



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 2024** Scientific Consultant, FutureHouse Inc., San Francisco, CA
- Since 2024** Bioinformatics Visiting Scholar, MantleBio Inc., San Francisco, CA
- 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
- 2022 – 2023** Scientific Consultant, LatchBio Inc., San Francisco, CA

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

1. **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. Evolutionary origin and population diversity of a cryptic hybrid pathogen. **Nature Communications**. DOI: 10.1038/s41467-024-52639-1
2. **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
3. **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
4. **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
5. **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

AWARDS

- 2024** Frequency Bio Cohort 10 Member, Pillar Venture Capital
- 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** JXTX + CSHL Genome Informatics Scholarship, Biology of Genomes, Cold Spring Harbor Laboratory
- 2023** Honorable mention, Next Generation Faculty Symposium, Stanford.Berkeley.UCSF
- 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 of Health	Principal investigator, 08/19-08/22, Examining the loss of diverse DNA repair genes and long-term hypermutation in a lineage of budding yeasts, Ruth L. Kirschstein National Research Service Award, Individual Predoctoral Fellowship (Parent F31), \$88,128 (declined)
Ford Foundation Predoctoral Fellow	Principal investigator, 08/19-08/22, The consequences of aberrant cell cycle and DNA repair processes in budding yeast, Individual Predoctoral Fellowship, \$72,000 (declined)
Curb Center ArtLab Fellow	Principal investigator, 12/18-04/19, Bridging the gap between artist and scientist, ArtLab, Vanderbilt University, \$300

SOFTWARE

- 1) ClipKIT: a multiple sequence alignment-trimming software for accurate phylogenomic inference. [Publication PDF](#); [Documentation](#); [Source code](#)
- 2) PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data. [Publication PDF](#); [Documentation](#); [Source code](#)
- 3) BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data. [Publication PDF](#); [Documentation](#); [Source code](#)
- 4) OrthoHMM: Improved Inference of Ortholog Groups using Hidden Markov Models. [Publication PDF](#); [Documentation](#); [Source code](#)
- 5) OrthoSNAP: a tree splitting and pruning algorithm for retrieving single-copy orthologs from gene family trees. [Publication PDF](#); [Documentation](#); [Source code](#)
- 6) orthofisher: a broadly applicable tool for automated gene identification and retrieval. [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](#)
- 9) 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

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 Texas at Austin
2024	Englund Emerging Scholar Symposium, Department of Biological Chemistry, Johns Hopkins Medicine
2024	32 st Fungal Genetics Conference at Asilomar, Pacific Grove, CA
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	31 st 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	30 th 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, University of Melbourne (co-advised with Heroen Verbruggen)

Undergraduates

2024-Pres. Veronica L Uy, University of California, Berkeley

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

Since 2023 Advisor, ForensisGroup, Inc., Pasadena, CA

2022-2023 Scientific Advisor, WittGen Biotechnologies, CA

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

WORKSHOP TEACHING

2024	Instructor, Methods for Biological Data Workshop, University of Wisconsin-Madison
2024	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

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

2024	Life Sciences Research Foundation Fellows Annual Meeting, Chicago, IL
2023	Genome Informatics, Cold Spring Harbor Laboratory
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	30 th Fungal Genetics Conference at Asilomar, Pacific Grove, CA
2019	Asperfest pre-meeting at 30 th Fungal Genetics Conference at Asilomar, Pacific Grove, CA
2018	Cellular and Molecular Fungal Biology, Gordon Research Conference, Holderness, NH
2018	Cellular and Molecular Fungal Biology, Gordon Research Seminar, Holderness, NH
2018	Department of Biological Sciences Annual Retreat, Vanderbilt University, Nashville, TN
2015	Bumpus Symposium, Clark University, Worcester, MA
2015	Traina Scholars Presentation, Clark University, Worcester, MA
2015	Summer Research Presentation, Clark University, Worcester, MA

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

SERVICE

- 2024-Pres.** Member, Conferences Committee, Genetics Society of America
- 2024-Pres.** Co-chair, Postdocs Research Showcase, Molecular and Cell Biology, University of California, Berkeley
- 2023-Pres.** Mentor, Alumni Mentorship Program Early Career Mentorship Program, Genetics Society of America
- 2023-Pres.** Project Partner, Data Science Discovery Program, University of California, Berkeley
- 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>
- 2023-2024** Executive Board Member, Berkeley Postdoctoral Entrepreneurship Program, University of California, Berkeley
- 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
- 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, MEGAMicrobe, 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, MEGAMicrobe, Vanderbilt Institute for Infections, Immunology and Inflammation, Nashville, TN
- 2018-2019** Vice President, Inclusivity in Biosciences Association, Vanderbilt University, Nashville, TN
- 2013-2019** Administrator and Owner, Molecular Biology and Biochemistry for Researchers and Students Group, LinkedIn

- 2019** Peer review workshop leader, 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, MEGAMicrobe, Vanderbilt Institute for Infections, Immunology and Inflammation, Nashville, TN
- 2017-2018** Secretary, Graduate Student Association, Department of Biological Sciences, Vanderbilt University, Nashville, TN
- 2017** 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; Current Biology; PLOS Pathogens, GigaScience, 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

11. **Steenwyk, J.L.**[^] & T.J. Buida III (2025). ClipKIT in the Browser: Fast Online Trimming of Multiple Sequence Alignments for Phylogenetics. **Submitted**.
10. **Steenwyk, J.L.**[^], T.J. Buida III, A. Rokas, & N. King (2024). [^]Corresponding authors. OrthoHMM: Improved Inference of Ortholog Groups using Hidden Markov Models. **bioRxiv**. DOI: 10.1101/2024.12.07.627370.
9. **Steenwyk, J.L.**, & T.J. Buida III (2024). RCVT: a novel diagnostic to quantify compositional biases among taxa for phylogenomics. **bioRxiv**. DOI: 10.1101/2024.11.28.625917.
8. 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**.
7. Delbaje, E., L. Pontes, J. Rhodes, **J.L. Steenwyk**, L. Lu, T.F. dos Reis, A. Rokas & G.H. Goldman (2024). *Aspergillus fumigatus* mitogenomes and their influence on azole-resistant and -susceptible populations. **Submitted**.
6. Feng, B.^{*}, Y. Li^{*}, H. Liu^{*}, **J.L. Steenwyk**, K.T. David, X. Tian, B. Xu, C. Gonçalves, D.A. Opolente, 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[^] (2024). ^{*}Equal contributors; [^]Corresponding authors. Unique trajectory of gene family evolution from genomic analysis of nearly all known species in an ancient yeast lineage. **bioRxiv**. DOI: 10.1101/2024.06.05.597512.
5. 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 (2024). ^{*}Equal contributors. The Role of Metabolism in Shaping Enzyme Structures Over 400 Million Years of Evolution. **bioRxiv**. DOI: 10.1101/2024.05.27.596037
4. 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 (2024). The Genomes of Nematode-Trapping Fungi Provide Insights into the Origin and Diversification of Fungal Carnivorism. **bioRxiv**. DOI: 10.1101/2024.03.21.586190.
3. Turnbull, R.^{*}, **J.L. Steenwyk**^{*}, S. Mutch, P. Scholten, V.W. Salazar, J.L. Birch, & H. Verbruggen (2023). ^{*}Equal contributors. Orthoflow: phylogenomic analysis and diagnostics with one command. **Research Square**. DOI: 10.21203/rs.3.rs-3699210/v1
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

77. Moilanen, T., K. Visuri, J. Lehtinen, 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.
76. Li, N., D.M. Geiser, **J.L. Steenwyk**, C. Tsuchida, S. Koike, S. Slinski, & F.N. Martin (2024). 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.
75. **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. Evolutionary origin and population diversity of a cryptic hybrid pathogen. **Nature Communications**. DOI: 10.1038/s41467-024-52639-1.
74. 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). Diverse signatures of convergent evolution in cacti-associated yeasts. **PLOS Biology**. DOI: 10.1371/journal.pbio.3002832.
73. **Bjornson, S.**, H. Verbruggen, N. Upham[^], & **J.L. Steenwyk[^]** (2024). [^]Corresponding authors. Reticulate Evolution: Detection and Utility in the Phylogenomics Era. **Molecular Phylogenetics and Evolution**. DOI: 10.1016/j.ympev.2024.108197.
72. **Steenwyk, J.L.**, G.I. Martínez-Redondo, T.J. Buida III, E. Gluck-Thaler, X.-X. Shen, T. Gabaldón, A. Rokas, & R. Fernández (2024). PhyKIT: A Multitool for Phylogenomics. **Current Protocols**. DOI: 10.1002/cpz1.70016.
71. 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.
70. Pinzan, C.F., C. Valero, P.A. de Castro, J. Luiz da Silva, K. Earle, H. Liu, M.A.C. Horta, O. Knemeyer, 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. *Aspergillus fumigatus* conidial surface-associated proteome reveals factors for fungal evasion and host immunity modulation. **Nature Microbiology**. DOI: 10.1038/s41564-024-01782-y
69. Zhang, W., Y. Fan, W. Deng, Y. Chen, S. Wang, S. Kang, **J.L. Steenwyk**, M. Xiang, & X. Liu (2024). Characterization of Genome-wide Phylogenetic Conflict Uncovers Evolutionary Modes of Carnivorous Fungi. **mBio**. DOI: 10.1128/mbio.02133-24.
68. **Steenwyk, J.L.** (2024). The discovery of a new lifespan-extending gene in insects. **Crop Health**. DOI: 10.1007/s44297-024-00032-1.

67. **Steenwyk, J.L.** & N. King (2024). The Promise and Pitfalls of Synteny in Phylogenomics. ***PLOS Biology***. DOI: 10.1371/journal.pbio.3002632.
66. Brown, A., **J.L. Steenwyk**, & A. Rokas (2024). Genome-wide patterns of non-coding sequence variation in the major fungal pathogen *Aspergillus fumigatus*. ***G3 Genes/Genomes/Genetics***. DOI: 10.1093/g3journal/jkae091
65. 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.
64. **Balamurugan, C.**, **J.L. Steenwyk**^, G.H. Goldman, & A. Rokas^ (2024). ^Corresponding authors. The evolution of the gliotoxin biosynthetic gene cluster in *Penicillium* fungi. ***G3 Genes/Genomes/Genetics***. DOI: 10.1093/g3journal/jkae063
63. **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). Phylogenomics reveals extensive misidentification of fungal strains from the genus *Aspergillus*. ***mSpectrum***. DOI: 10.1128/spectrum.03980-23
62. O'Meara, M.^, J. Rapala, C.B. Nichols, C. Alexandre, B. Billmyre, **J.L. Steenwyk**, J.A. Alspaugh, & T. O'Meara^ (2024). ^Corresponding authors. CryptoCEN: A Co-Expression Network for *Cryptococcus neoformans* reveals novel proteins involved in DNA damage repair. ***PLOS Genetics***. DOI: 10.1371/journal.pgen.1011158
61. Haase, M.A.B.^, **J.L. Steenwyk**, & J.D. Boeke (2024). ^Corresponding author. Gene loss and cis-regulatory novelty shaped core histone gene evolution in the apiculate yeast *Hanseniaspora uvarum*. ***Genetics***. DOI: 10.1093/genetics/iyae008
60. Wang, J.-T.J., **J.L. Steenwyk**, & R. Brem (2024). Natural trait variation across *Saccharomycotina* species. ***FEMS Yeast Research***. DOI: 10.1093/femsyr/foae002
59. 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
58. **Steenwyk, J.L.**^, A. Rokas, & G.H. Goldman (2023). ^Corresponding author. Know the enemy and know yourself: addressing cryptic fungal pathogens and beyond. ***PLOS Pathogens***. DOI: 10.1371/journal.ppat.1011704
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*. **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 non-coding sequence divergence between the major human pathogen *Aspergillus fumigatus* 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. Gonçalves, 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. **PNAS**. 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:

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