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

Jacob L. Steenwyk

PROFESSIONAL POSITIONS

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

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

1. **Steenwyk, J.L.**, Y. Li, X. Zhou, X.-X. Shen, & A. Rokas (2023). Incongruence in the phylogenomics era. ***Nature Reviews Genetics***. DOI: 10.1038/s41576-023-00620-x
2. **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
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***. DOI: 10.1093/bioinformatics/btab096
4. **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***. DOI: 10.1371/journal.pbio.3001007
5. **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

AWARDS

2023	Howard Hughes Medical Institute Awardee, Life Sciences Research Foundation
2022	Fifty 50 Community Fellow, Fifty Years Industries, LLC
2022	Berkeley Science Fellow, Berkeley Postdoctoral Entrepreneurship Program, University of California, Berkeley
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

FUNDING

Life Sciences Research Foundation	Principal investigator, 08/23-08/26, Investigating the molecular underpinnings of complex traits like multicellularity, $231,000. Funding generously provided by the Howard Hughes Medical Institute.
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 investigator, 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	Principal investigator, 08/19-08/22, 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)
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 colorblind friendly figures with ggplot2. Publication PDF; Documentation & source code

INVITED TALKS

2023	Seminar, Stowers Institute
2023	Innovative Genomics Institute and the Department of Electrical Engineering and Computer Sciences, University of California, Berkeley
2023	CanFunNet, Acadia University
2023	Lightening Talk, Southern California Systems Biology Conference, University of Southern California
2023	Departmental Seminar, Plant Pathology and Environmental Microbiology, The Pennsylvania State University
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

2023 Plant and Microbial Biology, Postdoc Seminar Series, University of California, Berkeley, Berkeley, CA
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

TRAINEE ADVISING

Graduate Students

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

Undergraduates

2023-Pres. Nhoelle Rocero (co-advised with Nicole King at University of California, Berkeley)

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

COMPANY ADVISING

Since 2023 Advisor, ForensisGroup, Inc., Pasadena, CA
Since 2022 Scientific Advisor, WittGen Biotechnologies, CA
2022-2023 Scientific Consultant, Latch AI Inc., San Francisco, CA
2017-2018 Scientific Consultant, Little Harpeth Brewing, Nashville, TN

WORKSHOP TEACHING

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

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

2023 The International Choanoflagellates & Friends Workshop
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 30th Fungal Genetics Conference at Asilomar, Pacific Grove, CA
2019 Asperfest pre-meeting at 30th 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

EDUCATION

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

SERVICE

2023-Pres. Project Partner, Data Science Discovery Program, University of California, Berkeley
2023-Pres. Executive Board Member, Berkeley Postdoctoral Entrepreneurship Program, University of California, Berkeley
2023-Pres. Representative for Early Career Scientists, Allied Program Committee, The Allied Genetics Conference 2024
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
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 Vanderbilt Student Volunteers for Science, Volunteer Science Teacher, West End Middle School, 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
2014-2015 Science Education Outreach Blogger, C-DEBI Sci-Curious Blog
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 Communications; Proceedings of the National Academy of Sciences, Molecular Biology and Evolution; Systematic Biology; PLOS Pathogens, Methods in Ecology and Evolution; Genome Biology and Evolution; Genetics; G3 Genes|*Genomes*|*Genetics; FEMS Yeast Research;* 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 (Trainees and I are in **bold** font.)

Preprints/Submitted

15. **Bjornson, S.**, N. Upham, H. Verbruggen, & **J.L. Steenwyk** (2023). Methods for phylogenomic inference, divergence-time calibration, and characterizing reticulate evolution. Preprint. DOI: 10.20944/preprints202309.0905.v1.

14. **Steenwyk, J.L.** & N. King (2023). From Genes to Genomes: Opportunities and Challenges for Synteny-based Phylogenomics. Preprints. DOI: 10.20944/preprints202309.0495.v1.

13. Liu, H.*, **J.L. Steenwyk***, X. Zhou, D.T. Schultz, K.M. Kocot, X.-X. Shen, A. Rokas^, & Y. Li^ (2023). *Equal contributors; ^Corresponding authors. A genome-scale Opisthokonta tree of life: toward phylogenomic resolution of ancient divergences. *Submitted*.

12. Yea, R., M. Biango-Daniels, **J.L. Steenwyk**, A. Rokas, N. Louwa, R. Nardellaa, & B.E. Wolfe (2023). Genomic, transcriptomic, and ecological diversity of *Penicillium* species in the cheese rind microbiome. *Submitted.*

11. Haase, M.A.B.^, **J.L. Steenwyk**, & J.D. Boeke (2023). ^Corresponding author. Gene loss and cis-regulatory novelty shaped core histone gene evolution in the apiculate yeast *Hanseniaspora uvarum*. bioRxiv. DOI: 10.1101/2023.08.28.551515

10. Valero, C.*, Pinzan, C.F.*, P.A. de Castro, N. van Rhijn, K. Earle, H. Liu, M.A.C. Horta, O. Kniemeyer, T. Krüger, A. Pschibul, A.A. Brakhage, **J.L. Steenwyk**, M.E. Mead, A. Rokas, S.G. Filler, H. Cabral, E. Deljabe, M.J. Bromley, G. Palmisano, A.S. Ibrahim, S. Gago^, T.F. dos Reis^ & G.H. Goldman^ (2023). *Equal contributors; ^Corresponding authors. A phylogenetic approach to explore the *Aspergillus fumigatus* conidial surface-associated proteome and its role in pathogenesis. bioRxiv. DOI: 10.1101/2023.08.22.553365v1

9. O'Meara, M.^, J. Rapala, C.B. Nichols, C. Alexandre, B. Billmyre, **J.L. Steenwyk**, J.A. Alspaugh, & T. O'Meara^ (2023). ^Corresponding authors. CryptoCEN: A Co-Expression Network for *Cryptococcus neoformans* reveals novel proteins involved in DNA damage repair. bioRxiv. DOI: 10.1101/2023.08.17.553567.

8. **Steenwyk, J.L.**, A. Rokas, & G.H. Goldman (2023). Know the enemy and know yourself: addressing cryptic fungal pathogens and beyond. *Submitted.*

7. **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^ (2023). ^Corresponding authors. Evolutionary origin, population diversity, and diagnostics for a cryptic hybrid pathogen. bioRxiv. DOI: 10.1101/2023.07.03.547508.

6. Wang, J.-T.J., **J.L. Steenwyk**, & R. Brem (2023). Natural trait variation across Saccharomycotina species. *Submitted.*

5. 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^ (2023). *Equal co-first authors; [#]Equal co-second authors; ^Corresponding authors. Genomic and ecological factors shaping specialism and generalism across an entire subphylum. bioRxiv. DOI: 10.1101/2023.06.19.545611.

4. **Balamurugan, C.**, **J.L. Steenwyk**^, G.H. Goldman, & A. Rokas^ (2023). ^Corresponding authors. The evolution of the gliotoxin biosynthetic gene cluster in *Penicillium* fungi. bioRxiv. DOI: 10.1101/2023.01.17.524442.

3. **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 (2022). Phylogenomics reveals extensive misidentification of fungal strains from the genus *Aspergillus*. bioRxiv. DOI: 10.1101/2022.11.22.517304

2. Le, H.G.B.H.^,*, **J.L. Steenwyk***, N. Manske, M. Smolin, A. Abdulali, A. Kamat, R. Kanchana, K. Giffin, A. Andere, & K. Workman^ (2022). *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

1. **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

Peer Review Published

57. Liu, C., X. Han, **J.L. Steenwyk**, & X.-X. Shen (2023). 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.

56. **Steenwyk, J.L.**, Y. Li, X. Zhou, X.-X. Shen, & A. Rokas (2023). Incongruence in the phylogenomics era. Nature Reviews Genetics. DOI: 10.1038/s41576-023-00620-x.

55. Drewell, R.A., T.C. Cormier, **J.L. Steenwyk**, J. St. Denis, J.F. Tabima, J.M. Dresch, & D.A. Larochelle (2023). The *Dictyostelium discoideum* genome lacks significant DNA methylation and uncovers palindromic sequences as a source of false positives in bisulfite sequencing. NAR Genomics and Bioinformatics. DOI: 10.1093/nargab/lqad035.

54. 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). COVID-19 Associated Pulmonary Aspergillosis isolates are genomically diverse but similar to each other in their responses to infection-relevant stresses. mSpectrum. DOI: 10.1128/spectrum.05128-22.

53. 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*. Proceedings of the National Academy of Sciences of the United States of America (PNAS). DOI: 10.1073/pnas.2214076120.

52. **Steenwyk, J.L.**^ & A. Rokas^ (2023). The dawn of relaxed phylogenetics. ^Corresponding authors. PLOS Biology. DOI: 10.1371/journal.pbio.3001998

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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. DOI: 10.1371/journal.pbio.3001185

35. **Steenwyk, J.L.** (2021). Evolutionary divergence in the DNA damage response among fungi. mBio. DOI: 10.1128/mBio.03348-20

34. Shen, X.-X., **J.L. Steenwyk**, & A. Rokas (2021). Dissecting incongruence between concatenation- and quartet-based approaches in phylogenomic data. Systematic Biology. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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. 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

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. DOI: 10.1186/s12864-016-3044-0