

# Jacob L. Steenwyk

Berkeley Science Fellow & Howard Hughes Medical Institute Awardee of the Life Sciences Research Foundation. Howard Hughes Medical Institute and University of California, Berkeley. jlsteenwyk@berkeley.edu www.jlsteenwyk.com 626-840-7950

#### **ACADEMIC APPOINTMENTS**

Since 2023 Howard Hughes Medical Institute Awardee, Life Sciences Research Foundation

Since 2022 Postdoctoral Associate, Laboratory of Dr. King, University of California, Berkeley

Since 2022 Berkeley Science Fellow, University of California, Berkeley

#### **OTHER POSITIONS**

Since 2024 Scientific Consultant, FutureHouse Inc., San Francisco, CA

2024 - 2025 Bioinformatics Visiting Scholar, MantleBio Inc., San Francisco, CA

2022 - 2023 Scientific Consultant, LatchBio Inc., San Francisco, CA

#### **EDUCATION**

2016 - 2022 Vanderbilt University	Biological Sciences	Ph.D., GPA: 3.97
<b>2015 - 2016</b> Clark University	Biochemistry and Molecular Biology	M.S., GPA: 3.98
<b>2011 - 2015</b> Clark University	Biochemistry and Molecular Biology	B.A., GPA: 3.84

# FIVE HIGHLIGHTED PUBLICATIONS (Trainees and I are in **bold** font.)

- Steenwyk, J.L.<sup>^</sup>, J.T. Loucks, & T.J. Buida III (2025). <sup>^</sup>Corresponding author. <u>ClipKIT in the Browser: Fast Online Trimming of Multiple Sequence Alignments for Phylogenetics</u>. *Nucleic Acids Research*. DOI: 10.1093/nar/gkaf325.
- Steenwyk, J.L., S. Knowles, R.W. Bastos, C. Balamurugan, D. Rinker, M.E. Mead, C.D. Roberts, H.A. Raja, Y. Li, A.C. Colabardini, P.A. de Castro, T.F. dos Reis, D. Canóvas, R.L. Sanchez, K. Lagrou, E. Torrado, F. Rodrigues, N.H. Oberlies, X. Zhou, G.H. Goldman<sup>^</sup>, & A. Rokas<sup>^</sup> (2024). Corresponding authors. Evolutionary origin and population diversity of a cryptic hybrid pathogen. Nature Communications. DOI: 10.1038/s41467-024-52639-1
- 3. **Steenwyk, J.L.**, Y. Li, X. Zhou, X.-X. Shen, & A. Rokas (2023). <u>Incongruence in the phylogenomics era</u>. *Nature Reviews Genetics*. DOI: 10.1038/s41576-023-00620-x
- Steenwyk, J.L.<sup>^</sup>, T.J. Buida III, A.L. LaBella, Y. Li, X.-X. Shen, & A. Rokas<sup>^</sup> (2021). <u>PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data</u>.

   Corresponding authors. *Bioinformatics*. DOI: 10.1093/bioinformatics/btab096
- Steenwyk, J.L.<sup>^</sup>, T.J. Buida III, Y. Li, X.-X. Shen, & A. Rokas<sup>^</sup> (2020). <u>ClipKIT: a multiple sequence alignment-trimming software for accurate phylogenomic inference</u>.
   ^Corresponding authors. *PLOS Biology*. DOI: 10.1371/journal.pbio.3001007

#### **FUNDING**

Life Sciences Principal investigator, Investigating the molecular Research underpinnings of complex traits like multicellularity, \$231,000. Funding provided by the Howard Hughes Medical Institute. 08/23-08/26 Foundation **Howard Hughes** Principal investigator. The evolution of pathways responsible for genome **Medical Institute** integrity in early animals and close relatives, Hanna H. Gray Finalist, \$10,000.09/22 **Howard Hughes** Principal investigator, Examining the loss of diverse DNA repair genes **Medical Institute** and long-term hypermutation in a lineage of budding yeasts, Gilliam Fellowship, Individual Predoctoral Fellowship, \$150,000, 09/19-09/22

National Principal investigator, Examining the loss of diverse DNA repair genes and long-term hypermutation in a lineage of budding yeasts, of Health Ruth L. Kirschstein National Research Service Award, Individual Predoctoral Fellowship (Parent F31), \$88,128 (declined). 08/19-08/22

Ford Foundation Principal investigator, The consequences of aberrant cell cycle and DNA repair processes in budding yeast, Individual Predoctoral

**Fellow** Fellowship, \$72,000 (declined). 08/19-08/22

**Curb Center** Principal investigator, Bridging the gap between artist and scientist, ArtLab, Vanderbilt University, \$300. 12/18-04/19

#### ADDITIONAL AWARDS AND RECOGNITION

Research	Recognition
2025	Next Wave of Faculty in Genomics Symposium, Genomics Institute of the University of California, Santa Cruz
2024	Trailblazers of Tomorrow National Postdoctoral Symposium, The University of Texas at Austin
2024	Englund Emerging Scholar Award, Department of Biological Chemistry, Johns Hopkins Medicine
2023	Honorable mention, Next Generation Faculty Symposium, Stanford Berkeley. UCSF
2022	Graduate Student Excellence Award Finalist, Society for Molecular Biology and Evolution
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	Graduate Research Excellence Award in Biological Sciences, Vanderbilt University
2021	Smriti Bardhan Scholarship, Vanderbilt University
2020	Trainee-of-the-Year, Vanderbilt Institute for Infection, Immunology and Inflammation
2019	Ann Bernard Martin Award for Excellence in Graduate Research, Vanderbilt University

# **Conferences and Professional Development**

**2024** Frequency Bio Cohort 10 Member, Pillar Venture Capital

2023	JXTX + CSHL Genome Informatics Scholarship, Biology of Genomes, Cold Spring Harbor Laboratory
2022	Fifty 50 Community Fellow, Fifty Years Industries, LLC
2022	Edward Ferguson Jr. Graduate Award, Graduate School, Vanderbilt University
2022	
	Honorable mention, Next Generation Faculty Symposium, Stanford.Berkeley.UCSF
2021	Presentation award, Canadian Fungal Research Network and Great Lakes Mycology Conference
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	•
2020	Registration scholarship, SACNAS – The National Diversity in STEM Virtual Conference
2020	Best Talk Honorable Mention, Canadian Fungal Research Network Meeting
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
2010	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
_0.0	University
2017	Graduate student travel grant, Vanderbilt University
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2016	Graduate student council travel awards, 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

#### **Academic Excellence**

2015 Summa cum laude, Clark University2011 Jonas Clark Scholar, Clark University

# **SOFTWARE DEVELOPED**

# Lead developer

- 1) ClipKIT: a multiple sequence alignment-trimming software for accurate phylogenomic inference. <u>Publication PDF</u>; <u>Documentation</u>; <u>Source code</u>
- 2) PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data. <u>Publication PDF</u>; <u>Documentation</u>; <u>Source code</u>
- 3) BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data. <u>Publication PDF</u>; <u>Documentation</u>; <u>Source code</u>
- 4) OrthoHMM: Improved Inference of Ortholog Groups using Hidden Markov Models. <u>Publication PDF</u>; <u>Documentation</u>; <u>Source code</u>
- 5) OrthoSNAP: a tree splitting and pruning algorithm for retrieving single-copy orthologs from gene family trees. <u>Publication PDF</u>; <u>Documentation</u>; <u>Source code</u>

- 6) orthofisher: a broadly applicable tool for automated gene identification and retrieval. Publication PDF; Documentation; Source code
- treehouse: a user-friendly application to obtain subtrees from large phylogenies. 7) Publication PDF; Documentation & source code
- ggpubfigs: an R package for creating colorblind friendly figures with ggplot2. Publication 8) PDF; Documentation & source code

# Supporting developer

- Orthoflow: phylogenomic analysis and diagnostics with one command. Publication PDF; Documentation; Source code.
- 10) Solu a cloud platform for real-time genomic pathogen surveillance. Publication PDF; Platform.
- 11) LVBRS: a cloud-based suite of workflows for bulk RNA-seq quality control, analysis, and functional enrichment. Publication PDF; Documentation; Source code.

INVITED TALKS		
2025	The International Choanoflagellates & Friends Meeting, Institut Pasteur, France	
2025	Next Wave of Faculty in Genomics Symposium, The University of California, Santa	
	Cruz, Genomics Institute	
2025	DNA Sequences as Type, Westerdijk Fungal Biodiversity Institute	
2025	Department of Microbiology and Immunology, The University of California, San	
	Francisco	
2024	Bioinformatics Group, Utrecht University, Netherlands	
2024	Bioinformatics Group, Wageningen University, Netherlands	
2024	Evolutionary Rate Covariation and Related Methods Workshop, Oregon State	
	University and Colorado State University	
2024	Biochemistry, Molecular, and Structural Biology Graduate Program, The University	
	of California, Los Angeles	
2024	Southern California Evolutionary Genetics and Genomics Meeting, Caltech's Center	
	for Evolutionary Science and the University of California's Center for Ecological and	
	Evolutionary Dynamics, Caltech	
2024	Postdoc Research Showcase, Molecular and Cell Biology Department, University of	
	California, Berkeley	
2024	Trailblazers of Tomorrow National Postdoctoral Symposium, The University of	
0004	Texas at Austin	
2024	Englund Emerging Scholar Symposium, Department of Biological Chemistry, Johns	
0004	Hopkins Medicine	
2024	32 <sup>st</sup> Fungal Genetics Conference at Asilomar, Pacific Grove, CA	
2023	Seminar, Stowers Institute	
2023	Innovative Genomics Institute and the Department of Electrical Engineering and	
2022	Computer Sciences, University of California, Berkeley	
2023 2023	CanFunNet, Acadia University Lightening Talk, Southern California Systems Biology Conference, University of	
2023	Southern California	
2023	Departmental Seminar, Plant Pathology and Environmental Microbiology, The	
2023	Pennsylvania State University	
2022	Biology Department, Loras College	
	biology bopartitions, 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	, ,,
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	31 <sup>st</sup> 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 ( <u>Link</u> )
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
2020	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
CONTRI	BUTED TALKS
2023	Plant and Microbial Biology, Postdoc Seminar Series, University of California,
	Berkeley, Berkeley, CA
2021	Students' Mycology Colloquium, Mycological Society of America
2021	Evolution Seminar Series, Vanderbilt University ( <u>Link</u> )
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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 Tackalone Brewing Company, Nashville, TN

Nashville Science Club, Jackalope Brewing Company, Nashville, TN Mycological Society of America, University of Georgia, Athens, GA

2018 2017

2016	Mycological Society of America, University of California Berkeley, Berkeley, CA
2016	Graduate Student Multidisciplinary Conference, Clark University, Worcester, MA

# TRAINEE ADVISING

#### **Graduate Students**

**2023-Pres.** Saelin Bjornson, University of Melbourne (co-advised with Heroen Verbruggen)

### **Undergraduates**

- 2022-2024 Charu Balamurugan, Vanderbilt University (co-advised with Antonis Rokas)
- 2019-2022 Qianhui (Olivia) Zheng, Vanderbilt University (co-advised with Antonis Rokas)
- 2018-2021 Megan A. Phillips, Vanderbilt University (co-advised with Antonis Rokas)

#### **COMPANY ADVISING**

<b>Since 2023</b>	Advisor, ForensisGroup, Inc., Pasadena, CA
2022-2023	Scientific Advisor, WittGen Biotechnologies, CA

2017-2018 Scientific Consultant, Little Harpeth Brewing, Nashville, TN

#### **WORKSHOP TEACHING**

2026	Director, Phylogenomics and Evolutionary Genomics, Český Krumlov, Czech Republic
2024 2024	Instructor, Methods for Biological Data Workshop, University of Wisconsin-Madison Instructor, Phylogenomics and Population Genomics: Inference and Applications, University of Barcelona, Barcelona, Spain
2024	Lead instructor, Workshop on Phylogenomics, Evolution and Genomics, Český Krumlov, Czech Republic
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**

2	2025	Guest lecture, Evolution of Genomes, Cells, and Development, University of
		California, Berkeley, Berkeley, CA
2	2020	Guest lecture, Science Communication Tools and Techniques, Vanderbilt
		University, Nashville, TN
2	2017-2019	Teaching Assistant, Introductory Biology Lab, Vanderbilt University, Nashville, TN
2	2016	Teaching Assistant, Introduction to Biostatistics, Clark University, Worcester, MA
2	2014-2015	Teaching Assistant, Cell Biology, Clark University, Worcester, MA

#### **POSTER PRESENTATIONS**

2024	Life Sciences Research Foundation Fellows Annual Meeting, Boston, MA
2024	Life Sciences Research Foundation Fellows Annual Meeting, Chicago, IL
2023	Genome Informatics, Cold Spring Harbor Laboratory
2023	The International Choanoflagellates & Friends Meeting, The University of California,
	Berkeley and San Francisco

2022 2021 2021 2021	Decoding the Genome, Howard Hughes Medical Institute Gilliam Fellows Meeting, Howard Hughes Medical Institute Biology of Genomes, Cold Spring Harbor Laboratories Science Talk '21, Science Talk
2020 2020	Gilliam Fellows Meeting, Howard Hughes Medical Institute 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 <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
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SERVICE	
Service to Profession	
2025-Pres Mentor Life Sciences Research Foundation	

- **2025-Pres.** Mentor, Life Sciences Research Foundation
- **2025-Pres.** Member, Special Purpose Committee, International Mycological Congress
- 2024-Pres. Member, Conferences Committee, Genetics Society of America
- **2023-Pres.** Chair of Alumni Affairs, The Evolutionary Studies Initiative at Vanderbilt, Vanderbilt University, Nashville, TN
- 2020-Pres. Founder and Chief Officer, SciArt with Purpose, https://jlsteenwyk.com/sciart.html
- **2023-2025** Mentor, Alumni Mentorship Program Early Career Mentorship Program, Genetics Society of America
- **2023-2024** Chair, TAGC Undergraduate Travel Award Subcommittee, Genetics Society of America
- **2023-2024** Representative for Early Career Scientists, Allied Program Committee, The Allied Genetics Conference 2024, Genetics Society of America
- 2022 Panelist at the Diversity, Equity, and Inclusion Discussion, Yeast Genetics Conference, Genetics Society of America
- 2017-2022 Educational outreach booth design and execution, MEGAMicrobe, 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
- **2020** Panelist at the Communication and Outreach Workshop, The Allied Genetics Conference, Genetics Society of America
- **2019** Peer review workshop leader, 30<sup>th</sup> Fungal Genetics Conference at Asilomar, Pacific Grove, CA

- **2017** Vanderbilt Student Volunteers for Science, Volunteer Science Teacher, West End Middle School, Nashville, TN
- 2014-2015 Science Education Outreach Blogger, C-DEBI Sci-Curious Blog

#### Service to Institution

- 2023-2025 Project Partner, Data Science Discovery Program, University of California, Berkeley
- **2023-2024** Executive Board Member, Berkeley Postdoctoral Entrepreneurship Program, University of California, Berkeley
- 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** Member of the Dean of Graduate Student's survey quantitative analysis subgroup, Graduate Diversity and Inclusion Committee, Vanderbilt University, Nashville, TN
- **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
- **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
- **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
- **2014-2015** Director, Clark University Emergency Medical Services, Clark University, Worcester, MA
- **2014-2015** Subcommittee for Department of Chemistry, Biochemistry and Molecular Biology Faculty Search Committee, Clark University, Worcester, MA
- 2013-2014 Secretary, Clark University Emergency Medical Services, Clark University, Worcester, MA

#### **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 Methods; Nature Communications; Proceedings of the National Academy of Sciences, Molecular Biology and Evolution; Systematic Biology; Current Biology; PLOS Pathogens; GigaScience; Methods in Ecology and Evolution; Genome Biology and Evolution; Genetics; G3 Genes|Genomes|Genetics; FEMS Yeast Research; and others

#### **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

#### **SCI-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

### PUBLICATIONS (Trainees and I are in **bold** font.) Google Scholar Profile

# First-Author or Corresponding Author Peer Review Published

- 31. **Steenwyk, J.L.**^, J.T. Loucks, & T.J. Buida III (2025). ^Corresponding author. <u>ClipKIT in the Browser: Fast Online Trimming of Multiple Sequence Alignments for Phylogenetics</u>. *Nucleic Acids Research*. DOI: 10.1093/nar/gkaf325.
- 30. **Steenwyk, J.L.**, S. Knowles, R.W. Bastos, **C. Balamurugan**, D. Rinker, M.E. Mead, C.D. Roberts, H.A. Raja, Y. Li, A.C. Colabardini, P.A. de Castro, T.F. dos Reis, D. Canóvas, R.L. Sanchez, K. Lagrou, E. Torrado, F. Rodrigues, N.H. Oberlies, X. Zhou, G.H. Goldman^, & A. Rokas^ (2024). ^Corresponding authors. <u>Evolutionary origin and population diversity of a cryptic hybrid pathogen</u>. *Nature Communications*. DOI: 10.1038/s41467-024-52639-1.
- 29. **Bjornson, S.**, H. Verbruggen, N. Upham^, & **J.L. Steenwyk**^ (2024). ^Corresponding authors. <u>Reticulate Evolution</u>: <u>Detection and Utility in the Phylogenomics Era</u>. *Molecular Phylogenetics and Evolution*. DOI: 10.1016/j.ympev.2024.108197.

- 28. **Steenwyk, J.L.**, G.I. Martínez-Redondo, T.J. Buida III, E. Gluck-Thaler, X.-X. Shen, T. Gabaldón, A. Rokas, & R. Fernández (2024). <u>PhyKIT: A Multitool for Phylogenomics</u>. *Current Protocols*. DOI: 10.1002/cpz1.70016.
- 27. **Steenwyk**, J.L. (2024). <u>The discovery of a new lifespan-extending gene in insects</u>. *Crop Health*. DOI: 10.1007/s44297-024-00032-1.
- 26. **Steenwyk**, **J.L.** & N. King (2024). <u>The Promise and Pitfalls of Synteny in Phylogenomics</u>. *PLOS Biology*. DOI: 10.1371/journal.pbio.3002632.
- 25. **Balamurugan, C., J.L. Steenwyk**^, G.H. Goldman, & A. Rokas^ (2024). ^Corresponding authors. <u>The evolution of the gliotoxin biosynthetic gene cluster in *Penicillium* fungi</u>. **G3 Genes|Genomes|Genetics**. DOI: 10.1093/g3journal/jkae063
- 24. **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 (2024). <a href="https://example.com/Phylogenomics reveals extensive misidentification of fungal strains from the genus">https://example.com/Phylogenomics reveals extensive misidentification of fungal strains from the genus | Aspergillus</a>. <a href="https://example.com/Phylogenomics reveals extensive misidentification of fungal strains from the genus | Aspergillus</a>. <a href="https://example.com/Phylogenomics reveals extensive misidentification of fungal strains from the genus | Aspergillus</a>. <a href="https://example.com/Phylogenomics reveals extensive misidentification of fungal strains from the genus | Aspergillus</a>. <a href="https://example.com/Phylogenomics reveals extensive misidentification of fungal strains from the genus | Aspergillus</a>. <a href="https://example.com/Phylogenomics reveals extensive misidentification of fungal strains from the genus | Aspergillus</a>. <a href="https://example.com/Phylogenomics reveals extensive misidentification of fungal strains from the genus | Aspergillus</a>. <a href="https://example.com/Phylogenomics reveals extensive misidentification of fungal strains from the genus | Phylogenomics reveals extensive misidentification of fungal strains from the genus | Phylogenomics reveals | Phylogenomics revea
- 23. **Steenwyk, J.L.**^, A. Rokas, & G.H. Goldman (2023). ^Corresponding author. <u>Know the enemy and know yourself: addressing cryptic fungal pathogens and beyond</u>. *PLOS Pathogens*. DOI: 10.1371/journal.ppat.1011704
- 22. **Steenwyk, J.L.**, Y. Li, X. Zhou, X.-X. Shen, & A. Rokas (2023). <u>Incongruence in the phylogenomics era</u>. *Nature Reviews Genetics*. DOI: 10.1038/s41576-023-00620-x.
- 21. **Steenwyk**, **J.L.**^ & A. Rokas^ (2023). <u>The dawn of relaxed phylogenetics</u>. ^Corresponding authors. *PLOS Biology*. DOI: 10.1371/journal.pbio.3001998
- Steenwyk, J.L.<sup>^</sup>, D.C. Goltz, T.J. Buida III, Y. Li, X.-X. Shen, & A. Rokas<sup>^</sup> (2021).
   OrthoSNAP: a tree splitting and pruning algorithm for retrieving single-copy orthologs from gene family trees. <sup>^</sup>Corresponding authors. *PLOS Biology*. DOI: 10.1371/journal.pbio.3001827
- 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> (2022). <u>BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data</u>.
   ^Corresponding authors. *Genetics*. DOI: 10.1093/genetics/iyac079
- Steenwyk, J.L., M.A. Phillips, F. Yang, S.S. Date, T. Graham, J. Berman, C.T. Hittinger, & A. Rokas (2022). <u>An orthologous gene coevolution network provides insight into</u> <u>eukaryotic cellular and genomic structure and function</u>. *Science Advances*. DOI: 10.1126/sciadv.abn0105
- 17. **Steenwyk, J.L.**^ & A. Rokas^ (2021). <u>agpubfigs: colorblind friendly color palettes and agplot2 graphic system extensions for publication-quality scientific figures</u>. \*Corresponding authors. *Microbiology Resource Announcements*. DOI: 10.1128/MRA.00871-21
- 16. 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. DOI: 10.1093/gbe/evab219
- 15. **Steenwyk, J.L.** & A. Rokas (2021). <u>orthofisher: a broadly applicable tool for automated gene identification and retrieval</u>. **G3 Genes|Genomes|Genetics**. DOI: 10.1093/g3journal/jkab250

- 14. Mead, M.E.\*, **J.L. Steenwyk**\*, L.P. Silva, P.A. de Castro, N. Saeed, F. Hillmann, G.H. Goldman, & A. Rokas (2021). <u>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</u>
- 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*. DOI: 10.1128/Spectrum.00010-21
- 12. **Steenwyk**, **J.L.** (2021). Evolutionary divergence in the DNA damage response among fungi. *mBio*. DOI: 10.1128/mBio.03348-20
- Steenwyk, J.L.<sup>^</sup>, T.J. Buida III, A.L. LaBella, Y. Li, X.-X. Shen, & A. Rokas<sup>^</sup> (2020). <u>PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data</u>. <u>^Corresponding authors</u>. Bioinformatics. DOI: 10.1093/bioinformatics/btab096
- 10. **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**. DOI: 10.1002/yea.3518
- Steenwyk, J.L.<sup>^</sup>, T.J. Buida III, Y. Li, X.-X. Shen, & A. Rokas<sup>^</sup> (2020). <u>ClipKIT: a multiple sequence alignment-trimming software for accurate phylogenomic inference</u>.
   ^Corresponding authors. *PLOS Biology*. DOI: 10.1371/journal.pbio.3001007
- 8. **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). <u>Biosynthetic gene clusters, secondary metabolite profiles, and cards of virulence in the closest nonpathogenic relatives of Aspergillus fumigatus.</u> \*Equal contributors. *Genetics*. DOI: 10.1534/genetics.120.303549
- 7. **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*. DOI: 10.1016/j.cub.2020.04.071
- 6. **Steenwyk, J.L.** & A. Rokas (2019). <u>treehouse: a user-friendly application to obtain subtrees from large phylogenies</u>. *BMC Research Notes*. DOI: 10.1186/s13104-019-4577-5
- 5. **Steenwyk, J.L.**, X.-X. Shen, A.L. Lind, G.H. Goldman, & A. Rokas (2019). <u>A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera *Aspergillus* and *Penicillium*. *mBio*. DOI: 10.1128/mBio.00925-19</u>
- 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. Corresponding authors. *PLOS Biology*. DOI: 10.1371/journal.pbio.3000255
- 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
- 2. **Steenwyk**, **J.** & A. Rokas (2017). Extensive Copy number variation in fermentation-related

- genes among Saccharomyces cerevisiae wine strains. **G3 Genes|Genomes|Genetics**. DOI: 10.1534/g3.117.040105
- Steenwyk J.L., J.S. Soghigian, J.R. Perfect, & J.G. Gibbons (2016). <u>Copy number</u> variation contributes to cryptic genetic variation in outbreak lineages of *Cryptococcus gattii* from the North American Pacific Northwest. *BMC Genomics*. DOI: 10.1186/s12864-016-3044-0

# First-Author or Corresponding Author Preprints/Submitted

- 7. Gonçalves, C.\*, **J.L. Steenwyk**\*, D.C. Rinker, D.A. Opulente, A.L. LaBella, M.-C. Harrison, J.F. Wolters, X. Zhou, X.-X. Shen, S. Covo, M. Groenewald, C.T. Hittinger, & A. Rokas (2025). \*Equal co-first authors. <u>Stable hypermutators revealed by the genomic landscape</u> of DNA repair genes among yeast species. *bioRxiv*. DOI: 10.1101/2025.03.15.643480
- 6. **Steenwyk**, **J.L.**^ & T.J. Buida III (2025). ^Corresponding author. <u>RCVT: a novel diagnostic to quantify compositional biases among taxa for phylogenomics</u>. *bioRxiv*. DOI: 10.1101/2024.11.28.625917.
- 5. **Steenwyk, J.L.**^ & N. King^ (2025). ^Corresponding authors. <u>Integrative phylogenomics positions sponges at the root of the animal tree</u>. *Submitted*.
- 4. **Steenwyk, J.L.**^, T.J. Buida III, A. Rokas, & N. King (2024). ^Corresponding author. OrthoHMM: Improved Inference of Ortholog Groups using Hidden Markov Models. **bioRxiv.** DOI: 10.1101/2024.12.07.627370.
- 3. Turnbull, R.\*, **J.L. Steenwyk**\*, S. Mutch, P. Scholten, V.W. Salazar, J.L. Birch, & H. Verbruggen (2023). \*Equal contributors. <u>Orthoflow: phylogenomic analysis and diagnostics with one command</u>. *Research Square*. DOI: 10.21203/rs.3.rs-3699210/v1
- 2. Le, H.G.B.H.<sup>^,\*</sup>, **J.L. Steenwyk**\*, N. Manske, M. Smolin, A. Abdulali, A. Kamat, R. Kanchana, K. Giffin, A. Andere, & K. Workman<sup>^</sup> (2022). \*Equal contributors; 
  ^Corresponding authors. <u>Latch Verified Bulk-RNA Seq toolkit: a cloud-based suite of workflows for bulk RNA-seq quality control, analysis, and functional enrichment</u>. **bioRxiv**. DOI: 10.1101/2022.11.10.516016.
- 1. **Zheng, Q.**, **J.L. Steenwyk**^, & A. Rokas^ (2022). <u>Lack of universal mutational biases in a fungal phylum.</u> \*Corresponding authors. *bioRxiv*. DOI: 10.1101/2022.03.29.486229

#### Middle Author Peer Review Published

- 51. Fan, Y., M. Du, W. Zhang, W. Deng, E. Yang, S. Wang, L. Yan, L. Zhang, S. Kang, J.L. Steenwyk, Z. An, X. Liu, & M. Xiang (2025). The Genomes of Nematode-Trapping Fungi Provide Insights into the Origin and Diversification of Fungal Carnivorism. *Molecular Phylogenetics and Evolution*. DOI: 10.1016/j.ympev.2025.108423.
- O. Lemke\*, B.M. Heineike\*, S. Viknander, N. Cohen, J.L. Steenwyk, L. Spranger, F. Li, F. Agostini, C.T. Lee, S.K. Aulakh, J. Nielsen, A. Rokas, J. Berman, A. Zelezniak, T.I. Gossmann, & M. Ralser (2025). \*Equal contributors. <u>The Role of Metabolism in Shaping Enzyme Structures Over 400 Million Years of Evolution</u>. *Nature*. DOI: 10.1038/s41586-025-09205-6.
- 49. Feng, B.\*, Y. Li\*, H. Liu\*, **J.L. Steenwyk**, K.T. David, X. Tian, B. Xu, C. Gonçalves, D.A. Opulente, A.L. LaBella, M.-C. Harrison, J.F. Wolters, S. Shao, Z. Chen, K.J. Fisher, M. Groenewald, C.T. Hittinger, X.-X. Shen, A. Rokas^, X. Zhou^, & Y. Li^ (2025). \*Equal contributors; \*Corresponding authors. Unique trajectory of gene family evolution from

- genomic analysis of nearly all known species in an ancient yeast lineage. *Molecular Systems Biology*. DOI: 10.1038/s44320-025-00118-0
- 48. Delbaje, E., L. Pontes, J. Rhodes, **J.L. Steenwyk**, L. Lu, T.F. dos Reis, A. Rokas & G.H. Goldman (2025). *Aspergillus fumigatus* mitogenomes and their influence on azole-resistant and -susceptible populations. *npj Antimicrobials and Resistance*. DOI: 10.1038/s44259-025-00083-6.
- 47. Li, N., D.M. Geiser, **J.L. Steenwyk**, C. Tsuchida, S. Koike, S. Slinski, & F.N. Martin (2025). A systematic approach for identifying unique genomic sequences for *Fusarium oxysporum* f. sp. *lactucae* race 1 and development of molecular diagnostic tools. *Phytopathology*. DOI: 10.1094/PHYTO-04-24-0142-R.
- 46. Moilanen, T., K. Visuri, J. Lehitenen, I. Ortega-Sanz, **J.L. Steenwyk**, & S. Sihvonen (2025). Solu: a cloud platform for real-time genomic pathogen surveillance. **BMC Bioinformatics**. DOI: 10.1186/s12859-024-06005-z.
- 45. Goncalves, C., M.-C. Harrison, **J.L. Steenwyk**, D.A. Opulente, A.L. LaBella, J.F. Wolters, X. Zhou, X.-X. Shen, M. Groenewald, C.T. Hittinger, & A. Rokas (2024). <u>Diverse signatures of convergent evolution in cacti-associated yeasts</u>. *PLOS Biology*. DOI: 10.1371/journal.pbio.3002832.
- 44. Liu, H., **J.L. Steenwyk**, X. Zhou, D.T. Schultz, K.M. Kocot, X.-X. Shen, A. Rokas^, & Y. Li^ (2024). A taxon-rich and genome-scale phylogeny of Opisthokonta. **PLOS Biology**. DOI: 10.1371/journal.pbio.3002794.
- 43. Pinzan, C.F., C. Valero, P.A. de Castro, J. Luiz da Silva, K. Earle, H. Liu, M.A.C. Horta, O. Kniemeyer, T. Krüger, A. Pschibul, D.N. Cömert, T. Heinekamp, A.A. Brakhage, J.L. Steenwyk, M.E. Mead, N. Hermsdorf, S.G. Filler, N.G. da Rosa-Garzon, E. Delbaje, M.J. Bromley, H. Cabral, C. Diehl, C.B. Angeli, G. Palmisano, A.S. Ibrahim, D.C. Rinker, T.J.C. Sauters, K. Steffen, A. Gumilang, A. Rokas^, S. Gago^, & T.F. dos Reis^, G.H. Goldman^ (2024). ^Corresponding authors. <u>Aspergillus fumigatus conidial surface-associated proteome reveals factors for fungal evasion and host immunity modulation</u>. *Nature Microbiology*. DOI: 10.1038/s41564-024-01782-y
- 42. Zhang, W., Y. Fan, W. Deng, Y. Chen, S. Wang, S. Kang, **J.L. Steenwyk**, M. Xiang, & X. Liu (2024). <u>Characterization of Genome-wide Phylogenetic Conflict Uncovers Evolutionary Modes of Carnivorous Fungi</u>. *mBio*. DOI: 10.1128/mbio.02133-24.
- 41. Brown, A., **J.L. Steenwyk**, & A. Rokas (2024). <u>Genome-wide patterns of non-coding sequence variation in the major fungal pathogen *Aspergillus fumigatus*. **G3 Genes|Genomes|Genetics**. DOI: 10.1093/g3journal/jkae091</u>
- 40. Opulente, D.A.\*, A.L. LaBella\*, M.-C. Harrison\*, J.F. Wolters\*, C. Liu, Y. Li, J. Kominek, J.L. Steenwyk, H.R. Stoneman, J. VanDenAvond, C.R. Miller, Q.K. Langdon, M. Silva, C. Goncalves, E.J. Ubbelohde, Y. Li, K.V. Buh, M. Jarzyna, M.A.B. Haase, C.A. Rosa, N. Cadez, D. Libkind, J.H. DeVirgilio, A.B. Hulfachor, C.P. Kurtzman, J.P. Sampaio, P. Goncalves, X. Zhou, X.-X. Shen, M. Groenewald, A. Rokas^, & C.T. Hittinger^ (2024). \*Equal co-first authors; \*Equal co-second authors; \*Corresponding authors. Genomic factors shape carbon and nitrogen metabolic niche breadth across Saccharomycotina yeasts. Science. DOI: 10.1126/science.adj4503.
- 39. O'Meara, M.^, J. Rapala, C.B. Nichols, C. Alexandre, B. Billmyre, **J.L. Steenwyk**, J.A. Alspaugh, & T. O'Meara^ (2024). ^Corresponding authors. <u>CryptoCEN: A Co-Expression</u>

- Network for *Cryptococcus neoformans* reveals novel proteins involved in DNA damage repair. *PLOS Genetics*. DOI: 10.1371/journal.pgen.1011158
- 38. Haase, M.A.B.^, **J.L. Steenwyk**, & J.D. Boeke (2024). ^Corresponding author. <u>Gene loss and cis-regulatory novelty shaped core histone gene evolution in the apiculate yeast Hanseniaspora uvarum</u>. **Genetics**. DOI: 10.1093/genetics/iyae008
- 37. Wang, J.-T.J., **J.L. Steenwyk**, & R. Brem (2024). <u>Natural trait variation across</u>
  <u>Saccharomycotina species</u>. **FEMS Yeast Research**. DOI: 10.1093/femsyr/foae002
- Yea, R., M. Biango-Daniels, J.L. Steenwyk, A. Rokas, N. Louwa, R. Nardellaa, & B.E. Wolfe (2024). Genomic, transcriptomic, and ecological diversity of *Penicillium* species in the cheese rind microbiome. *Fungal Genetics and Biology*. DOI: 10.1016/j.fgb.2023.103862
- 35. Liu, C., X. Han, **J.L. Steenwyk**, & X.-X. Shen (2023). <u>Temporal transcriptomics provides insight into host-pathogen interactions: a case study of *Didymella pinodella* and disease-resistant and -susceptible pea varieties. *Crop Health*. DOI: 10.1007/s44297-023-00005-w.</u>
- 34. Drewell, R.A., T.C. Cormier, **J.L. Steenwyk**, J. St. Denis, J.F. Tabima, J.M. Dresch, & D.A. Larochelle (2023). <u>The *Dictyostelium discoideum* genome lacks significant DNA methylation and uncovers palindromic sequences as a source of false positives in bisulfite sequencing</u>. *NAR Genomics and Bioinformatics*. DOI: 10.1093/nargab/lqad035.
- 33. Mead, M.E., P.A. de Castro, **J.L. Steenwyk**, J. Gangeux, M. Hoenigl, J. Prattes, R. Rautemaa-Richardson, H. Guegan, C.B. Moore, C. Lass-Flörl, F. Reizine, C. Valero, N. Van Rhijn, M.J. Bromley, A. Rokas, G.H. Goldman, & S. Gago (2023). <u>COVID-19</u>
  <u>Associated Pulmonary Aspergillosis isolates are genomically diverse but similar to each other in their responses to infection-relevant stresses</u>. *mSpectrum*. DOI: 10.1128/spectrum.05128-22.
- 32. 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 (2023). A Global Phylogenomic Analysis of the Shiitake Genus Lentinula. PNAS. DOI: 10.1073/pnas.2214076120.
- 31. 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. <u>Contrasting modes of macro- and micro-synteny evolution in a eukaryotic subphylum</u>. *Current Biology*. DOI: 10.1016/j.cub.2022.10.025
- 30. Brown, A., M.E. Mead, **J.L. Steenwyk**, G.H. Goldman, & A. Rokas (2022). Extensive non-coding sequence divergence between the major human pathogen Aspergillus fumigatus and its relatives. **Frontiers in Fungal Biology**. DOI: 10.3389/ffunb.2022.802494
- 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<sup>^</sup>, & G.H. Goldman<sup>^</sup> (2022). Examination of genome-wide ortholog variation in clinical and environmental isolates of the fungal pathogen Aspergillus fumigatus. <sup>^</sup>Corresponding authors. mBio. DOI: 10.1128/mbio.01519-22

- 28. Bradley, N.P.\*, K.L. Wahl\*, **J.L. Steenwyk**, A. Rokas, & B.F. Eichman (2022). <u>Resistance-guided mining of bacterial genotoxins defines a family of DNA glycosylases</u>. \*Equal contributors. *mBio*. DOI: 10.1128/mbio.03297-21
- 27. 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). <u>Regulation of gliotoxin biosynthesis and protection in *Aspergillus* species. *PLOS Genetics*. DOI: 10.1371/journal.pgen.1009965</u>
- 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). <u>Examining signatures of natural selection in</u> <u>antifungal resistance genes across Aspergillus fungi</u>. <sup>^</sup>Corresponding authors. *Frontiers in Fungal Biology*. DOI: 10.3389/ffunb.2021.723051
- 25. 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). <a href="https://doi.org/10.1012/nmbio.01682-21"><u>Aspergillus fumigatus acetate utilization impacts virulence traits and pathogenicity</u>. *mBio*. DOI: 10.1128/mBio.01682-21</a>
- 24. LaBella, A.L., D. Opulente, **J.L. Steenwyk**, C.T. Hittinger, & A. Rokas (2021). <u>Signatures of optimal codon usage in metabolic genes inform budding yeast ecology</u>. *PLOS Biology*. DOI: 10.1371/journal.pbio.3001185
- 23. Shen, X.-X., **J.L. Steenwyk**, & A. Rokas (2021). <u>Dissecting incongruence between concatenation- and quartet-based approaches in phylogenomic data</u>. **Systematic Biology**. DOI: 10.1093/sysbio/syab011
- 22. 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). <u>A genome-scale phylogeny of the kingdom Fungi</u>. ^Corresponding authors. *Current Biology*. DOI: 10.1016/j.cub.2021.01.074
- 21. Li, Y., K.T. David, X.-X. Shen, **J.L. Steenwyk**, K.M. Halanych, & A. Rokas (2020). <u>Feature Frequency Profile-based phylogenies are inaccurate</u>. *PNAS*. DOI: 10.1073/pnas.2013143117
- 20. 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). <u>Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota</u>. \*Corresponding authors. *Science Advances*. DOI: 10.1126/sciadv.abd0079
- Santos, R.A.C., O. Rivero-Menendez, J.L. Steenwyk, M.E. Mead, G.H. Goldman<sup>^</sup>, A. Alastruey-Izquierdo, & A. Rokas<sup>^</sup> (2020). <u>Draft genome sequences of four Aspergillus section Fumigati clinical strains</u>. <sup>^</sup>Corresponding authors. *Microbiology Resource Announcements*. DOI: 10.1128/MRA.00856-20
- 18. 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*. DOI: 10.1128/mBio.02458-20

- 17. 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). <a href="https://doi.org/10.1008/jhtml.com/html/pat/4008/jhtml/pat/400
- 16. 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*. DOI: 10.1093/gbe/evaa107
- 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<sup>^</sup>, & A. Rokas<sup>^</sup> (2020). Genomic and phenotypic heterogeneity of clinical isolates of the human pathogens Aspergillus fumigatus, Aspergillus lentulus and Aspergillus fumigatiaffinis. <sup>^</sup>Corresponding contributors. Frontiers in Genetics. DOI: 10.3389/fgene.2020.00459
- 14. 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). <u>Functional characterization of clinical isolates of the opportunistic fungal pathogen Aspergillus nidulans</u>. <u>mSphere</u>. DOI: 10.1128/mSphere.00153-20
- 13. Rokas, A., M.E. Mead, **J.L. Steenwyk**, N.H. Oberlies, & G.H. Goldman (2020). <u>Evolving moldy murderers: Aspergillus section Fumigati</u> as a model for studying the repeated evolution of fungal pathogenicity. **PLOS Pathogens**. DOI: 10.1371/journal.ppat.1008315
- Knowles, S.L., M.E. Mead, L.P. Silva, H.A. Raja, J.L. Steenwyk, G.H. Gustavo, A. Rokas, & N.H. Oberlies (2020). <u>Gliotoxin, a known virulence factor in the major human pathogen Aspergillus fumigatus</u>, is also biosynthesized by the non-pathogenic relative *A. fischeri*. mBio. DOI: 10.1128/mBio.03361-19
- 11. Libkind, D., D. Peris, F.A. Cubillos, **J.L. Steenwyk**, D.A. Opulente, Q.K. Langdon, N. Bellora, A. Rokas, & C.T. Hittinger (2020). <u>Into the wild: new yeast genomes from natural environments and new tools for their analysis</u>. *FEMS Yeast Research*. DOI: 10.1093/femsyr/foaa008
- Rokas, A., M.E. Mead, J.L. Steenwyk, H.A. Raja, & N.H., Oberlies (2020). <u>Biosynthetic gene clusters and the evolution of fungal chemodiversity</u>. *Natural Product Reports*. DOI: 10.1039/c9np00045c
- 9. Bodinakku, I., J. Shaffer, A.B. Connors, **J.L. Steenwyk**, E. Kastman, A. Rokas, A. Robbat, B. Wolfe (2019). <u>Rapid phenotypic and metabolomics domestication of wild *Penicillium* molds on cheese. *mBio*. DOI: 10.1128/mBio.02445-19</u>
- 8. Mead, M.E.\*, H.A. Raja\*, **J.L. Steenwyk**, S.L. Knowles, N.H. Oberlies^, & A. Rokas^ (2019). <u>Draft genome sequence of the griseofulvin-producing fungus *Xylaria* <u>flabelliformis strain G536</u>. \*Equal contributors; ^Corresponding authors. *Microbiology Resource Announcements*. DOI: 10.1128/MRA.00890-19</u>
- 7. 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**. DOI: 10.1371/journal.pgen.1008304
- 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). <u>Nutritional heterogeneity among Aspergillus fumigatus strains has consequences for virulence in a strain- and host-dependent manner</u>. Frontiers in Microbiology. DOI: 10.3389/fmicb.2019.00854
- 5. 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**. DOI: 10.1128/mSphere.00018-19
- 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). <u>Mapping</u> the Fungal Battlefield: <u>Using in situ Chemistry and Deletion Mutants to Monitor Interspecific</u> <u>Chemical Interactions between Fungi</u>. *Frontiers in Microbiology*. DOI: 10.3389/fmicb.2019.00285
- 3. 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**. DOI: 10.1186/s12920-018-0426-y
- 2. 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. <u>Tempo and mode of genome evolution in the budding yeast subphylum</u>. *Cell*. DOI: 10.1016/j.cell.2018.10.023
- 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. DOI: 10.1128/mBio.02048-18

# Middle Author Preprints/Submitted

- 5. **Bjornson, S.**, T.T. Bringloe, K. Uthanumallian, R. De Paoli-Iseppi, M. B. Clark, C.M.C. Cremen, R. Hossen, O. McGinley, T. Jalali, J. West, F. Leliaert, R. Wetherbee, O. De Clerck, S. Duchene, **J.L. Steenwyk**, & H. Verbruggen (2025). <u>Stepwise evolutionary transitions in Cladophorales plastid genomes reveals origins of hairpin chromosomes</u>. *Submitted.*
- 4. O'Donnell, S., N. Li, **J.L. Steenwyk**, D. Geiser, F.N. Martin, & E. Gluck-Thaler (2025). PAQman: reference-free ensemble evaluation of long-read eukaryotic genome assemblies. **bioRxiv.** DOI: 10.1101/2025.09.11.675652
- 3. David, K.T., L. Horianopoulos, C. Goncalves, **J.L. Steenwyk**, A. Pontes, P. Goncalves, C.T. Hittinger, M. Pennell, & A. Rokas (2025). <u>Discovery of additional ancient genome duplications in yeasts</u>. **bioRxiv**. DOI: 10.1101/2025.08.31.673279
- 2. Cao, X.\*, C. Liu\*, D. Liu\*, J.L. Steenwyk, X. Zhong, Y. Wang, H. Liu, Y. Wang, Q. Zhang,

- X.-X. Shen, Z. Qu<sup>^</sup>, Yuanning Li<sup>^</sup> (2025). \*Equal co-first authors; ^Corresponding authors. <u>The evolution and function of eukaryote-to-cyanobacteria horizontal gene transfer.</u> **Submitted.**
- 1. Ros-Rocher, N., J. Reyes-Rivera, U. Horo, C. Combredet, Y. Foroughijabbari, B.T. Larson, M.C. Coyle, E.A.T. Houtepen, M.J.A. Vermeij, N. King, **J.L. Steenwyk**, & T. Brunet (2024). Clonal-aggregative multicellularity entrained by salinity in one of the closest relatives of animals. **Submitted.**