

Kamil Slowikowski

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🌐 slowkow.com

EDUCATION

- PhD in Bioinformatics and Integrative Genomics** 2012–Present
Harvard University. Boston, Massachusetts.
Anticipated graduation date: December 2018.
- 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. 2012 – Present
[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
Extensions for the computer game *Half-Life*, with 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

- ggrepel** (R, C++). Repel overlapping text labels away from each other. Over **900K** 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.
- CENTIPEDE.tutorial** (R). How to use **CENTIPEDE** to test if a transcription factor is bound.

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

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

TALKS

Transcriptomics reveals the role of synovial fibroblasts in rheumatoid arthritis. <i>Leena Peltonen School of Human Genomics. Les Diablerets, Switzerland.</i>	2018-08-19
An introduction to ggrepel. <i>Partners R User Group Meeting. Massachusetts General Hospital, Boston, MA.</i>	2018-07-19
Insights into RA pathogenesis from single cell transcriptomics of synovial tissue. <i>Federation of Clinical Immunology Societies (FOCIS). Chicago, IL.</i>	2017-06-14
AMP rheumatoid arthritis phase 1: single-cell RNA-seq with CEL-seq2. <i>Accelerating Medicines Partnership (AMP). Houston, TX.</i>	2017-02-15
Single-cell transcriptomics reveals disease-associated fibroblast subsets in rheumatoid arthritis. <i>Joint Biology Consortium. Brigham and Women's Hospital, Boston, MA.</i>	2017-01-27
<i>Medical and Population Genetics Seminar Series. Broad Institute, Boston, MA.</i>	2016-04-28
<i>Immunogenomics 2015. HudsonAlpha Institute, Huntsville, AL.</i>	2015-09-30
<i>Cell Circuits and Epigenomics Program Seminar Series. Broad Institute, Boston, MA.</i>	2015-06-22

POSTERS

Identifying transcriptional regulators central to rheumatoid arthritis: transcriptomics of IL-17 dose-response and time series in stromal cells. <i>American College of Rheumatology (ACR) Annual Meeting. San Diego, CA.</i>	2017-11-04
<i>Immune Profiling in Health and Disease. Seattle, WA.</i>	2016-10-03
Single-cell transcriptomics identifies pathogenic synovial fibroblasts in rheumatoid arthritis. <i>National Human Genome Research Institute (NHGRI) Annual Meeting. Bethesda, MD.</i>	2016-04-07
<i>4th Annual Single Cell Analysis Investigators Meeting. Bethesda, MD.</i>	2016-03-02
<i>Program in Quantitative Genomics Conference. Boston, MA.</i>	2015-11-05
SNPSEA: an algorithm to identify cell types, tissues, and pathways affected by risk loci. <i>Harvard Graduate Women in Science and Engineering (HGWISE) Symposium. Cambridge, MA.</i>	2015-04-25
<i>Harvard Biological and Biomedical Sciences (BBS) Retreat. Provincetown, MA.</i>	2014-08-05
Reverse transcriptase SuperScript III adds non-template bases during cDNA polymerization. <i>Summer Undergraduate Research Symposium. Santa Cruz, CA.</i>	2011-08-12
Retrotransposon-associated minisatellites in the soybean genome. <i>Great Lakes Bioinformatics Conference. Athens, OH.</i>	2011-05-03
<i>Loyola Undergraduate Research Symposium. Chicago, IL.</i>	2011-04-16
<i>Chicago Area Undergraduate Research Symposium. Chicago, IL.</i>	2011-04-02

PUBLICATIONS

SELECTED ARTICLES

[Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types](#)
HK Finucane, YA Reshef, V Anttila, **K Slowikowski**, A Gusev, A Byrnes, ...
Nature Genetics, 2018.

[Functionally distinct disease-associated fibroblast subsets in rheumatoid arthritis](#)

F Mizoguchi*, **K Slowikowski***, K Wei, JL Marshall, DA Rao, SK Chang, ...
Nature Communications, 2018.

[Functional genomics of stromal cells in chronic inflammatory diseases](#)

K Slowikowski, K Wei, MB Brenner, S Raychaudhuri
Current Opinion in Rheumatology, 2018.

[Methods for high-dimensional analysis of cells dissociated from cryopreserved synovial tissue](#)

LT Donlin, DA Rao, K Wei, **K Slowikowski**, MJ McGeachy, JD Turner, ...
Arthritis Research and Therapy, 2018.

[Refining the role of de novo protein-truncating variants in neurodevelopmental disorders by using population reference samples](#)

JA Kosmicki, KE Samocha, DP Howrigan, SJ Sanders, **K Slowikowski**, ...
Nature Genetics, 2017.

[Pathologically expanded peripheral T helper cell subset drives B cells in rheumatoid arthritis](#)

DA Rao, MF Gurish, JL Marshall, **K Slowikowski**, CY Fonseka, Y Liu, ...
Nature, 2017.

[A method to decipher pleiotropy by detecting underlying heterogeneity driven by hidden subgroups applied to autoimmune and neuropsychiatric diseases](#)

B Han, JG Pouget, **K Slowikowski**, E Stahl, CH Lee, D Diogo, X Hu, ...
Nature Genetics, 2016.

[Disentangling the Effects of Colocalizing Genomic Annotations to Functionally Prioritize Non-coding Variants within Complex-Trait Loci](#)

G Trynka, HJ Westra, **K Slowikowski**, X Hu, H Xu, BE Stranger, RJ Klein, ...
The American Journal of Human Genetics, 2015.

[Regulation of gene expression in autoimmune disease loci and the genetic basis of proliferation in CD4+ effector memory T cells](#)

X Hu, H Kim, T Raj, PJ Brennan, G Trynka, N Teslovich, **K Slowikowski**, ...
PLoS Genetics, 2014.

[SNPSEA: an algorithm to identify cell types, tissues and pathways affected by risk loci](#)

K Slowikowski, X Hu, S Raychaudhuri
Bioinformatics, 2014.

PREPRINTS

[A genome-wide innateness gradient defines the functional state of human innate T cells](#)

M Gutierrez-Arcelus, N Teslovich, AR Mola, H Kim, S Hannes, ...
bioRxiv, 2018.

[Mixed Effects Association of Single Cells Identifies an Expanded Th1-Skewed Cytotoxic Effector CD4+ T Cell Subset in Rheumatoid Arthritis](#)

CY Fonseka, DA Rao, NC Teslovich, I Korsunsky, SK Hannes, ...
bioRxiv, 2018.

[UBiT2: a client-side web-application for gene expression data analysis](#)

J Fan, D Fan, **K Slowikowski**, N Gehlenborg, P Kharchenko
bioRxiv, 2017.

[Discovering in vivo eQTL interactions with interferon status and drug exposure from a lupus clinical trial](#)

EE Davenport, T Amariuta, M Gutierrez-Arcelus, **K Slowikowski**, ...
bioRxiv, 2017.

Updated October 11, 2018