sciences; joint with Jay Shendure), 2015-present
 Serena Liu (Genome Sciences), 2015-present

Rotation students:

Andria Ellis (Genome Sciences), Spring 2017
 Gesine Cauer (Genome Sciences), Winter 2017
 April Lo (Genome Sciences), Fall 2016
 Eliah Overbey (Genome Sciences), Winter 2016
 Jonathan Packer (Genome Sciences), Fall 2015
 Sanjay Srivatsan (MSTP Program), Summer 2015
 Lauren Saunders (Molecular and Cellular Biology), Spring 2015
 Serena Liu (Genome Sciences), Winter 2015

Andrew Hill (Genome Sciences), Winter 2015
 Hannah Pliner (Genome Sciences; joint with Jay Shendure), Fall 2014
 Xiaojie Qiu (Molecular and Cellular Biology), Summer 2014

TRAINEE (In addition to own trainees)

COMMITTEES

Graduate students:

Jun Cao, Molecular and Cellular Biology, 2016-present
 Andrew Hill, Genome Sciences, 2015-present
 Lauren Saunders, Molecular and Cellular Biology, 2015-present
 Andrew McDavid, Statistics, 2015-present
 Vijay Ramani, Genome Sciences, 2015-present
 Timothy Durham, Genome Sciences, 2015-present
 Cecilia Noecker, Genome Sciences, 2015-present
 Claire Williams, Molecular and Cellular Biology, 2015-present

Other trainees:

Matthew Hartmann, M.D. K08 Advisory Committee, 2015-present, Advisors: John Stam, Mike LaFlamme

FACULTY

RESPONSIBILITIES

Member, Genome Sciences faculty search committee. 2017
 Member, Genome Sciences graduate admission committee. 2017
 Organizer, Genome Sciences departmental retreat. 2016
 Organizer, Genome Sciences departmental retreat. 2015
 Member, Seminar Series Committee (Genome Sciences). 2015

PATENTS

High-throughput methodology for identifying RNA-Protein interactions transcriptome-wide. (issued: 13/911,429)

PUBLICATIONS

Submitted:

1. Xiaojie Qiu, Arman Rahimzamani, Li Wang, Qi Mao, Timothy Durham, Jose L McFaline-Figueroa, Lauren Saunders, **Cole Trapnell**[†], Sreeram Kannan[†], Towards inferring causal gene regulatory networks from single cell expression measurements *bioRxiv* doi:10.1101/426981 (2018)
2. Naresh K. Hanchate, Eun Jeong Lee, Andria Ellis, Kunio Kondoh, Donghui Kuang, Ryan Basom, **Cole Trapnell**, Linda B. Buck, Connect-seq to superimpose molecular on anatomical neural circuit maps. *bioRxiv* doi:10.1101/454835 (2018)

*Equal contribution

[†]Co-corresponding author

3. Heather Feldman, Chad Toledo, Sonali Arora, Pia Hoellerbauer, Philip Corrin, Lucas Carter, Megan Kufeld, Hamid Bolouri, Ryan Basom, Jeffrey Delrow, Joshua Meier, Feng Zhang, José McFaline-Figueroa, **Cole Trapnell**, Steven Pollard, Christopher Plaisier, Patrick Paddison, CRISPR-Cas9 Screens Reveal Genes Regulating a G0-like State in Human Neural Progenitors.
bioRxiv doi:10.1101/446344 (2018)
4. Ken Jean-Baptiste, Jose L. McFaline-Figueroa, Cristina M Alexandre, Michael W Dorrity, Lauren Saunders, Kerry L Bubb, **Cole Trapnell**, Stanley Fields, Christine Queitsch, Josh T Cuperus, Developmental and conditional dynamics of gene expression in single root cells of *A. thaliana*
bioRxiv doi:10.1101/448514 (2018)
5. Molly Gasperini[†], Andrew Hill, José L. McFaline-Figueroa, Beth Martin, **Cole Trapnell**, Nadav Ahituv, Jay Shendure[†], crisprQTL mapping as a genome-wide association framework for cellular genetic screens.
bioRxiv doi:10.1101/314344 (2018)
6. John R Sinnamon, Kristof A Torkenczy, Michael W Linhoff, Sarah A Vitak, Hannah A Pliner, **Cole Trapnell**, Frank J Steemers, Gail Mandel, Andrew C Adey, The accessible chromatin landscape of the hippocampus at single-cell resolution.
bioRxiv doi:10.1101/407668 (2018)

Journal Articles:

1. Junyue Cao, Darren A. Cusanovich*, Vijay Ramani*, Delasa Aghamirzaie, Hannah A. Pliner, Andrew J. Hill, Riza M. Daza, Jose L. McFaline-Figueroa, Jonathan S. Packer, Lena Christiansen, Frank J. Steemers, Andrew C. Adey, **Cole Trapnell**[†], Jay Shendure[†], Joint profiling of chromatin accessibility and gene expression in thousands of single cells
Science 361: 6409, 13801385 (2018)
2. 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, **Cole Trapnell**[†], Jay Shendure[†], A first-generation atlas of in vivo mammalian chromatin accessibility at single cell resolution.
Cell 174:5 1309-1324 (2018)
3. Jonathan Packer, Bob Waterston, **Cole Trapnell**, Single-Cell Multi-omics: An Engine for New Quantitative Models of Gene Regulation.
Trends in Genetics 34:9 6530-665(2018).
4. Michelle N. Wray-Dutra, Raghav Chawla, Kerri R. Thomas, Brenda J. Seymour, Tanvi Arkatkar, Karen M. Sommer, Socheath Khim, **Cole Trapnell**, Richard G. James, David J. Rawlings, Activated CARD11 accelerates germinal center kinetics, promoting mTORC1 and terminal differentiation.
Journal of Experimental Medicine 215 (9): 2445 (2018)
5. Hannah A. Pliner, Jonathan Packer, José L. McFaline-Figueroa, Darren Cusanovich, Riza Daza, Sanjay Srivatsan, Xiaojie Qiu, Dana Jackson, Anna Minkina, Andrew Adey, Frank Steemers, Jay Shendure[†], **Cole Trapnell**[†], Cicero predicts cis-regulatory DNA interactions from single-cell chromatin accessibility data.
Molecular Cell 71:5 858-871 (2018)

6. Davide Cacchiarelli[†], 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**[†], Aligning single-cell developmental and reprogramming trajectories identifies molecular determinants of reprogramming outcome. *Cell Systems* 7:3 258-268 (2018)
7. 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* 36 428-431 (2018)
8. Darren Cusanovich*, James Reddington*, David Garfield*, Riza Daza, Raquel Marco-Ferreres, Lena Christiansen, Xiaojie Qiu, Frank Steemers, **Cole Trapnell**, Jay Shendure[†], Eileen Furlong[†], The cis-regulatory dynamics of embryonic development at single cell resolution. *Nature* 555 538-542 (2018)
9. Alistair B. Russell, **Cole Trapnell**, Jesse D. Bloom, Extreme heterogeneity of influenza virus infection in single cells. *eLife* 7:e32303 (2018)
10. Andrew Hill*, Jose L. McFaline-Figueroa*, Jay Shendure[†], **Cole Trapnell**[†], On the design of CRISPR-based single cell molecular screens. *Nature Methods* 15, pages 271274 (2018).
11. 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[†], **Cole Trapnell**[†], Jay Shendure[†], Comprehensive single cell transcriptional profiling of a multicellular organism by combinatorial indexing. *Science* 357: 6352 661-667. (2017)
12. 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, 979–982. (2017)
13. 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 6680. (2017)
14. 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)
15. Serena Liu and **Cole Trapnell**. Single-cell transcriptome sequencing: recent advances and remaining challenges. *F1000 Faculty Reviews*. (2016) *Invited paper*.

16. **Cole Trapnell**, Defining cell types and states with single-cell genomics.
Genome Research, 25:1491-1498. (2015) *Invited paper*.
17. Naresh K. Hanchate, Kunio Kondoh, Zhonghua Lu, Donghui Kuang, Xiaolan Ye, Xiaojie Qiu, Lior Pachter, **Cole Trapnell**[†], Linda B. Buck[†], Single-cell transcriptomics reveals receptor transformations during olfactory neurogenesis,
Science, 350:6265. (2015)
18. Davide Cacchiarelli*, **Cole Trapnell***, Michael J. Ziller*, Magali Soumillon, Marcella Cesana, Rahul Karnik, Zachary D. Smith, Sutheera Ratanasirintra-woot 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, 162:2 412-424. (2015)
19. 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)
20. 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)
21. **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)
22. 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)
23. 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)
24. 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)
25. 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)
26. 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)
27. 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)
28. Lei Sun^{*}, Loyal A Goff^{*}, **Cole Trapnell**^{*}, Ryan Alexander, Kinyui Alice Lo, Ezgi Haciosuleyman, 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)
29. **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, 46–53. (2013)
30. **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, 562–578. (2012)
31. 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)
32. 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)
33. Adam Roberts, Harold Pimentel, **Cole Trapnell**[†], and Lior Pachter[†], Identification of novel transcripts in annotated genomes using RNA-Seq. *Bioinformatics*, 27 (17): 2325-2329. (2011)
34. 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)
35. 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)

36. Manuel Garber, Manfred Grabherr, Mitchell Guttman, and **Cole Trapnell**, Computational Methods for Transcriptome Annotation and Quantification. *Nature Methods*, 8, 469-477. (2011)
37. 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)
38. **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)
39. 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)
40. **Cole Trapnell** and Steven L. Salzberg, How to map billions of short reads onto genomes. *Nature Biotechnology*, 27, 455-457. (2009)
41. **Cole Trapnell***, Michael C. Schatz*, Optimizing Data Intensive GPGPU Computations for DNA Sequence Alignment. *Parallel Computing*, 35:8-9. (2009)
42. **Cole Trapnell**, Lior Pachter, and Steven L. Salzberg, TopHat: discovering splice junctions with RNA-Seq. *Bioinformatics* 25(9):1105-1111. (2009)
43. 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)
44. Steven L. Salzberg *et al*, Genome sequence and rapid evolution of the rice pathogen *Xanthomonas oryzae* pv. *oryzae* PXO99. *BMC Genomics* 9:204. (2008)
45. 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)

ACTIVE GRANT	1DP2OD020868-01 (Trapnell)	09/01/15-08/31/20
SUPPORT	NIH New Innovator Award National Institutes of Health <i>Charting the regulatory topography of the cell differentiation landscape with single-cell RNA-Seq</i> The goal of the project is to use single-cell gene expression analysis to map the landscape of cellular states and then identify the key genes that govern each cell's path over the landscape, in order to better direct stem cells toward target fates as part of cell-based therapies.	
	U54 DK107979 (MPI Shendure and Noble) NIH/NIDDK <i>University of Washington Center for Nuclear Organization and Function</i> This project will develop novel experimental and computational methods to characterize genome 3D architecture, validate the methods using mouse and human cells, and demonstrate the utility of the resulting data for improving our understanding of fundamental biology and human disease Role: Co-investigator	09/01/15-08/31/20
	W.M. Keck Foundation (Trapnell) This project aims to broadly capture the molecular consequences of perturbing thousands of genes in a multitude of combinations by evaluating the resulting signatures of cell states in a high-throughput manner. This technique will markedly accelerate the discovery of sets of genes that functionally collaborate, e.g. in signaling pathways, as molecular machines, or for cellular reprogramming.	07/01/16-06/30/19
	RC2 DK114777 (Bernstein, Rafii and Trapnell) NIH/NIDDK <i>Niche signals in HSC genesis</i> The overall goal of this project is map the signaling interactions regulating hematopoietic stem cell specification and self-renewal from embryonic hemogenic precursors or reprogrammed adult endothelial cells in the context of the their niche.	09/01/17-08/31/22
	12357 (Shendure) Paul G. Allen Frontiers Group <i>Allen Discovery Center for Cell Lineage Tracing</i> The goal of this project is to develop and employ genome-editing based lineage tracing technologies to reconstruct the cell lineage of mouse and zebrafish. By coupling this technique with single-cell genomics and RNA FISH, we will also annotate the lineages with complete gene expression profiles. Role: Co-investigator	09/01/17-08/31/22
	R01 (Buck) NIH <i>Odor blocking of fear and stress</i> This project aims to understand the molecular regulation and neural circuitry that mediates fear and other stress responses using an approach that combines viral labeling and single-cell transcriptomics. Role: Co-investigator	04/01/18- 3/31/23
	R01 (Bruce C. Trapnell and Cole Trapnell) NIH	05/01/18- 04/30/22

Pulmonary Macrophage Transplantation for Pulmonary Alveolar Proteinosis The goal of this project is to understand the molecular regulation of conversion of macrophages to an alveolar phenotype during pulmonary macrophage transplantation.

PAST GRANT
SUPPORT

Alfred P. Sloan Foundation Fellowship (Trapnell) **09/15/15-09/14/17**

Alfred P. Sloan Foundation

This project aims to develop basic computational methods for single-cell genomic analysis of cell differentiation, including finding important regulators of cell differentiation using machine learning

Dale F. Frey Award for Breakthrough Scientists **09/01/14-08/31/16**

Damon Runyon Cancer Research Foundation

The aim of this grant is to use single cell genomics to dissect the corrupted gene regulatory networks that drive cancer.

TALKS

RNA-Seq: getting to clinical data you can interpret and believe

Individualizing Medicine, Mayo Clinic (2015)

Differential analysis of branched single-cell gene expression trajectories

Genome Informatics, Cold Spring Harbor (2015)

Australasian genomics technology association, Hunter Valley, Australia (2015)

Single cell trajectory analysis with Monocle

Bioconductor Developer Day (BioC) 2015

Single cell trajectory alignment uncovers defects in direct lineage reprogramming

International society of stem cell research, Stockholm, Sweden (2015)

International Society of Heart Research, North American meeting, Seattle (2015)

Pseudotemporal ordering of single cells reveals regulators of cell differentiation and reprogramming

Tri-con Molecular Medicine, San Francisco (2015)

University of California, San Francisco, Gladstone Institute (2014)

Emerging Leaders in Systems-level biology, Cincinnati Children's Hospital (2014)

Princeton University, Lewis Sieglar Institute (2014)

Harvard University, Department of Stem Cell and Regenerative Biology (2014)

Cornell University, Department of Molecular Biology and Genetics (2014)

University of Washington, Department of Genome Sciences (2014)

Georgia Institute of Technology, Department of Biology seminar series (2013)

University of Georgia, Institute of Bioinformatics (2013)

University of Minnesota, Department of Genetics, Cell Biology, and Development (2013)

Investigating the role of long, noncoding RNAs in cellular differentiation

Boston University Bioinformatics Student-Organized Symposium. (2013)

Broad Institute retreat. (2012)

Isoform-resolution differential expression analysis with RNA-Seq

VIZBI: Visualizing Biological Data (2013)

Cincinnati Children's Hospital Medical Center. (2012)

UC Berkeley *-Seq I. (2012)

Biomatters Geneious User Group meeting. (2011)

Assembly, quantification, and cloning of human long, noncoding RNAs

Roche RNA-Seq BARN. (2011)

Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation

UNC Charlotte Bioinformatics Dept. (2011)

Johns Hopkins Biostatistics Dept. (2010)

RNA-seq analysis with TopHat and Cufflinks

Illumina live global webcast. (2010)

Life Technologies platform user webinar. (2010)

The Tuxedo Tools: ultrafast short read mapping

UC San Diego Next-Generation Sequencing Meeting. (2008)

Illumina. (2008)

UC Berkeley Mathematics Dept. (2008)

Bowtie: ultrafast and memory-efficient alignment of short DNA sequences to the human genome

Applied Biosystems. (2008)

Transcriptome discovery and quantitation with the Tuxedo tools

Short-SIG: Next Generation Sequencing and Algorithms for Short Read Analysis, ISMB. (2009)

MGED 12, Phoenix, Arizona. (2009)

Broad Institute Computational Biology and Bioinformatics program seminar series. (2009)

Long noncoding RNAs regulate adipogenesis

Invited speaker, Keystone Symposium on the Genetic and Molecular Basis of Obesity and Body Weight Regulation. (2012)

Investigating the role of long, noncoding RNAs in pluripotency and self renewal

Invited seminar, Harvard Stem Cell and Regenerative Biology departmental seminar series. (2012)

Invited seminar, Quantitative Biology departmental seminar series, Cold Spring Harbor Laboratory. (2012)

"The Clone Wars:" Mechanistic characterization of long, noncoding RNAs

Invited seminar, Broad Epigenomics seminar (2011)