

## Cole Trapnell, Ph.D.

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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 EXPERIENCE **University of Washington** 2019 - pres.  
Associate Professor (with tenure), Department of Genome Sciences

**University of Washington** 2014 - 2019.  
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
- ISCB Overton Prize, 2018
  - NIH Director's New Innovator Award, 2015
  - Alfred P. Sloan Foundation Research Fellowship, 2015
  - Damon Runyon Dale F. Frey Award for Breakthrough Scientists, 2014
  - Damon Runyon Postdoctoral Fellowship, 2011-2014
  - Finalist, Burroughs-Wellcome Career Award at the Scientific Interface, 2013
  - Genome Biology Award, *BioMed Central*, 2010. (Bowtie, with Langmead, *et al*)
  - Next-Generation Sequencing Paper of the Year, 2009. *Bioinformatics* (TopHat)
  - Teaching Excellence Award, 2007, University of Maryland Computer Science Department
- SOFTWARE
- Monocle:** Time-series and differential expression analysis for single-cell RNA-Seq.
  - Cufflinks:** Transcriptome assembly and differential expression with RNA-Seq.  
Citations for related article<sup>†</sup> Trapnell *et al*, 2010: 4,402  
Highlighted as a notable breakthrough in Computational Biology, 2010.  
See: H. Craig Mak, *Nature Biotechnology* Vol. 29, 45 (2011)
  - TopHat:** Spliced short read alignment for RNA-Seq.  
Citations for related article<sup>†</sup> Trapnell *et al*, 2009: 4,933
  - Bowtie:** Ultrafast short read mapping (with Ben Langmead)  
Citations for related article<sup>†</sup> Langmead *et al*, 2009: 8,578
  - Spats:** RNA structure with SHAPE-Seq (with Sharon Aviran)
  - MUMmerGPU:** Fast sequence alignment on the GPU (with Michael Schatz)
- TEACHING
- Co-instructor** for UW GENOME 551: Gene Regulation (with John Stam). Winter 2016
  - 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.
  - 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.
  - Recitation teaching assistant** for University of Maryland CMSC 212: Intro to Hardware-level Programming, Fall 2006 and Spring 2007.
- OUTREACH
- RNA-Seq informatics workshops:**
    - Hanson-Wade RNA-Seq Summit (Boston) 2015
    - Tufts Computational Biology Initiative Transcriptomics Symposium 2012
    - Broad-E workshop series, Summer 2012 and 2013
    - Functional Genomics Data Society (FGED) meeting, 2009.

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<sup>†</sup>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  
Dejun Lin, Ph.D. 2016-present (with Noble lab)  
Raghav Chawla, M.D., Ph.D., 2016-2018  
Delasa Aghamirzaie, Ph.D. 2016-2018

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), 2014-2018  
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  
Elijah 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. Jonathan S. Packer\*, Qin Zhu\*, Chau Huynh, Priya Sivaramakrishnan, Elicia Preston, Hannah Dueck, Derek Stefanik, Kai Tan, *Cole Trapnell*, Junhyong Kim<sup>†</sup>, Robert H. Waterston<sup>†</sup>, John I. Murray<sup>†</sup>, A lineage-resolved molecular atlas of *C. elegans* embryogenesis at single cell resolution.

*bioRxiv* doi:10.1101/565549 (2019)

2. Hannah Pliner, Jay Shendure<sup>†</sup>, **Cole Trapnell**<sup>†</sup>, Supervised classification enables rapid annotation of cell atlases.

*bioRxiv* doi:10.1101/538652 (2019)

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\*Equal contribution

<sup>†</sup>Co-corresponding author

3. Lauren M. Saunders, Abhishek K. Mishra, Andrew J. Aman, Victor M. Lewis, Matthew B. Toomey, Jonathan S. Packer, Xiaojie Qiu, Jose L. McFaline-Figueroa, Joseph C. Corbo, **Cole Trapnell**<sup>†</sup>, David M. Parichy<sup>†</sup>, Thyroid hormone regulates distinct paths to maturation in pigment cell lineages.  
*bioRxiv* doi:10.1101/527341 (2019)
4. Xiaojie Qiu, Arman Rahimzamani, Li Wang, Qi Mao, Timothy Durham, Jose L. McFaline-Figueroa, Lauren Saunders, **Cole Trapnell**<sup>†</sup>, Sreeram Kannan<sup>†</sup>, Towards inferring causal gene regulatory networks from single cell expression measurements  
*bioRxiv* doi:10.1101/426981 (2018)
5. 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)
6. 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)

Journal Articles:

1. Junyue Cao\*, Malte Spielmann\*, Xiaojie Qiu, Xingfan Huang, Daniel M. Ibrahim, Andrew J. Hill<sup>1</sup>, Fan Zhang, Stefan Mundlos, Lena Christiansen, Frank J. Steemers, **Cole Trapnell**<sup>†</sup>, and Jay Shendure<sup>†</sup>, The single-cell transcriptional landscape of mammalian organogenesis.  
*Nature* doi:10.1038/s41586-019-0969-x (2019)
2. Nadav Sharon\*, Raghav Chawla\*, Jonas W. Mueller, Jordan Vanderhooft, Benjamin Rosenthal, Mads Gurtler, Dmitry Shvartsman, David K. Gifford, **Cole Trapnell**<sup>†</sup>, Doug Melton<sup>†</sup>, A peninsular structure coordinates asynchronous differentiation with morphogenesis to generate pancreatic islets.  
*Cell* doi:10.1016/j.cell.2018.12.003 (2019)
3. John R Sinnamon, Kristof A Torkenczy, Michael W Linhoff, Sarah A Vitak, Ryan Mulqueen, Hannah A Pliner, **Cole Trapnell**, Frank J Steemers, Gail Mandel, Andrew C Adey, The accessible chromatin landscape of the hippocampus at single-cell resolution.  
*Genome Research* doi:10.1101/gr.243725.118 (2019)
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*  
*The Plant Cell* doi:10.1105/tpc.18.00785 (2019)
5. Molly Gasperini\*<sup>†</sup>, Andrew Hill\*, José L. McFaline-Figueroa, Beth Martin, Seungsoo Kim, Melissa D. Zhang, Dana Jackson, Anh Leith, Jacob Schreiber, William S. Noble, **Cole Trapnell**, Nadav Ahituv, Jay Shendure<sup>†</sup>, A genome-wide framework for mapping gene regulation via cellular genetic screens  
*Cell* doi:10.1016/j.cell.2018.11.029 (2019)

6. 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**<sup>†</sup>, Jay Shendure<sup>†</sup>, Joint profiling of chromatin accessibility and gene expression in thousands of single cells  
*Science* 361: 6409, 13801385 (2018)
7. 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**<sup>†</sup>, Jay Shendure<sup>†</sup>, A first-generation atlas of in vivo mammalian chromatin accessibility at single cell resolution.  
*Cell* 174:5 1309-1324 (2018)
8. 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).
9. 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)
10. 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<sup>†</sup>, **Cole Trapnell**<sup>†</sup>, Cicero predicts cis-regulatory DNA interactions from single-cell chromatin accessibility data.  
*Molecular Cell* 71:5 858-871 (2018)
11. 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.  
*Cell Systems* 7:3 258-268 (2018)
12. 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)
13. 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)
14. Alistair B. Russell, **Cole Trapnell**, Jesse D. Bloom, Extreme heterogeneity of influenza virus infection in single cells.  
*eLife* 7:e32303 (2018)
15. 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).

16. 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)
17. 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)
18. Jin Zhang, Sutheera Ratanasirintraooot, 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, Yuin-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)
19. 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)
20. Serena Liu and **Cole Trapnell**. Single-cell transcriptome sequencing: recent advances and remaining challenges. *F1000 Faculty Reviews*. (2016) *Invited paper*.
21. **Cole Trapnell**, Defining cell types and states with single-cell genomics. *Genome Research*, 25:14911498. (2015) *Invited paper*.
22. 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*, 350:6265. (2015)
23. Davide Cacchiarelli\*, **Cole Trapnell**\*, Michael J. Ziller\*, Magali Soumillon, Marcella Cesana, Rahul Karnik, Zachary D. Smith, Sutheera Ratanasirintraooot 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 412424. (2015)
24. 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)
25. 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)

26. **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)
27. 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)
28. 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)
29. 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)
30. 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)
31. 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)
32. 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)
33. 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)
34. **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)
35. **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)
36. 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)
  37. 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)
  38. 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)
  39. 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)
  40. 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)
  41. Manuel Garber, Manfred Grabherr, Mitchell Guttman, and **Cole Trapnell**, Computational Methods for Transcriptome Annotation and Quantification.  
*Nature Methods*, 8, 469-477. (2011)
  42. 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)
  43. **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)
  44. 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)
  45. **Cole Trapnell** and Steven L. Salzberg, How to map billions of short reads onto genomes.  
*Nature Biotechnology*, 27, 455-457. (2009)
  46. **Cole Trapnell**\*, Michael C. Schatz\*, Optimizing Data Intensive GPGPU Computations for DNA Sequence Alignment.  
*Parallel Computing*, 35:8-9. (2009)
  47. **Cole Trapnell**, Lior Pachter, and Steven L. Salzberg, TopHat: discovering splice junctions with RNA-Seq.  
*Bioinformatics* 25(9):1105-1111. (2009)

48. 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)
49. Steven L. Salzberg *et al*, Genome sequence and rapid evolution of the rice pathogen *Xanthomonas oryzae* pv. *oryzae* PXO99. *BMC Genomics* 9:204. (2008)
50. 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 SUPPORT	<p><b>1DP2OD020868-01</b> (Trapnell) <span style="float: right;"><b>09/01/15-08/31/20</b></span>          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.</p> <p><b>U54 DK107979</b> (MPI Shendure and Noble) <span style="float: right;"><b>09/01/15-08/31/20</b></span>          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</p> <p><b>W.M. Keck Foundation</b> (Trapnell) <span style="float: right;"><b>07/01/16-06/30/19</b></span>          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.</p> <p><b>RC2 DK114777</b> (Bernstein, Rafii and Trapnell) <span style="float: right;"><b>09/01/17-08/31/22</b></span></p>
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NIH/NIDDK

*Niche signals in HSC genesis*

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.

**12357** (Shendure)**09/01/17-08/31/22**

Paul G. Allen Frontiers Group

*Allen Discovery Center for Cell Lineage Tracing*

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

**R01DC016442** (Buck)**04/01/18- 3/31/23**

NIH

*Odor blocking of fear and stress* 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

**R01HL118342** (Bruce C. Trapnell and Cole Trapnell)**05/01/18- 04/30/22**

NIH

*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.

**1U54HL145611** (Cai, Trapnell, Shendure)**09/20/18 - 06/30/22**

NIH

*A spatially resolved molecular atlas of human endothelium* This project aims to establish a Tissue Mapping Center for the NIH Human Biomolecular Atlas Project. Our Center will provide a spatially resolved transcriptome and chromatin accessibility map for the human vascular system.

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 Siegler 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)