Kamil Slowikowski

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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

Postdoctoral Associate. Massachusetts General Hospital.   2019 – Present
Dr. Chloé Villani. Center for Immunology and Inflammatory Diseases.
Dr. Bo Li. Center for Immunology and Inflammatory Diseases.

Graduate Research Assistant. Harvard Medical School.   2013 – 2019
Dr. Soumya Raychaudhuri. Department of Biomedical Informatics.
Dr. Michael B. Brenner. Division of Rheumatology, Immunology and Allergy,
Brigham and Women's Hospital.

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.

SOFTWARE AND TUTORIALS

○ **Cell Guide** (HTML, Javascript). Navigate large-scale scRNA-seq datasets in your web browser.
⬈ **Immunogenomics.io** (R, HTML, Javascript). Websites for RNA-seq data visualization.
○ **ggrepel** (R, C++). Repel overlapping text labels away from each other. **Over 5 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.
○ **harmonypy** (Python). Harmony is a data integration algorithm (Korsunsky *et al.* 2019).

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

SCHOLARSHIPS AND AWARDS ───────────────────────────────

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

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

TALKS ───

7. Web-based data browsers make RNA-seq data accessible to a wide audience.
   - *Federation of Clinical Immunology Societies (FOCIS)*. San Diego, CA. 2020-10-31

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. ggrepel: Automatically positioning non-overlapping text labels with 'ggplot2'
   - *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 ───

7. Unravelling immune and cellular responses associated with acute COVID-19 infection, symptoms and lethality at single-cell resolution
   - *FOCIS 2020*. San Diego, CA. 2020-10-29

6. ggrepel: Automatically positioning non-overlapping text labels with 'ggplot2'
   - *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.

- *MGH Division of Rheumatology, Allergy, and Immunology Annual Retreat.* North Falmouth, MA. — 2019-10-18
- *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

SELECTED PEER REVIEWED ARTICLES

6. Single-cell transcriptomics in cancer: computational challenges and opportunities
Jean Fan, **Kamil Slowikowski**, Fan Zhang
EMM, 2020.

5. 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
PNAS, 2020. ⧉ View the data

4. 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

3. 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.

2. Functional genomics of stromal cells in chronic inflammatory diseases
   Kamil Slowikowski, Kevin Wei, Michael B. Brenner, Soumya Raychaudhuri
   Current Opinion in Rheumatology, 2018.

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

PEER REVIEWED ARTICLES

18. Synoviocyte-targeted therapy synergizes with TNF inhibition in arthritis reversal
    Mattias N. D. Svensson, Martina Zoccheddu, Shen Yang1, Gyrid Nygaard, Christian Secchi, Karen M. Doody, **Kamil Slowikowski**, Fumitaka Mizoguchi, Frances Humby, Rebecca Hands, Eugenio Santelli, Cristiano Sacchetti, Kuninobu Wakabayashi, Dennis J. Wu, Christopher Barback, Rizi Ai, Wei Wang, Gary P. Sims, Piotr Mydel, Tsuyoshi Kasama, David L. Boyle, Francesco Galimi, David Vera, Michel L. Tremblay, Soumya Raychaudhuri, Michael B. Brenner, Gary S. Firestein, Costantino Pitzalis, Anna-Karin H. Ekwall, Stephanie M. Stanford and Nunzio Bottini
    Science Advances, 2020.

17. A positively selected FBN1 missense variant reduces height in Peruvian individuals
    Samira Asgari, Yang Luo, Ali Akbari, Gillian M. Belbin, Xinyi Li, Daniel N. Harris, Martin Selig, Eric Bartell, Roger Calderon, **Kamil Slowikowski**, Carmen Contreras, Rosa Yataco, Jerome T. Galea, Judith Jimenez, Julia M. Coit, Chandel Farroñay, Rosalynn M. Nazarian, Timothy D. O'Connor, Harry C. Dietz, Joel N. Hirschhorn, Heinner Guio, Leonid Lecca, Eimear E. Kenny, Esther E. Freeman, Megan B. Murray Soumya Raychaudhuri
    Nature, 2020.

16. Using genetics to prioritize diagnoses for rheumatology outpatients with inflammatory arthritis
    Rachel Knevel, Saskia le Cessie, Chikashi C. Terao, **Kamil Slowikowski**, Jing Cui, Tom W.J. Huizinga, Karen H. Costenbader, Katherine P. Liao, Elizabeth W. Karlson, Soumya Raychaudhuri
    Science Translational Medicine, 2020.

15. Fast, sensitive and accurate integration of single-cell data with Harmony
    Ilya Korsunsky, Nghia Millard, Jean Fan, **Kamil Slowikowski**, Fan Zhang, Kevin Wei, Yuriy Baglaenko, Michael Brenner, Po-ru Loh, Soumya Raychaudhuri
    Nature Methods, 2019. ⤷ Learn about Harmony

14. 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.

13. 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 Dall'Era, 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

12. 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

11. 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.

10. 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.

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. 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.

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. [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.

5. [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.

4. [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.

3. [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.

2. [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.

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.

PREPRINTS

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](#)

Updated November 4, 2020