# Jacob L. Steenwyk

Berkeley Science Fellow
Howard Hughes Medical Institute
University of California, Berkeley
jlsteenwyk@berkeley.edu
www.jlsteenwyk.com

## CURRENT POSITIONS

**Since 2022** Postdoctoral Scholar, Laboratory of Dr. Nicole King
Dept. of Molecular & Cell Biology, University of California, Berkeley

**Since 2022** Berkeley Science Fellow
Berkeley Postdoctoral Entrepreneurship Program, University of California, Berkeley

## EDUCATION

**2022** Ph.D., Biological Sciences — **Vanderbilt University**
Advisor: Dr. Antonis Rokas
GPA: 3.97

**2016** M.S., Biochemistry and Molecular Biology — **Clark University**
Advisor: Dr. John G. Gibbons
GPA: 3.98

**2015** B.A., Biochemistry and Molecular Biology — **Clark University**
Advisor: Dr. Denis Larochelle
Cumulative GPA: 3.84; Science GPA: 3.84

## AWARDS

**2022** Graduate Student Excellence Award Finalist, Society for Molecular Biology and Evolution
**2022** Hanna H. Gray Fellows Finalist, Howard Hughes Medical Institute
**2022** Edward Ferguson Jr. Graduate Award, Graduate School, Vanderbilt University
**2022** James F. Crow Early Career Researcher Award Finalist, Genetics Society of America
**2022** Harold M. Weintraub Graduate Student Award, Fred Hutchinson Cancer Research Center
**2021** Sandler Fellows Finalist, University of California, San Francisco
**2021** Honorable mention, Next Generation Faculty Symposium, Stanford.Berkeley.UCSF
**2021** Presentation award, Canadian Fungal Research Network and Great Lakes Mycology Conference
**2021** Graduate Research Excellence Award in Biological Sciences, Vanderbilt University
**2021** Smriti Bardhan Scholarship, Vanderbilt University
**2021** Registration award, Science Talk '21
**2020** Favorite Artist Award, Catalyst: A Virtual Sci-Art Exhibition
**2020** Oral presentation award, SACNAS – The National Diversity in STEM Virtual Conference
**2020** Registration scholarship, SACNAS – The National Diversity in STEM Virtual Conference
**2020** Best Talk Honorable Mention, Canadian Fungal Research Network Meeting
**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
**2019** Graduate student travel grant, Vanderbilt University
**2019** Curb Center Fellow, ArtLab, Vanderbilt University
**2018** *GENETICS* Peer Review Training Program, Genetics Society of America

**2018** Best poster award, Cellular and Molecular Fungal Biology, Gordon Research Seminar
**2018** Best poster award, Cellular and Molecular Fungal Biology, Gordon Research Conference
**2018** Best poster award, Department of Biological Sciences, Vanderbilt University
**2018** T-shirt design contest winner, Department of Biological Sciences, Vanderbilt University
**2017** Graduate student travel grant, Vanderbilt University
**2016** Graduate student council travel awards, Clark University
**2015** Summa cum laude, Clark University
**2014** Bridging the gaps scholar, 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

## TEN HIGHLIGHTED FIRST AUTHOR PUBLICATIONS

### Evolutionary and Comparative Genomics

(1) **Steenwyk, J.L.**, M.A. Phillips, F. Yang, S.S. Date, T. Graham, J. Berman, C.T. Hittinger, & A. Rokas (2022). An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function. ***Science Advances***. DOI: 10.1126/sciadv.abn0105

(2) **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

(3) **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^, & A. Rokas^ (2019). Extensive loss of cell cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. ^Corresponding authors. ***PLOS Biology***. PMID: 31112549; PMCID: PMC6528967; DOI: 10.1371/journal.pbio.3000255

(4) **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

(5) **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

### Software Engineering

(1) **Steenwyk, J.L.**^, D.C. Goltz, T.J. Buida III, Y. Li, X.-X. Shen, & A. Rokas^ (2022). OrthoSNAP: a tree splitting and pruning algorithm for retrieving single-copy orthologs from gene family trees. ^Corresponding authors. ***PLOS Biology***. DOI: 10.1371/journal.pbio.3001827

(2) **Steenwyk, J.L.**^, T.J. Buida III, Y. Li, X.-X. Shen, & A. Rokas^ (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

(3) **Steenwyk, J.L.**^, T.J. Buida III, A.L. LaBella, Y. Li, X.-X. Shen, & A. Rokas^ (2021). PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data. ^Corresponding authors. ***Bioinformatics***. PMID: 33560364; PMCID: PMC8388027; DOI: 10.1093/bioinformatics/btab096

(4) **Steenwyk, J.L.**^, 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^ (2022). BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data. ^Corresponding authors. ***Genetics***. DOI: 10.1093/genetics/iyac079

(5) **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

## FUNDING

| | |
|---|---|
| **Howard Hughes Medical Institute** | Principal investigator, 09/22, The evolution of pathways responsible for genome integrity in early animals and close relatives, Hanna H. Gray Finalist, $10,000 |
| **Howard Hughes Medical Institute** | 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 |
| **National Institutes of Health** | 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) |
| **Ford Foundation Predoctoral Fellow** | 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) |
| **Curb Center ArtLab Fellow** | Principal investigator, 12/18-04/19, Bridging the gap between artist and scientist, ArtLab, Vanderbilt University, $300 |

## SOFTWARE

1) ClipKIT: a multiple sequence alignment-trimming software for accurate phylogenomic inference. Publication PDF; Documentation; Source code

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

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

4) OrthoSNAP: a tree splitting and pruning algorithm for retrieving single-copy orthologs from gene family trees. Publication PDF; Documentation; Source code

5) orthofisher: a broadly applicable tool for automated gene identification and retrieval. Publication

PDF; Documentation; Source code

6) LVBRS: a cloud-based suite of workflows for bulk RNA-seq quality control, analysis, and functional enrichment. Publication PDF; Documentation; Source code

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

8) ggpubfigs: an R package for creating color blind friendly figures with ggplot2. Publication PDF; Documentation & source code

## INVITED TALKS

**2023** Mycological Society of America Annual Meeting
**2022** Biology Department, Loras College
**2022** Yeast Genetics Meeting, Genetics Society of America
**2022** Hanna H. Gray Fellows Finalists Meeting, Howard Hughes Medical Institute
**2022** Molecular mycology meeting, Technion - Israel Institute of Technology
**2022** Evolution, Am. Soc. of Naturalists, Soc. for the Study of Evo., and the Soc. of Sys. Biologists, Cleveland, OH (declined due to scheduling conflict)
**2022** James F. Crow Early Career Researcher Award Finalist, Genetics Society of America
**2022** Department of Biological Sciences, George Washington University
**2022** 31st Fungal Genetics Conference at Asilomar, Pacific Grove, CA
**2021** Artist-in-Residence program, Vanderbilt Institute for Infection, Immunology and Inflammation
**2021** CanFunNet and Great Lakes Mycology Conference
**2021** Sandler Fellows Finalists 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** 30th 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**
**2022-Pres.** Charu Balamurugan
**2019-2022** Qianhui (Olivia) Zheng
**2018-2021** Megan A. Phillips

## 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

**2022** Decoding the Genome, Howard Hughes Medical Institute
**2021** Gilliam Fellows Meeting, Howard Hughes Medical Institute
**2021** Biology of Genomes, Cold Spring Harbor Laboratories
**2021** Science Talk '21, Science Talk
**2020** 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** 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$^{th}$ Fungal Genetics Conference at Asilomar, Pacific Grove, CA
**2019** Asperfest pre-meeting at 30$^{th}$ 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

**2022-Pres.** Nicole King Lab at University of California, Berkeley, and Howard Hughes Medical Institute, Berkeley, CA. Post-doctoral Research. The evolution of animal genome function.

**2016-2022** 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
**2022** Panelist at the Diversity, Equity, and Inclusion Discussion, Yeast Genetics Conference, Genetics Society of America
**2022** Scientist-Artist: Embracing Duality, ArtLab, Vanderbilt University
**2019-2022** Member, Steering Committee, Early Career Leadership Program, Genetics Society of America
**2019-2022** Inclusion Coordinator, The Evolutionary Studies Initiative at Vanderbilt, Vanderbilt University, Nashville, TN
**2019-2022** Graphic Illustrator, The Evolutionary Studies Initiative at Vanderbilt, Vanderbilt University, Nashville, TN
**2017-2022** Educational outreach booth design and execution, MEGA*Microbe*, Nashville, TN
**2017-2022** Member of the Dean of Graduate Student's survey quantitative analysis subgroup, Graduate Diversity and Inclusion Committee, Vanderbilt University, Nashville, TN
**2017-2022** 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, MEGA*Microbe*, 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, 30th 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, MEGA*Microbe*, 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

## SOCIETIES

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

## 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; Fungal Biology and Biotechnology; BMC Genomics; Nature Communications Biology; PLOS One; Molecular Genetics and Genomics;* and others

## 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

## POPULAR SCIENCE ARTICLES

(6) **Steenwyk, J.L.** & K. Giffin. The silver lining of bioinformatics. *Genes to Genomes*. September 12, 2022

(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/Submitted

(6) **Steenwyk, J.L.**, C. Balamurugan, H.A. Raja, C. Goncalves, N. Li, F. Martin, J. Berman, N.H. Oberlies, J.G. Gibbons, G.H. Goldman, D.M. Geiser, D.S. Hibbett, A. Rokas. Phylogenomics reveals extensive misidentification of fungal strains from the genus *Aspergillus*. bioRxiv. DOI: 10.1101/2022.11.22.517304

(5) **Steenwyk, J.L.**, Y. Li, X. Zhou, X.-X. Shen, A. Rokas. Incongruence in the Tree of Life. Submitted, under review at *Nature Reviews Genetics*.

(4) Le, H.G.B.H.^,*, **J.L. Steenwyk***, N. Manske, M. Smolin, A. Abdulali, A. Kamat, R. Kanchana, K. Giffin, A. Andere, K. Workman^. *Equal contributors; ^Corresponding authors. Latch Verified Bulk-RNA Seq toolkit: a cloud-based suite of workflows for bulk RNA-seq quality control, analysis, and functional enrichment. bioRxiv. DOI: 10.1101/2022.11.10.516016

(3) Sierra-Patev, S, B. Min, M. Naranjo-Ortiz, B. Looney, Z. Konkel, J.C. Slot, Y. Sakamoto, **J.L. Steenwyk**, A. Rokas, J. Carro, S. Camarero, P. Ferreira, G. Molpeceres, F.J. Ruiz-Dueñas, A. Serrano, B. Henrissat, E. Drula, K.W. Hughes, J.L. Mata, N.K. Ishikawa, R. Vargas-Isla, S. Ushijima, C.A. Smith, S. Ahrendt, W. Andreopoulos, G. He, K. LaButti, A. Lipzen, V. Ng, R. Riley, L. Sandor, K. Barry, A.T. Martínez, Y. Xiao, J.G. Gibbons, K. Terashima, I.V. Grigoriev, & D. Hibbett (2022). A Global Phylogenomic Analysis of the Shiitake Genus *Lentinula*. Submitted, in revision at *Proceedings of the National Academy of Sciences of the United States of America*.

(2) Zheng, Q., **J.L. Steenwyk**^, & A. Rokas^ (2022). Lack of universal mutational biases in a fungal phylum. ^Corresponding authors. bioRxiv. DOI: 10.1101/2022.03.29.486229

(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

(51) Li, Y.^, H Liu, **J.L. Steenwyk**, A.L. LaBella, M.C. Harrison, M. Groenewald, X. Zhou, X.-X. Shen, T. Zhao, C.T. Hittinger, & A. Rokas^ (2022). ^Corresponding authors. Contrasting modes of macro- and micro-synteny evolution in a eukaryotic subphylum. Current Biology. DOI: 10.1016/j.cub.2022.10.025

(50) **Steenwyk, J.L.**^, D.C. Goltz, T.J. Buida III, Y. Li, X.-X. Shen, & A. Rokas^ (2021). OrthoSNAP: a tree splitting and pruning algorithm for retrieving single-copy orthologs from gene family trees. ^Corresponding authors. PLOS Biology. PMID: 36228036 DOI: 10.1371/journal.pbio.3001827

(49) Brown, A., M.E. Mead, **J.L. Steenwyk**, G.H. Goldman, & A. Rokas (2022). Extensive sequence divergence of non-coding regions between *Aspergillus fumigatus*, a major fungal pathogen of humans, and its relatives. Frontiers in Fungal Biology. DOI:

10.3389/ffunb.2022.802494

(48) Horta, M.A., **J.L. Steenwyk**, M.E. Mead, L.H.B. dos Santos, S. Zhao, J.G. Gibbons, M. Marcet-Houben, T. Gabaldón, A. Rokas^, & G.H. Goldman^ (2022). Examination of genome-wide ortholog variation in clinical and environmental isolates of the fungal pathogen *Aspergillus fumigatus*. ^Corresponding authors. mBio. PMID: 35766381; PMCID: PMC9426589; DOI: 10.1128/mbio.01519-22

(47) **Steenwyk, J.L.**^, 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^ (2022). BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data. ^Corresponding authors. Genetics. PMID: 35536198; DOI: 10.1093/genetics/iyac079

(46) **Steenwyk, J.L.**, M.A. Phillips, F. Yang, S.S. Date, T. Graham, J. Berman, C.T. Hittinger, & A. Rokas (2022). An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function. Science Advances. PMID: 35507651; PMCID: PMC9067921; DOI: 10.1126/sciadv.abn0105

(45) Bradley, N.P.*, K.L. Wahl*, **J.L. Steenwyk**, A. Rokas, & B.F. Eichman (2022). Resistance-guided mining of bacterial genotoxins defines a family of DNA glycosylases. *Equal contributors. mBio. PMID: 35311535; PMCID: PMC9040887; DOI: 10.1128/mbio.03297-21

(44) 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 (2022). Regulation of gliotoxin biosynthesis and protection in *Aspergillus* species. PLOS Genetics. PMID: 35041649; PMCID: PMC8797188; DOI: 10.1371/journal.pgen.1009965

(43) **Steenwyk, J.L.**^ & A. Rokas^ (2021). ggpubfigs: colorblind friendly color palettes and ggplot2 graphic system extensions for publication-quality scientific figures. ^Corresponding authors. Microbiology Resource Announcements. PMID: 34734767; PMCID: PMC8567791; DOI: 10.1128/MRA.00871-21

(42) Phillips, M.A., **J.L. Steenwyk**^, X.-X. Shen, & A. Rokas^ (2021). Examination of gene loss in the DNA mismatch repair pathway and its mutational consequences in a fungal phylum. ^Corresponding authors. Genome Biology and Evolution. PMID: 34554246; PMCID: PMC8597960; 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^, & A. Rokas^ (2021). Examining signatures of natural selection in antifungal resistance genes across *Aspergillus* fungi. ^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. Aimanianda, F. Rodrigues, R. Gonçales, 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^, G.H. Goldman^, A. Rokas^ (2021). Genomic and phenotypic analysis of COVID-19-associated pulmonary aspergillosis isolates of *Aspergillus fumigatus*. ^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.**^, T.J. Buida III, A.L. LaBella, Y. Li, X.-X. Shen, & A. Rokas^ (2020). PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data. ^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^, A. Rokas^ (2020). A genome-scale phylogeny of the kingdom Fungi. ^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.**^, T.J. Buida III, Y. Li, X.-X. Shen, & A. Rokas^ (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. Opulente, 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 fumigatiaffinis*. ^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^, & A. Rokas^ (2019). Extensive loss of cell cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. ^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. Opulente*, 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^, C.T. Hittinger^ & A. Rokas^ (2018). *Equal contributors; ^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