

## Abbreviated CV



# Jacob L. Steenwyk

Howard Hughes Medical Institute  
Gilliam Fellow, Vanderbilt University  
jacob.steenwyk@vanderbilt.edu  
<http://jlsteenwyk.com/>

## BRIEF BIOGRAPHY

---

I am a Howard Hughes Medical Institute Gilliam Fellow and Ph.D. candidate in the Department of Biological Sciences at Vanderbilt University, Nashville TN. I received my undergraduate degree in Biochemistry and Molecular Biology from Clark University, Worcester MA (2015) where I graduated Summa Cum Laude (GPA: 3.84). I then received an accelerated master's degree in Biochemistry and Molecular Biology from the same institution (2016) before starting my doctoral work.

My research focuses on understanding genome function and evolution with an emphasis on technologically and medically important fungi. I also develop bioinformatic command-line toolkits that process and analyze diverse data types such as phylogenomic and sequence data. More broadly, I aim to elucidate the evolutionary processes that underpin fungal lifestyle as well as reconstruct the tree of life.

My project proposals have been accepted for funding by multiple agencies, including Howard Hughes Medical Institute (2019), the National Institutes of Health (2019), and the Ford Foundation (2019). My research has been recognized by multiple awards, including Trainee-of-the-Year at the Vanderbilt Institute for Infection, Immunology and Inflammation (2020), Graduate Research Excellence Awards (2019 & 2020), and presentation awards at multiple conferences (e.g., 2018, 2020, 2021).

These scientific projects have been successful in part because of my stance of diversity, equity, and inclusion as well as my professional etiquette. I believe that diversity is essential for excellence and that inclusion is required for everyone to benefit from diversity. To this end, I currently serve as the Inclusion Coordinator at The Evolutionary Studies Initiative at Vanderbilt University, was the former president of the Inclusivity in the Biosciences Association at Vanderbilt University, and participate in several other activities that promote diversity, equity, and inclusion in my department, university, and beyond.

## SELECT AWARDS

---

2021	Graduate Research Excellence Award in Biological Sciences, Vanderbilt University
2020	Oral presentation award, SACNAS – The National Diversity in STEM Virtual Conference
2020	Trainee-of-the-Year, Vanderbilt Institute for Infection, Immunology and Inflammation
2019	Gilliam Predoctoral Fellowship, Howard Hughes Medical Institute
2019	Ann Bernard Martin Award for Excellence in Graduate Research, Vanderbilt University
2019	Ruth L. Kirschstein National Research Service Award, National Institutes of Health
2019	Ford Foundation Predoctoral Fellowship, Ford Foundation

## SELECT INVITED TALKS

---

2021	Department of Ecology, Evolution, and Organismal Biology, Iowa State University
2021	MicroSeminar, International Society for Microbial Ecology ( <a href="#">Link</a> )
2020	Institute of Insect Sciences, Zhejiang University
2020	The National Diversity in STEM Conference, SACNAS
2020	Trainee-of-the-year talk, Vanderbilt Institute for Infection, Immunology and Inflammation
2019	Gordon Research Conference, Molecular Mechanisms in Evolution, Easton, MA
2019	30 <sup>th</sup> Fungal Genetics Conference at Asilomar, Pacific Grove, CA

## FIFTEEN HIGHLIGHTED PUBLICATIONS

---

### First author

- (1) **Steenwyk, J.L.**<sup>^</sup>, *et al.* (2021). BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data. <sup>^</sup>Corresponding author. *bioRxiv*. DOI: 10.1101/2021.10.02.462868
- (2) **Steenwyk, J.L.**, *et al.* (2021). A gene coevolution network provides insight into eukaryotic cellular and genomic structure and function. *bioRxiv*. DOI: 10.1101/2021.07.09.451830
- (3) **Steenwyk, J.L.**<sup>^</sup>, *et al.* (2021) PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data. <sup>^</sup>Corresponding author. *Bioinformatics*. DOI: 10.1093/bioinformatics/btab096
- (4) Mead, M.E.\* , **J.L. Steenwyk\***, *et al.* (2021). An evolutionary genomic approach reveals both conserved and species-specific genetic elements related to human disease in closely related *Aspergillus* fungi. \*Equal contributors. *Genetics*. DOI: 10.1093/genetics/iyab066
- (5) **Steenwyk, J.L.**<sup>^</sup>, *et al.* (2020). ClipKIT: a multiple sequence alignment-trimming software for accurate phylogenomic inference. <sup>^</sup>Corresponding author. *PLOS Biology*. DOI: 10.1371/journal.pbio.3001007
- (6) **Steenwyk, J.L.\***, A.L. Lind\*, *et al.* (2020). Pathogenic allodiploid hybrids of *Aspergillus* fungi. \*Equal contributors. *Current Biology*. DOI: 10.1016/j.cub.2020.04.071
- (7) **Steenwyk, J.L.**, *et al.* (2020). Biosynthetic gene clusters, secondary metabolite profiles, and cards of virulence in the closest nonpathogenic relatives of *Aspergillus fumigatus*. *Genetics*. DOI: 10.1534/genetics.120.303549
- (8) **Steenwyk, J.L.**, *et al.* (2019). Extensive loss of cell cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. *PLOS Biology*. DOI: 10.1371/journal.pbio.3000255
- (9) **Steenwyk, J.L.**, *et al.* (2019). A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera *Aspergillus* and *Penicillium*. *mBio*. DOI: 10.1128/mBio.00925-19
- (10) **Steenwyk, J.L.** & A. Rokas (2018). Copy number variation in fungi and its implications for wine yeast genetic diversity and adaptation. *Frontiers in Microbiology*. DOI: 10.3389/fmicb.2018.00288

### Middle author

- (11) Shen, Xing-Xing<sup>^</sup>, **J.L. Steenwyk**, & A. Rokas (2021). Dissecting incongruence between concatenation- and quartet-based approaches in phylogenomic data. <sup>^</sup>Corresponding author. *Systematic Biology*. DOI: 10.1093/sysbio/syab011
- (12) Li, Y., **J.L. Steenwyk**, *et al.* (2021). A genome-scale phylogeny of the kingdom Fungi. *Current Biology*. DOI: 10.1016/j.cub.2021.01.074
- (13) LaBella, A.L., D. Opulente, **J.L. Steenwyk**, C.T. Hittinger, & A. Rokas (2021). Signatures of optimal codon usage in metabolic genes inform budding yeast ecology. *PLOS Biology*. DOI: 10.1371/journal.pbio.3001185
- (14) Shen, X.-X.<sup>^</sup>, **J.L. Steenwyk**, *et al.* (2020). Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. <sup>^</sup>Corresponding author. *Science Advances*. DOI: 10.1126/sciadv.abd0079
- (15) Shen, X.-X.\* , D.A. Opulente\*, J. Kominek\*, X. Zhou\*, **J.L. Steenwyk**, *et al.* (2018). \*Equal contributors. Tempo and mode of genome evolution in the budding yeast subphylum. *Cell*. DOI: 10.1016/j.cell.2018.10.023

## Full length CV



# Jacob L. Steenwyk

Howard Hughes Medical Institute  
Gilliam Fellow, Vanderbilt University  
jacob.steenwyk@vanderbilt.edu  
<http://jlsteenwyk.com/>

## EDUCATION

<b>Present</b>	Ph.D. Candidate, Biological Sciences Advisor: Antonis Rokas GPA: 3.97	<b>Vanderbilt University</b>
<b>2016</b>	M.S. Biochemistry and Molecular Biology Advisor: John G. Gibbons GPA: 3.98	<b>Clark University</b>
<b>2015</b>	B.A. Biochemistry and Molecular Biology Advisor: Denis Larochelle Cumulative GPA: 3.84 Science GPA: 3.84	<b>Clark University</b>

## AWARDS

<b>2021</b>	Honorable mention, Next Generation Faculty Symposium, Stanford.Berkeley.UCSF
<b>2021</b>	Presentation award, Canadian Fungal Research Network and Great Lakes Mycology Conference
<b>2021</b>	Graduate Research Excellence Award in Biological Sciences, Vanderbilt University
<b>2021</b>	Smriti Bardhan Scholarship, Vanderbilt University
<b>2021</b>	Registration award, Science Talk '21
<b>2020</b>	Favorite Artist Award, Catalyst: A Virtual Sci-Art Exhibition
<b>2020</b>	Oral presentation award, SACNAS – The National Diversity in STEM Virtual Conference
<b>2020</b>	Registration scholarship, SACNAS – The National Diversity in STEM Virtual Conference
<b>2020</b>	Best Talk Honorable Mention, Canadian Fungal Research Network Meeting
<b>2020</b>	Trainee-of-the-Year, Vanderbilt Institute for Infection, Immunology and Inflammation
<b>2019</b>	Gilliam Predoctoral Fellowship, Howard Hughes Medical Institute
<b>2019</b>	Ann Bernard Martin Award for Excellence in Graduate Research, Vanderbilt University
<b>2019</b>	Ruth L. Kirschstein National Research Service Award, National Institutes of Health
<b>2019</b>	Ford Foundation Predoctoral Fellowship, Ford Foundation
<b>2019</b>	Graduate student travel grant, Vanderbilt University
<b>2019</b>	Curb Center Fellow, ArtLab, Vanderbilt University
<b>2018</b>	<i>GENETICS</i> Peer Review Training Program, Genetics Society of America
<b>2018</b>	Best poster award, Cellular and Molecular Fungal Biology, Gordon Research Seminar
<b>2018</b>	Best poster award, Cellular and Molecular Fungal Biology, Gordon Research Conference
<b>2018</b>	Best poster award, Department of Biological Sciences, Vanderbilt University
<b>2018</b>	T-shirt design contest winner, Department of Biological Sciences, Vanderbilt University
<b>2017</b>	Graduate student travel grant, Vanderbilt University
<b>2016</b>	Graduate student council travel awards, Clark University
<b>2015</b>	Summa cum laude, Clark University
<b>2014</b>	Summer research scholar, Bridging the gaps, University of Southern California Keck School of Medicine

**2013** Global environmental microbiology scholar, Center for dark energy biosphere investigations, University of Southern California  
**2011** Jonas Clark Scholar, Clark University

## RESEARCH INTERESTS

---

- Evolution of technologically and medically significant fungi
- Evolution and function of DNA repair
- Genome and gene evolution
- Phylogenomics and phylogenetics
- Software development

## SOFTWARE

---

ClipKIT: a multiple sequence alignment-trimming software for accurate phylogenomic inference.

[Publication PDF](#); [Documentation](#); [Source code](#)

PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data. [Publication PDF](#); [Documentation](#); [Source code](#)

BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data. [Publication PDF](#); [Documentation](#); [Source code](#)

orthofisher: a broadly applicable tool for automated gene identification and retrieval. [Documentation](#); [Source code](#)

treehouse: a user-friendly application to obtain subtrees from large phylogenies. [Publication PDF](#); [Documentation & source code](#)

ggpubfigs: an R package for creating color blind friendly figures with ggplot2. [Zenodo record](#); [Documentation & source code](#)

## SOCIETIES

---

*Genetics Society of America, American Society for Microbiology, Mycological Society of America, Society for the Advancement of Chicanos/Hispanics and Native Americans in Science*

## FUNDING

---

<b>Howard Hughes Medical Institute</b>	Principal co-investigator (shared with Antonis Rokas), 09/19-09/22, Examining the loss of diverse DNA repair genes and long-term hypermutation in a lineage of budding yeasts, Gilliam Fellowship, Individual Predoctoral Fellowship, \$150,000
<b>National Institutes of Health</b>	Principal investigator, 08/19-08/22, Examining the loss of diverse DNA repair genes and long-term hypermutation in a lineage of budding yeasts, Ruth L. Kirschstein National Research Service Award, Individual Predoctoral Fellowship (Parent F31), \$88,128 (declined)
<b>Ford Foundation Predoctoral Fellow</b>	Principal investigator, 08/19-08/22, The consequences of aberrant cell cycle and DNA repair processes in budding yeast, Individual Predoctoral Fellowship, \$72,000 (declined)
<b>Curb Center ArtLab Fellow</b>	Principal investigator, 12/18-04/19, Bridging the gap between artist and scientist, ArtLab, Vanderbilt University, \$300

## INVITED TALKS

---

- 2021 Artist-in-Residence program, Vanderbilt Institute for Infection, Immunology and Inflammation
- 2021 CanFunNet and Great Lakes Mycology Conference
- 2021 Sandler Fellows Seminar, University of California, San Francisco
- 2021 Department of Ecology, Evolution, and Organismal Biology, Iowa State University
- 2021 Medical Mycology Trainee Seminar Series, University of Utah ([Link](#))
- 2021 Mycology Graduate Student Organization, University of Georgia
- 2021 MicroSeminar, International Society for Microbial Ecology ([Link](#))
- 2021 Alliance for Diversity in Science and Engineering, Young Researchers Conference
- 2021 Andrew Murray Lab seminar, Harvard University, Cambridge
- 2020 Institute of Insect Sciences, Zhejiang University
- 2020 Evan Eichler Lab seminar, University of Washington, Seattle
- 2020 Genetics Society of America, Early Career Scientist Seminar Series
- 2020 Nicole King Lab seminar, University of California Berkeley
- 2020 The National Diversity in STEM Conference, SACNAS
- 2020 Canadian Fungal Research Network Meeting
- 2020 Trainee-of-the-year talk, Vanderbilt Institute for Infection, Immunology and Inflammation
- 2020 Day of Wond'ry, Vanderbilt University, Nashville, TN
- 2019 Genetics Society of America, Early Career Scientist Seminar Series
- 2019 Gordon Research Conference, Molecular Mechanisms in Evolution, Easton, MA
- 2019 Gordon Research Seminar, Molecular Mechanisms in Evolution, Easton, MA (declined)
- 2019 Focal Point, ArtLab, Vanderbilt University, Nashville, TN
- 2019 30<sup>th</sup> Fungal Genetics Conference at Asilomar, Pacific Grove, CA
- 2019 Phylogenomics and Evolution Group, North Carolina State University, Raleigh, NC
- 2018 ArtLab Seminar Series, Vanderbilt University, Nashville, TN
- 2015 TedXClarkUniversity, Clark University, Worcester, MA

## CONTRIBUTED TALKS

---

- 2021 Students' Mycology Colloquium, Mycological Society of America
- 2020 Evolution Seminar Series, Vanderbilt University ([Link](#))
- 2019 DNA Damage and Response Journal Club, Vanderbilt University, Nashville, TN
- 2019 Research in Progress Seminar, Vanderbilt University, Nashville, TN
- 2019 Biological Sciences Annual Retreat, Vanderbilt University, Nashville, TN
- 2019 Science club at the library, Nashville Public Library, Nashville, TN
- 2018 Nashville Science Club, Jackalope Brewing Company, Nashville, TN
- 2017 Mycological Society of America, University of Georgia, Athens, GA
- 2016 Mycological Society of America, University of California Berkeley, Berkeley, CA
- 2016 Graduate Student Multidisciplinary Conference, Clark University, Worcester, MA

## ADVISING

---

### Undergraduates

- 2019-Pres. Olivia Zheng
- 2018-2021 Megan A. Phillips
- 2018-2019 Benjamin Buckman
- 2018 Devin G. Arrants

## WORKSHOP TEACHING

---

- 2019 Organizer and instructor, Values-based leadership, Vanderbilt University, Nashville, TN

- 2019** Founder and instructor, ‘A beginner’s guide to making figures in R’, Vanderbilt University, Nashville, TN
- 2019** Instructor, Workshop on Phylogenomics, Evolution and Genomics, Český Krumlov, Czech Republic
- 2019** Instructor, Workshop on Genomics, Evolution and Genomics, Český Krumlov, Czech Republic

## TEACHING EXPERIENCE

---

- 2020** Guest lecture, Science Communication Tools and Techniques, Vanderbilt University, Nashville, TN
- 2017-2019** Teaching Assistant, Introductory Biology Lab, Vanderbilt University, Nashville, TN
- 2016** Teaching Assistant, Introduction to Biostatistics, Clark University, Worcester, MA
- 2014-2015** Teaching Assistant, Cell Biology, Clark University, Worcester, MA

## POSTER PRESENTATIONS

---

- 2021** HHMI Gilliam Fellows Meeting, Howard Hughes Medical Institute
- 2021** Biology of Genomes, Cold Spring Harbor Laboratories
- 2021** Science Talk '21, Science Talk
- 2020** HHMI Gilliam Fellows Meeting, Howard Hughes Medical Institute
- 2020** Vanderbilt Institute for Infection, Immunology and Inflammation Annual Symposium, Virtual Conference
- 2020** The Allied Genetics Conference, Virtual Conference
- 2019** HHMI Investigators Science Meeting, Howard Hughes Medical Institute, Bethesda, MD
- 2019** Gilliam Fellows Annual Meeting, Howard Hughes Medical Institute, Bethesda, MD
- 2019** Molecular Mechanisms in Evolution, Gordon Research Conference, Easton, MA
- 2019** Molecular Mechanisms in Evolution, Gordon Research Seminar, Easton, MA
- 2019** 30<sup>th</sup> Fungal Genetics Conference at Asilomar, Pacific Grove, CA
- 2019** Asperfest pre-meeting at 30<sup>th</sup> Fungal Genetics Conference at Asilomar, Pacific Grove, CA
- 2018** Cellular and Molecular Fungal Biology, Gordon Research Conference, Holderness, NH
- 2018** Cellular and Molecular Fungal Biology, Gordon Research Seminar, Holderness, NH
- 2018** Department of Biological Sciences Annual Retreat, Vanderbilt University, Nashville, TN
- 2015** Bumpus Symposium, Clark University, Worcester, MA
- 2015** Traina Scholars Presentation, Clark University, Worcester, MA
- 2015** Summer Research Presentation, Clark University, Worcester, MA

## RESEARCH EXPERIENCE

---

- 2016-Pres.** Antonis Rokas Lab at Vanderbilt University, Nashville, TN. Doctoral Research. Evolution of medically and technologically significant fungi.
- 2015-2016** John Gibbons Lab at Clark University, Worcester, MA. Undergraduate and Master’s Research. Copy number variation in the human pathogen, *Cryptococcus gattii*.
- 2015-2016** Robert Drewell Lab at Clark University, Worcester, MA. Undergraduate and Master’s Research. Genome-wide methylation patterns in the social amoeba, *Dictyostelium discoideum*.
- 2014** Ite A. Laird-Offringa Lab at University of Southern California, Los Angeles, CA. Bridging the Gaps Summer Scholar. Mapping the autoimmune triggering epitope of *ELAVL4* in small cell lung cancer.
- 2013** John Heidelberg and Eric Webb Labs at University of Southern California, Los Angeles, CA. Global Environmental Microbiology Summer Scholar. Fresh and marine water microbial diversity.

## SERVICE

---

- 2020-Pres.** Founder and Chief Officer, SciArt with Purpose, <https://jlsteenwyk.com/sciart.html>
- 2019-Pres.** Member, Steering Committee, Early Career Leadership Program, Genetics Society of America
- 2019-Pres.** Inclusion Coordinator, The Evolutionary Studies Initiative at Vanderbilt, Vanderbilt University, Nashville, TN
- 2019-Pres.** Graphic Illustrator, The Evolutionary Studies Initiative at Vanderbilt, Vanderbilt University, Nashville, TN
- 2017-Pres.** Educational outreach booth design and execution, MEGAMicrobe, Nashville, TN
- 2017-Pres.** Member of the Dean of Graduate Student's survey quantitative analysis subgroup, Graduate Diversity and Inclusion Committee, Vanderbilt University, Nashville, TN
- 2017-Pres.** Judge, Middle Tennessee Science and Engineering Fair, Belmont University, Nashville, TN
- 2019-2021** Co-chair, Communication and Outreach Subcommittee, Genetics Society of America
- 2018-2021** Volunteer Deputy, American Society of Microbiology Vanderbilt University Chapter, Nashville, TN
- 2017-2021** Communications chair, Inclusivity in Biosciences Association, Vanderbilt University, Nashville, TN
- 2020** Panelist at the Communication and Outreach Workshop, The Allied Genetics Conference, Genetics Society of America
- 2019-2020** President, Inclusivity in Biosciences Association, Vanderbilt University, Nashville, TN
- 2019-2020** Co-chair, MEGAMicrobe, Vanderbilt Institute for Infections, Immunology and Inflammation, Nashville, TN
- 2018-2019** Vice President, Inclusivity in Biosciences Association, Vanderbilt University, Nashville, TN
- 2013-2019** Administrator and Owner, Molecular Biology and Biochemistry for Researchers and Students Group, LinkedIn
- 2019** Peer review workshop leader, 30<sup>th</sup> Fungal Genetics Conference at Asilomar, Pacific Grove, CA
- 2018-2019** Vice President, Graduate Student Association, Department of Biological Sciences, Vanderbilt University, Nashville, TN
- 2018-2019** Vice co-chair, MEGAMicrobe, Vanderbilt Institute for Infections, Immunology and Inflammation, Nashville, TN
- 2017-2018** Secretary, Graduate Student Association, Department of Biological Sciences, Vanderbilt University, Nashville, TN
- 2017-2018** Scientific consultant, Little Harpeth Brewing, Nashville, TN
- 2017** Vanderbilt Student Volunteers for Science, Volunteer Science Teacher, West End Middle School, Nashville, TN
- 2014-2015** Undergraduate Subcommittee for Department of Chemistry, Biochemistry and Molecular Biology Faculty Search Committee, Clark University, Worcester, MA
- 2014-2015** Science Education Outreach Blogger, C-DEBI Sci-Curious Blog

## ART SHOWS

---

- 2021** Science Talk '21, Science Talk
- 2020** Catalyst: A Virtual Sci-Art Exhibition, Michigan State University
- 2020** Day of Wond'ry, Vanderbilt University, Nashville, TN
- 2020** Fire-Exhibition, Kefi Collective at Vanderbilt University, Nashville, TN
- 2019** Biomedical Sciences Winter Show, Vanderbilt University, Nashville, TN
- 2019** Focal point, ArtLab, Vanderbilt University, Nashville, TN
- 2019** Connecting the Dots, ArtLab, Vanderbilt University, Nashville, TN



- 2018 ArtLab opening reception, ArtLab, Vanderbilt University, Nashville, TN  
2018 The Intersection between Art and Science, ArtLab, Vanderbilt University, Nashville, TN

## MANUSCRIPT REVIEWER

*Nature Communications; Molecular Biology and Evolution; Systematic Biology; Methods in Ecology and Evolution; Genome Biology and Evolution; Genetics; Microbial Genomics; G3: Genes | Genomes | Genetics; FEMS Yeast Research; BMC Genomics; Nature Communications Biology; PLOS One; Molecular Genetics and Genomics; and others*

## POPULAR SCIENCE ARTICLES

- (5) Simopoulos, M.A.C., A.F. Cisneros, A.D. Mendoza, C. Bautista, **J.L. Steenwyk**, N. Ahmad. Hurdles and advances to making science gender-neutral, *ecrLife*. November 26, 2020
- (4) Mendoza, A.D., C. Bautista, E.A. Marnik, C.M.A. Simopoulos, & **J.L. Steenwyk**. Navigating fake news as a scientist, *ecrLife*. October 8, 2020
- (3) **Steenwyk, J.L.** & M. Jonika. How to get started in science communication, *ecrLife*. August 21, 2020
- (2) **Steenwyk, J.L.** & A. Rokas. A new hybrid fungus is found in hospitals and linked to lung disease, *The Conversation*. June 4, 2020
- (1) **Steenwyk, J.L.** & A. Rokas. An outlaw yeast thrives with genetic chaos – and could provide clues for understanding cancer growth, *The Conversation*. May 21, 2019

## PUBLICATIONS

### Preprints

- (4) **Steenwyk, J.L.**<sup>^</sup>, T.J. Buida III, C. Gonçalves, D.C. Goltz, G. Morales, M. Mead, A.L. LaBella, C.M. Chavez, J.E. Schmitz, M. Hadjifrangiskou, Y. Li, & A. Rokas<sup>^</sup> (2021). BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data. <sup>^</sup>Corresponding authors. bioRxiv. DOI: 10.1101/2021.10.02.462868
- (3) de Castro, P.A., A. Moraes, A.C. Colabardini, M.A.C. Horta, S.L. Knowles, H.A. Raja, N.H. Oberlies, Y. Koyama, M. Ogawa, K. Gomi, **J.L. Steenwyk**, A. Rokas, L.N.A. Ries, G.H. Goldman (2021). Regulation of gliotoxin biosynthesis and protection in *Aspergillus* species. bioRxiv. DOI: 10.1101/2021.08.16.456458
- (2) **Steenwyk, J.L.**, M.A. Phillips, F. Yang, S.S. Date, T. Graham, J. Berman, C.T. Hittinger, A. Rokas (2021). A gene coevolution network provides insight into eukaryotic cellular and genomic structure and function. bioRxiv. DOI: 10.1101/2021.07.09.451830
- (1) **Steenwyk, J.**, J. St. Denis, J. Dresch, D. Larochelle, & R. Drewell (2017). Whole genome bisulfite sequencing reveals a sparse, but robust pattern of DNA methylation in the *Dictyostelium discoideum* genome. bioRxiv. DOI: 10.1101/166033

### Peer Review Published

- (43) **Steenwyk, J.L.**<sup>^</sup> & A. Rokas<sup>^</sup> (2021). ggpubfigs: colorblind friendly color palettes and ggplot2 graphic system extensions for publication-quality scientific figures. <sup>^</sup>Corresponding authors. Microbiology Resource Announcements. *in press*.
- (42) Phillips, M.A., **J.L. Steenwyk**<sup>^</sup>, X.-X. Shen, & A. Rokas<sup>^</sup> (2021). Examination of gene loss in the DNA mismatch repair pathway and its mutational consequences in a fungal phylum. <sup>^</sup>Corresponding authors. Genome Biology and Evolution. PMID: 34554246; DOI:



10.1093/gbe/evab219.

- (41) Santos, R.A.C., M.E. Mead, **J.L. Steenwyk**, O. Rivero-Menéndez, A. Alastruey-Izquierdo, G.H. Goldman<sup>^</sup>, & A. Rokas<sup>^</sup> (2021). Examining signatures of natural selection in antifungal resistance genes across *Aspergillus* fungi. <sup>^</sup>Corresponding authors. *Frontiers in Fungal Biology*. DOI: 10.3389/ffunb.2021.723051
- (40) **Steenwyk, J.L.** & A. Rokas (2021). orthofisher: a broadly applicable tool for automated gene identification and retrieval. *G3 Genes|Genomes|Genetics*. PMID: 34544141; PMCID: PMC8496211; DOI: 10.1093/g3journal/jkab250
- (39) Ries, L., P. de Castro, L. Silva, C. Valero, T. dos Reis, R. Saborano, I. Duarte, G. Persinoti, **J.L. Steenwyk**, A. Rokas, F. Almeida, J. Costa, T. Fill, S.S.W. Wong, V. Aimaniananda, F. Rodrigues, R. Gonçalves, C. Duarte-Oliveira, A. Carvalho, & G.H. Goldman (2021). *Aspergillus fumigatus* acetate utilization impacts virulence traits and pathogenicity. *mBio*. PMID: 34311583; PMCID: PMC8406206; DOI: 10.1128/mBio.01682-21
- (38) Mead, M.E.\* , **J.L. Steenwyk\***, L.P. Silva, P.A. de Castro, N. Saeed, F. Hillmann, G.H. Goldman, & A. Rokas (2021). An evolutionary genomic approach reveals both conserved and species-specific genetic elements related to human disease in closely related *Aspergillus* fungi. \*Equal contributors. *Genetics*. PMID: 33944921; PMCID: PMC8225353; DOI: 10.1093/genetics/iyab066
- (37) **Steenwyk, J.L.**, M.E. Mead, P.A. Castro, C. Valero, A. Damasio, R.A.C. Santos, A.L. LaBella, Y. Li, S.L. Knowles, H.A. Raja, N.H. Oberlies, X. Zhou, O.A. Cornely, F. Fuchs, P. Koehler<sup>^</sup>, G.H. Goldman<sup>^</sup>, A. Rokas<sup>^</sup> (2021). Genomic and phenotypic analysis of COVID-19-associated pulmonary aspergillosis isolates of *Aspergillus fumigatus*. <sup>^</sup>Corresponding authors. *Microbiology Spectrum*. PMID: 34106569; PMCID: PMC7654854; DOI: 10.1128/Spectrum.00010-21
- (36) LaBella, A.L., D. Opulente, **J.L. Steenwyk**, C.T. Hittinger, & A. Rokas (2021). Signatures of optimal codon usage in metabolic genes inform budding yeast ecology. *PLOS Biology*. PMID: 33872297; PMCID: PMC8084343; DOI: 10.1371/journal.pbio.3001185
- (35) **Steenwyk, J.L.** (2021). Evolutionary divergence in the DNA damage response among fungi. *mBio*. PMID: 33727357; PMCID: PMC8092291; DOI: 10.1128/mBio.03348-20
- (34) Shen, Xing-Xing, **J.L. Steenwyk**, & A. Rokas (2021). Dissecting incongruence between concatenation- and quartet-based approaches in phylogenomic data. *Systematic Biology*. PMID: 33616672; DOI: 10.1093/sysbio/syab011
- (33) **Steenwyk, J.L.**<sup>^</sup>, T.J. Buida III, A.L. LaBella, Y. Li, X.-X. Shen, & A. Rokas<sup>^</sup> (2020). PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data. <sup>^</sup>Corresponding authors. *Bioinformatics*. PMID: 33560364; PMCID: PMC8388027; DOI: 10.1093/bioinformatics/btab096
- (32) Li, Y., **J.L. Steenwyk**, Y. Chang, Y. Wang, T.Y. James, J.E. Stajich, J.W. Spatafora, M. Groenewald, C. Dunn, C.T. Hittinger, X.-X. Shen<sup>^</sup>, A. Rokas<sup>^</sup> (2020). A genome-scale phylogeny of the kingdom Fungi. <sup>^</sup>Corresponding authors. *Current Biology*. PMID: 33607033; PMCID: PMC8347878; DOI: 10.1016/j.cub.2021.01.074
- (31) **Steenwyk, J.L.** (2021). A portrait of budding yeasts: A symbol of the arts, sciences and a whole greater than the sum of its parts. *Yeast*. PMID: 32869892; DOI: 10.1002/yea.3518
- (30) **Steenwyk, J.L.**<sup>^</sup>, T.J. Buida III, Y. Li, X.-X. Shen, & A. Rokas<sup>^</sup> (2020). ClipKIT: a multiple sequence alignment-trimming software for accurate phylogenomic inference.

^Corresponding authors. PLOS Biology. PMID: 33264284; PMCID: PMC7735675; DOI: 10.1371/journal.pbio.3001007

- (29) Li, Y., K.T. David, X.-X. Shen, **J.L. Steenwyk**, K.M. Halanych, & A. Rokas (2020). Feature Frequency Profile-based phylogenies are inaccurate. Proceedings of the National Academy of Sciences of the United States of America. PMID: 33234569; PMCID: PMC7749326; DOI: 10.1073/pnas.2013143117
- (28) Shen, X.-X.^, **J.L. Steenwyk**, A.L. LaBella, D.A. Ofulente, X. Zhou, J. Kominek, Y. Li, M. Groenewald, C.T. Hittinger, & A. Rokas^ (2020). Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. ^Corresponding authors. Science Advances. PMID: 33148650; PMCID: PMC7673691; DOI: 10.1126/sciadv.abd0079
- (27) Santos, R.A.C., O. Rivero-Menendez, **J.L. Steenwyk**, M.E. Mead, G.H. Goldman^, A. Alastruey-Izquierdo, & A. Rokas^ (2020). Draft genome sequences of four *Aspergillus* section *Fumigati* clinical strains. ^Corresponding authors. Microbiology Resource Announcements. PMID: 33004453; PMCID: PMC7530925; DOI: 10.1128/MRA.00856-20
- (26) Filho, A.P.C., G.T.P. Brancini, P.A. de Castro, J.A. Ferreira, L.P. Silva, M.C. Rocha, I. Malavazi, J.G.M. Pontes, T. Fill, R. Silva, F. Almeida, **J.L. Steenwyk**, A. Rokas, T.F. dos Reis, L.N.A. Ries, & G.H. Goldman (2020). *Aspergillus fumigatus* G-protein coupled receptors GprM and GprJ are important for the regulation of the cell wall integrity pathway, secondary metabolite production, and virulence. mBio. PMID: 33051372; PMCID: PMC7554674; DOI: 10.1128/mBio.02458-20
- (25) **Steenwyk, J.L.**, M.E. Mead\*, S.L. Knowles\*, H.A. Raja, C.D. Roberts, O. Bader, J. houbraken, G.H. Goldman, N.H. Oberlies, & A. Rokas (2020). Biosynthetic gene clusters, secondary metabolite profiles, and cards of virulence in the closest nonpathogenic relatives of *Aspergillus fumigatus*. \*Equal contributors. Genetics. PMID: 32817009; PMCID: PMC7536862; DOI: 10.1534/genetics.120.303549
- (24) Ries, L.N.A., L. Pardeshi, Z. Dong, K. Tan, **J.L. Steenwyk**, A.C. Colabardini, J.A.F. Filho, P.A. de Castro, L.P. Silva, N.W. Preite, F. Almeida, L.J. de Assis, R.A.C. dos Santos, P. Bowyer, M. Bromley, R.A. Owens, S. Doyle, M. Demasi, D.C.R. Hernández, L.E.S. Netto, M.T. Pupo, A. Rokas, F.V. Loures, K.H. Wong, & G.H. Goldman (2020). The *Aspergillus fumigatus* transcription factor RglT is important for gliotoxin biosynthesis and self-protection, and virulence. PLOS Pathogens. PMID: 32667960; PMCID: PMC7384679; DOI: 10.1371/journal.ppat.1008645
- (23) **Steenwyk, J.L.\***, A.L. Lind\*, L.N.A. Ries, T.F. dos Reis, L.P. Silva, F. Almeida, R.W. Bastos, T.F. de Campos Fraga da Silva, V.L.D. Bonato, A.M. Pessoni, F. Rodrigues, H.A. Raja, S.L. Knowles, N.H. Oberlies, K. Lagrou, G.H. Goldman^, A. Rokas^ (2020). Pathogenic allodiploid hybrids of *Aspergillus* fungi. \*Equal contributors; ^Corresponding authors. Current Biology. PMID: 32502407; PMCID: PMC7343619; DOI: 10.1016/j.cub.2020.04.071
- (22) Mead, M.E.\*, A.T. Borowsky\*, B. Joehnk, **J.L. Steenwyk**, X.-X. Shen, A. Sil, & A. Rokas (2020). Recurrent loss of *abaA*, a master regulator of asexual development in filamentous fungi, correlates with changes in genomic and morphological traits. \*Equal contributors. Genome Biology and Evolution. PMID: 32442273; PMCID: PMC7531577; DOI: 10.1093/gbe/evaa107
- (21) Santos, R.A.C., **J.L. Steenwyk**, O. Rivero-Menendez, M.E. Mead, L.P. Silva, R.W. Bastos, A. Alastruey-Izquierdo, G.H. Goldman^, & A. Rokas^ (2020). Genomic and phenotypic

heterogeneity of clinical isolates of the human pathogens *Aspergillus fumigatus*, *Aspergillus lentulus* and *Aspergillus fumigati*affinis. ^Corresponding contributors. *Frontiers in Genetics*. PMID: 32477406; PMCID: PMC7236307; DOI: 10.3389/fgene.2020.00459

- (20) Bastos, R.W., C. Valero, L.P. Silva, T. Schoen, M. Drott, V. Brauer, R. Silva-Rocha, A. Lind, **J.L. Steenwyk**, A. Rokas, F. Rodrigues, A. Resendiz-Sharpe, K. Lagrou, M. Marcet-Houben, T. Gabaldon, E. McDonnell, I. Reid, A. Tsang, B.R. Oakley, F. Loures, F. Almeida, A. Huttenlocher, N.P. Keller, L. Ries, G.H. Goldman (2020). Functional characterization of clinical isolates of the opportunistic fungal pathogen *Aspergillus nidulans*. *mSphere*. PMID: 32269156; PMCID: PMC7142298; DOI: 10.1128/mSphere.00153-20
- (19) Rokas, A., M.E. Mead, **J.L. Steenwyk**, N.H. Oberlies, & G.H. Goldman (2020). Evolving moldy murderers: *Aspergillus* section *Fumigati* as a model for studying the repeated evolution of fungal pathogenicity. *PLOS Pathogens*. PMID: 32106242; PMCID: PMC7046185; DOI: 10.1371/journal.ppat.1008315
- (18) Knowles, S.L., M.E. Mead, L.P. Silva, H.A. Raja, **J.L. Steenwyk**, G.H. Gustavo, A. Rokas, & N.H. Oberlies (2020). Gliotoxin, a known virulence factor in the major human pathogen *Aspergillus fumigatus*, is also biosynthesized by the non-pathogenic relative *A. fischeri*. *mBio*. PMID: 32047138; PMCID: PMC7018655; DOI: 10.1128/mBio.03361-19
- (17) Libkind, D., D. Peris, F.A. Cubillos, **J.L. Steenwyk**, D.A. Opulente, Q.K. Langdon, N. Bellora, A. Rokas, & C.T. Hittinger (2020). Into the wild: new yeast genomes from natural environments and new tools for their analysis. *FEMS Yeast Research*. PMID: 32009143; PMCID: PMC7067299; DOI: 10.1093/femsyr/foaa008
- (16) Rokas, A., M.E. Mead, **J.L. Steenwyk**, H.A. Raja, & N.H., Oberlies (2020). Biosynthetic gene clusters and the evolution of fungal chemodiversity. *Natural Product Reports*. PMID: 31898704; PMCID: PMC7332410; DOI: 10.1039/c9np00045c
- (15) Bodinakku, I., J. Shaffer, A.B. Connors, **J.L. Steenwyk**, E. Kastman, A. Rokas, A. Robbat, B. Wolfe (2019). Rapid phenotypic and metabolomics domestication of wild *Penicillium* molds on cheese. *mBio*. PMID: 31615965; PMCID: PMC6794487; DOI: 10.1128/mBio.02445-19
- (14) Mead, M.E.\*, H.A. Raja\*, **J.L. Steenwyk**, S.L. Knowles, N.H. Oberlies^, & A. Rokas^ (2019). Draft genome sequence of the griseofulvin-producing fungus *Xylaria flabelliformis* strain G536. \*Equal contributors; ^Corresponding authors. *Microbiology Resource Announcements*. PMID: 31537670; PMCID: PMC6753274; DOI: 10.1128/MRA.00890-19
- (13) **Steenwyk, J.L.** & A. Rokas (2019). treehouse: a user-friendly application to obtain subtrees from large phylogenies. *BMC Research Notes*. PMID: 31455362; PMCID: PMC6712805; DOI: 10.1186/s13104-019-4577-5
- (12) Labella, A.L., D.A. Opulente, **J.L. Steenwyk**, C.T. Hittinger, & A. Rokas (2019). Variation and selection on codon usage bias across an entire subphylum. *PLOS Genetics*. PMID: 31365533; PMCID: PMC6701816; DOI: 10.1371/journal.pgen.1008304
- (11) **Steenwyk, J.L.**, X.-X. Shen, A.L. Lind, G.H. Goldman, & A. Rokas (2019). A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera *Aspergillus* and *Penicillium*. *mBio*. PMID: 31289177; PMCID: PMC6747717; DOI: 10.1128/mBio.00925-19
- (10) **Steenwyk, J.L.**, D. Opulente, J. Kominek, X.-X. Shen, X. Zhou, A.L. LaBella, N.P. Bradley,

- B.F. Eichman, N. Čadež, D. Libkind, J. DeVirgilio, A.B. Hulfachor, C.P. Kurtzman, C.T. Hittinger<sup>^</sup>, & A. Rokas<sup>^</sup> (2019). Extensive loss of cell cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. <sup>^</sup>Corresponding authors. PLOS Biology. PMID: 31112549; PMCID: PMC6528967; DOI: 10.1371/journal.pbio.3000255
- (9) Ries, L.N.A., **J.L. Steenwyk**, P.A. de Castro, P.B.A. de Lima, F. Almeida, L.J. de Assis, A.O. Manfiolli, A. Takahashi-Nakaguchi, Y. Kusuya, D. Hagiwara, H. Takahashi, X. Wang, J. Obar, A. Rokas, & G.H. Goldman (2019). Nutritional heterogeneity among *Aspergillus fumigatus* strains has consequences for virulence in a strain- and host-dependent manner. Frontiers in Microbiology. PMID: 31105662; PMCID: PMC6492530; DOI: 10.3389/fmicb.2019.00854
  - (8) Mead M.E., S.L. Knowles, H.A. Raja, S.R. Beattie, C.H. Kowalski, **J.L. Steenwyk**, L.P. Silva, J. Chiaratto, L.N.A. Ries, G.G. Goldman, R.A. Cramer, N.H. Oberlies, & A. Rokas (2019). Characterizing the pathogenic, genomic, and chemical traits of *Aspergillus fischeri*, the closest sequenced relative of the major human fungal pathogen *Aspergillus fumigatus*. mSphere. PMID: 30787113; PMCID: PMC6382966; DOI: 10.1128/mSphere.00018-19
  - (7) Knowles, S.L., H.A. Raja, A.J. Wright, A.M.L. Lee, L.K. Caesar, N.B. Cech, M.E. Mead, **J.L. Steenwyk**, L.N.A. Ries, G.H. Goldman, A. Rokas, & N.H. Oberlies (2019). Mapping the Fungal Battlefield: Using *in situ* Chemistry and Deletion Mutants to Monitor Interspecific Chemical Interactions between Fungi. Frontiers in Microbiology. PMID: 30837981; PMCID: PMC6389630; DOI: 10.3389/fmicb.2019.00285
  - (6) Eidem, H.R., **J.L. Steenwyk**, J. Wisecaver, J.A. Capra, P. Abbot, & A. Rokas (2018). integRATE: a desirability-based data integration framework for the prioritization of candidate genes across heterogeneous ‘omics and its application to preterm birth. BMC Medical Genomics. PMID: 30453955; PMCID: PMC6245874; DOI: 10.1186/s12920-018-0426-y
  - (5) Shen, X.-X.\*, D.A. Oplente\*, J. Kominek\*, X. Zhou\*, **J.L. Steenwyk**, K.V. Buh, M.A.B. Haase, J.H. Wisecaver, M. Wang, D.T. Doering, J.T. Boudouris, R.M. Schneider, Q.K. Langdon, M. Ohkuma, R. Endoh, M. Takashima, R. Manabe, N. Čadež, D. Libkind, C.A. Rosa, J. DeVirgilio, A.B. Hulfachor, M. Groenewald, C.P. Kurtzman<sup>^</sup>, C.T. Hittinger<sup>^</sup> & A. Rokas<sup>^</sup> (2018). \*Equal contributors; <sup>^</sup>Corresponding authors. Tempo and mode of genome evolution in the budding yeast subphylum. Cell. PMID: 30415838; PMCID: PMC6291210; DOI: 10.1016/j.cell.2018.10.023
  - (4) Segal, E.S., V. Gritsenko, A. Levitan, B. Yadav, N. Dror, **J.L. Steenwyk**, Y. Silberberg, K. Mielich, A. Rokas, N.A.R. Gow, R. Kunze, R. Sharan, & J. Berman (2018). Gene Essentiality Analyzed by In Vivo Transposon Mutagenesis and Machine Learning in a Stable Haploid Isolate of *Candida albicans*. mBio. PMID: 30377286; PMCID: PMC6212825; DOI: 10.1128/mBio.02048-18
  - (3) **Steenwyk, J.L.** & A. Rokas (2018). Copy number variation in fungi and its implications for wine yeast genetic diversity and adaptation. Frontiers in Microbiology. PMID: 29520259; PMCID: PMC5826948; DOI: 10.3389/fmicb.2018.00288
  - (2) **Steenwyk, J.** & A. Rokas (2017). Extensive Copy number variation in fermentation-related genes among *Saccharomyces cerevisiae* wine strains. G3 Genes|Genomes|Genetics. PMID: 28292787; PMCID: PMC5427499; DOI: 10.1534/g3.117.040105
  - (1) **Steenwyk J.L.**, J.S. Soghigian, J.R. Perfect, & J.G. Gibbons (2016). Copy number variation contributes to cryptic genetic variation in outbreak lineages of *Cryptococcus gattii* from the

North American Pacific Northwest. BMC Genomics. PMID: 27590805; PMCID: PMC5009542; DOI: 10.1186/s12864-016-3044-0