Kamil Slowikowski

77 Avenue Louis Pasteur, Boston, MA 02115 ✉ kslowikowski@gmail.com ⌁ slowkow.com

EDUCATION

PhD in Bioinformatics and Integrative Genomics 2012–2019
Harvard University. Boston, Massachusetts.

BS in Bioinformatics 2007–2011
Loyola University Chicago. Chicago, Illinois.

GRANT SUPPORT

Predoctoral Individual National Research Service Award (F31-AR070582) 2016–2018
National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIAMS).
Title: *Transcriptomics in synoviocytes defines pathogenesis of rheumatoid arthritis.*

PROFESSIONAL ACTIVITIES

Graduate Research Assistant. Harvard Medical School. 2013 – 2019
Dr. Soumya Raychaudhuri. Department of Biomedical Informatics.

Undergraduate Research Assistant. Loyola University Chicago. Winter – Summer 2012
Dr. Sushma Reddy. Department of Biology.
Dr. Catherine Putonti. Department of Biology.

NSF Research Fellow. University of California Santa Cruz. Summer 2011
Dr. Todd M. Lowe. Department of Biomolecular Engineering.

Undergraduate Research Assistant. Loyola University Chicago. 2009–2011
Dr. Howard M. Laten. Department of Bioinformatics.

NSF Research Fellow. The Field Museum. Chicago, Illinois. Summer 2010
Dr. Scott Lidgard. Integrative Research Center.

Independent Software Developer. Chicago, Illinois. 2006–2010
Developed computer game extensions for 17 international clients.

EDUCATIONAL ACTIVITIES

Mentor for Harvard-Amgen Scholars. Harvard University. 2017
Student: Gopal Vashishtha. Harvard College.
Title: *Transcriptional dynamics of synovial fibroblasts in rheumatoid arthritis.*

Mentor for Research Science Institute (RSI). Harvard University. 2016 – 2017
Student: Sushil Upadhyayula.
Title: *Dissecting the heterogeneity of CD4+ T cell activation with single cell RNA-seq.*

Instructor. Grades 3-8. The Innovation Institute. Newton, MA.
Computer Programming for Future Entrepreneurs 2016 – 2017
Computer Programming for Future Scientists and Engineers 2015 – 2016

SOFTWARE AND TUTORIALS

⌁ **Immunogenomics.io** (R, HTML, Javascript). Websites for RNA-seq data visualization.
 ggrepel (R, C++). Repel overlapping text labels away from each other. Over 2 million downloads.
 SNPSEA (C++). Identify cell types and pathways affected by genetic risk loci.
 snakefiles (Python). Tutorial and Snakefiles for reproducible and scalable RNA-seq data analysis.

VOLUNTEER ACTIVITIES

Software Developer. cuSTEMized.org in Boston, MA. 2013–Present
Computer Programming Tutor. Loyola University Chicago (LUC). 2010–2011
Emergency Medical Technician - Basic. LUC Emergency Medical Services. 2008–2010

Fifty for the Future Award. Illinois Technology Foundation.	2011
Mulcahy Research Scholar. Loyola University Chicago.	2010–2011
Loyola Presidential Scholarship. Loyola University Chicago.	2007–2011
Dean's List. Loyola University Chicago.	2007–2011

TALKS

6. Identifying transcriptional regulators central to rheumatoid arthritis: transcriptomics of IL-17 dose-response and time series in stromal cells.
   - *Federation of Clinical Immunology Societies (FOCIS)*. Boston, MA. — 2019-06-20

5. Transcriptomics reveals the role of synovial fibroblasts in rheumatoid arthritis.
   - *Leena Peltonen School of Human Genomics*. Les Diablerets, Switzerland. — 2018-08-19

4. An introduction to ggrepel.
   - *Partners R User Group Meeting*. Massachusetts General Hospital, Boston, MA. — 2018-07-19

3. Insights into RA pathogenesis from single cell transcriptomics of synovial tissue.
   - *Federation of Clinical Immunology Societies (FOCIS)*. Chicago, IL. — 2017-06-14

2. AMP rheumatoid arthritis phase 1: single-cell RNA-seq with CEL-seq2.
   - *Accelerating Medicines Partnership (AMP)*. Houston, TX. — 2017-02-15

1. Single-cell transcriptomics reveals disease-associated fibroblast subsets in rheumatoid arthritis.
   - *Joint Biology Consortium*. Brigham and Women's Hospital, Boston, MA. — 2017-01-27
   - *Medical and Population Genetics Seminar Series*. Broad Institute, Boston, MA. — 2016-04-28
   - *Immunogenomics 2015*. HudsonAlpha Institute, Huntsville, AL. — 2015-09-30
   - *Cell Circuits and Epigenomics Program Seminar Series*. Broad Institute, Boston, MA. — 2015-06-22

POSTERS

6. Introduction to ggrepel.
   - *rstudio::conf 2019*. Austin, TX. — 2019-01-17

5. Identifying transcriptional regulators central to rheumatoid arthritis: transcriptomics of IL-17 dose-response and time series in stromal cells.
   - *Federation of Clinical Immunology Societies (FOCIS) 2019* Boston, MA. — 2019-06-20
   - *Broad Institute Annual Retreat*. Cambridge, MA. — 2018-12-17
   - *ISCB Conference on Regulatory and Systems Genomics*. New York, NY. — 2018-12-10
   - *American College of Rheumatology (ACR) Annual Meeting*. San Diego, CA. — 2017-11-04
   - *Immune Profiling in Health and Disease*. Seattle, WA. — 2016-10-03

4. Single-cell transcriptomics identifies pathogenic synovial fibroblasts in rheumatoid arthritis.
   - *National Human Genome Research Institute (NHGRI) Annual Meeting*. Bethesda, MD. — 2016-04-07
   - *4th Annual Single Cell Analysis Investigators Meeting*. Bethesda, MD. — 2016-03-02
   - *Harvard Program in Quantitative Genomics Conference*. Boston, MA. — 2015-11-05

3. SNPSEA: an algorithm to identify cell types, tissues, and pathways affected by risk loci.
   - *Harvard Graduate Women in Science and Engineering (HGWISE) Symposium*. Cambridge, MA. 2015-04-25

- *Harvard Biological and Biomedical Sciences (BBS) Retreat.* Provincetown, MA.   2014-08-05

2. Reverse transcriptase SuperScript III adds non-template bases during cDNA polymerization.
   - *Summer Undergraduate Research Symposium.* Santa Cruz, CA.   2011-08-12

1. Retrotransposon-associated minisatellites in the soybean genome.
   - *Great Lakes Bioinformatics Conference.* Athens, OH.   2011-05-03
   - *Loyola Undergraduate Research Symposium.* Chicago, IL.   2011-04-16
   - *Chicago Area Undergraduate Research Symposium.* Chicago, IL.   2011-04-02

PUBLICATIONS

PREPRINTS

3. CUX1 and IκBζ mediate the synergistic inflammatory response to TNF and IL-17A in stromal fibroblasts
   Kamil Slowikowski*, Hung N. Nguyen*, Erika H. Noss, Daimon P. Simmons, Fumitaka Mizoguchi, Gerald F.M. Watts, Michael F. Gurish, Michael B. Brenner, Soumya Raychaudhuri
   bioRxiv, 2019. ⬀ View the data

2. Fast, sensitive, and accurate integration of single cell data with Harmony
   Ilya Korsunsky, Jean Fan, **Kamil Slowikowski**, Fan Zhang, Kevin Wei, Yuriy Baglaenko, Michael Brenner, Po-Ru Loh, Soumya Raychaudhuri
   bioRxiv, 2018.

1. UBiT2: a client-side web-application for gene expression data analysis
   Jean Fan, David Fan, **Kamil Slowikowski**, Nils Gehlenborg, Peter Kharchenko
   bioRxiv, 2017. ⬀ Try the app

PEER REVIEWED ARTICLES

18. The immune cell landscape in kidneys of patients with lupus nephritis
    Arnon Arazi, Deepak A. Rao, Celine C. Berthier, Anne Davidson, Yanyan Liu, Paul J. Hoover, Adam Chicoine, Thomas M. Eisenhaure, A. Helena Jonsson, Shuqiang Li, David J. Lieb, Fan Zhang, **Kamil Slowikowski**, Edward P. Browne, Akiko Noma, Danielle Sutherby, Scott Steelman, Dawn E. Smilek, Patti Tosta, William Apruzzese, Elena Massarotti, Maria DallâĂŹEra, Meyeon Park, Diane L. Kamen, Richard A. Furie, Fernanda Payan-Schober, William F. Pendergraft III, Elizabeth A. McInnis, Jill P. Buyon, Michelle A. Petri, Chaim Putterman, Kenneth C. Kalunian, E. Steve Woodle, James A. Lederer, David A. Hildeman, Chad Nusbaum, Soumya Raychaudhuri, Matthias Kretzler, Jennifer H. Anolik, Michael B. Brenner, David Wofsy, Nir Hacohen, Betty Diamond the Accelerating Medicines Partnership in SLE network
    Nature Immunology, 2019. ⬀ View the data

17. Defining inflammatory cell states in rheumatoid arthritis joint synovial tissues by integrating single-cell transcriptomics and mass cytometry
    Fan Zhang*, Kevin Wei*, **Kamil Slowikowski***, Chamith Y. Fonseka*, Deepak A. Rao*, Stephen Kelly, Susan M. Goodman, Darren Tabechian, Laura B. Hughes, Karen Salomon-Escoto, Gerald F. M. Watts, William Apruzzese, David J. Lieb, David L. Boyle, Arthur M. Mandelin II, Accelerating Medicines Partnership: RA Phase 1, AMP RA/SLE, Brendan F. Boyce, Edward DiCarlo, Ellen M. Gravallese, Peter K. Gregersen, Larry Moreland, Gary S. Firestein, Nir Hacohen, Chad Nusbaum, James A. Lederer, Harris Perlman, Costantino Pitzalis, Andrew Filer, V. Michael Holers, Vivian P. Bykerk, Laura T. Donlin, Jennifer H. Anolik, Michael B. Brenner, Soumya Raychaudhuri
    Nature Immunology, 2019. ⬀ View the data

16. [Tubular Cell and Keratinocyte Single-cell Transcriptomics Applied to Lupus Nephritis Reveal Type I IFN and Fibrosis Relevant Pathways](#)
Evan Der, Hemant Suryawanshi, Pavel Morozov, Manjunath Kustagi, Beatrice Goilav, Saritha Ranabathou, Peter Izmirly, Michael Belmont, Robert Clancy, Mordecai Koenigsberg, Michele Mokrzycki, Helen Rominieki, Jay Graham, Juan Rocca, Nicole Bornkamp, Nicole Jordan, Emma Schulte, Ming Wu, James Pullman, **Kamil Slowikowski**, Soumya Raychaudhuri, Joel Guthridge, Judith James, Jill Buyon, Thomas Tuschl
Nature Immunology, 2019.

15. [Lymphocyte innateness defined by transcriptional states reflects a balance between proliferation and effector functions](#)
Maria Gutierrez-Arcelus, Nikola Teslovich, Alex R. Mola, Rafael B. Polidoro, Aparna Nathan, Hyun Kim, Susan Hannes, **Kamil Slowikowski**, Gerald F. M. Watts, Ilya Korsunsky, Michael B. Brenner, Soumya Raychaudhuri, Patrick J. Brennan
Nature Communications, 2019. ⬀ View the data

14. [Functionally distinct disease-associated fibroblast subsets in rheumatoid arthritis.](#)
Fumitaka Mizoguchi*, **Kamil Slowikowski***, Kevin Wei, Jennifer L. Marshall, Deepak A. Rao, Sook Kyung Chang, Hung N. Nguyen, Erika H. Noss, Jason D. Turner, Brandon E. Earp, Philip E. Blazar, John Wright, Barry P. Simmons, Laura T. Donlin, George D. Kalliolias, Susan M. Goodman, Vivian P. Bykerk, Lionel B. Ivashkiv, James A. Lederer, Nir Hacohen, Peter A. Nigrovic, Andrew Filer, Christopher D. Buckley, Soumya Raychaudhuri, Michael B. Brenner
Nature Communications, 2018.

13. [Mixed-effects association of single cells identifies an expanded effector CD4+ T cell subset in rheumatoid arthritis.](#)
Chamith Y. Fonseka*, Deepak A. Rao*, Nikola C. Teslovich, Ilya Korsunsky, Susan K. Hannes, **Kamil Slowikowski**, Michael F. Gurish, Laura T. Donlin, James A. Lederer, Michael E. Weinblatt, Elena M. Massarotti, Jonathan S. Coblyn, Simon M. Helfgott, Derrick J. Todd, Vivian P. Bykerk, Elizabeth W. Karlson, Joerg Ermann, Yvonne C. Lee, Michael B. Brenner, and Soumya Raychaudhuri
Science Translational Medicine, 2018.

12. [Discovering in vivo cytokine-eQTL interactions from a lupus clinical trial.](#)
Emma E. Davenport, Tiffany Amariuta, Maria Gutierrez-Arcelus, **Kamil Slowikowski**, Harm-Jan Westra, Yang Luo, Ciyue Shen, Deepak A. Rao, Ying Zhang, Stephen Pearson, David von Schack, Jean S. Beebe, Nan Bing, Sally John, Michael S. Vincent, Baohong Zhang and Soumya Raychaudhuri
Genome Biology, 2018.

11. [Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types.](#)
Hilary K. Finucane, Yakir A. Reshef, Verneri Anttila, **Kamil Slowikowski**, Alexander Gusev, Andrea Byrnes, Steven Gazal, Po-Ru Loh, Caleb Lareau, Noam Shoresh, Giulio Genovese, Arpiar Saunders, Evan Macosko, Samuela Pollack, The Brainstorm Consortium, John R. B. Perry, Jason D. Buenrostro, Bradley E. Bernstein, Soumya Raychaudhuri, Steven McCarroll, Benjamin M. Neale, Alkes L. Price
Nature Genetics, 2018.

10. [Functional genomics of stromal cells in chronic inflammatory diseases](#)
Kamil Slowikowski, Kevin Wei, Michael B. Brenner, Soumya Raychaudhuri
Current Opinion in Rheumatology, 2018.

9. [Methods for high-dimensional analysis of cells dissociated from cryopreserved synovial tissue](#)
Laura T. Donlin*, Deepak A. Rao*, Kevin Wei, **Kamil Slowikowski**, Mandy J. McGeachy, Jason D. Turner, Nida Meednu, Fumitaka Mizoguchi, Maria Gutierrez-Arcelus, David J. Lieb, Joshua Keegan, Kaylin Muskat, Joshua Hillman, Cristina Rozo, Edd Ricker, Thomas M. Eisenhaure, Shuqiang Li, Edward P. Browne, Adam Chicoine, Danielle Sutherby, Akiko Noma, Accelerating Medicines Partnership RA/SLE Network, Chad Nusbaum,

Stephen Kelly, Alessandra B. Pernis, Lionel B. Ivashkiv, Susan M. Goodman, William H. Robinson, Paul J. Utz, James A. Lederer, Ellen M. Gravallese, Brendan F. Boyce, Nir Hacohen, Costantino Pitzalis, Peter K. Gregersen, Gary S. Firestein, Soumya Raychaudhuri, Larry W. Moreland, V. Michael Holers, Vivian P. Bykerk, Andrew Filer, David L. Boyle, Michael B. Brenner and Jennifer H. Anolik
Arthritis Research and Therapy, 2018.

8. Pathologically expanded peripheral T helper cell subset drives B cells in rheumatoid arthritis
Deepak A. Rao, Michael F. Gurish, Jennifer L. Marshall, **Kamil Slowikowski**, Chamith Y. Fonseka, Yanyan Liu, Laura T. Donlin, Lauren A. Henderson, Kevin Wei, Fumitaka Mizoguchi, Nikola C. Teslovich, Michael E. Weinblatt, Elena M. Massarotti, Jonathan S. Coblyn, Simon M. Helfgott, Yvonne C. Lee, Derrick J. Todd, Vivian P. Bykerk, Susan M. Goodman, Alessandra B. Pernis, Lionel B. Ivashkiv, Elizabeth W. Karlson, Peter A. Nigrovic, Andrew Filer, Christopher D. Buckley, James A. Lederer, Soumya Raychaudhuri, Michael B. Brenner
Nature, 2017.

7. Refining the role of de novo protein-truncating variants in neurodevelopmental disorders by using population reference samples
Jack A Kosmicki, Kaitlin E Samocha, Daniel P Howrigan, Stephan J Sanders, **Kamil Slowikowski**, Monkol Lek, Konrad J Karczewski, David J Cutler, Bernie Devlin, Kathryn Roeder, Joseph D Buxbaum, Benjamin M Neale, Daniel G MacArthur, Dennis P Wall, Elise B Robinson, Mark J Daly
Nature Genetics, 2017.

6. A method to decipher pleiotropy by detecting underlying heterogeneity driven by hidden subgroups applied to autoimmune and neuropsychiatric diseases
Buhm Han, Jennie G Pouget, **Kamil Slowikowski**, Eli Stahl, Cue Hyunkyu Lee, Dorothee Diogo, Xinli Hu, Yu Rang Park, Eunji Kim, Peter K Gregersen, Solbritt Rantapää Dahlqvist, Jane Worthington, Javier Martin, Steve Eyre, Lars Klareskog, Tom Huizinga, Wei-Min Chen, Suna Onengut-Gumuscu, Stephen S Rich, Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium, Naomi R Wray, Soumya Raychaudhuri
Nature Genetics, 2016.

5. Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci
Gosia Trynka, Harm-Jan Westra, **Kamil Slowikowski**, Xinli Hu, Han Xu, Barbara E. Stranger, Robert J. Klein, Buhm Han, Soumya Raychaudhuri
The American Journal of Human Genetics, 2015.

4. SNPSEA: an algorithm to identify cell types, tissues and pathways affected by risk loci
Kamil Slowikowski, Xinli Hu, Soumya Raychaudhuri
Bioinformatics, 2014.

3. Common genetic variants modulate pathogen-sensing responses in human dendritic cells
Mark N. Lee*, Chun Ye*, Alexandra-Chloé Villani, Towfique Raj, Weibo Li, Thomas M. Eisenhaure, Selina H. Imboywa, Portia I. Chipendo, F. Ann Ran, **Kamil Slowikowski**, Lucas D. Ward, Khadir Raddassi, Cristin McCabe, Michelle H. Lee, Irene Y. Frohlich, David A. Hafler, Manolis Kellis, Soumya Raychaudhuri, Feng Zhang, Barbara E. Stranger, Christophe O. Benoist, Philip L. De Jager, Aviv Regev, Nir Hacohen
Science, 2014.

2. Regulation of gene expression in autoimmune disease loci and the genetic basis of proliferation in CD4+ effector memory T cells
Xinli Hu, Hyun Kim, Towfique Raj, Patrick J. Brennan, Gosia Trynka, Nikola Teslovich, **Kamil Slowikowski**, Wei-Min Chen, Suna Onengut, Clare Baecher-Allan, Philip L. De Jager, Stephen S. Rich, Barbara E. Stranger, Michael B. Brenner, Soumya Raychaudhuri
PLoS Genetics, 2014.

1. Computational and experimental analyses of retrotransposon-associated minisatellite DNAs in the soybean genome
Lauren S. Mogil*, **Kamil Slowikowski***, Howard M. Laten
BMC Bioinformatics 2012.

Updated June 22, 2019