



Berkeley Science Fellow & Howard Hughes Medical  
Institute Awardee of the Life Sciences Research  
Foundation. Howard Hughes Medical Institute and  
University of California, Berkeley.  
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# Jacob L. Steenwyk

## PROFESSIONAL POSITIONS

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**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.)

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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.**<sup>^</sup>, T.J. Buida III, A.L. LaBella, Y. Li, X.-X. Shen, & A. Rokas<sup>^</sup> (2021). PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data. <sup>^</sup>Corresponding authors. ***Bioinformatics***. DOI: 10.1093/bioinformatics/btab096
4. **Steenwyk, J.L.**<sup>^</sup>, T.J. Buida III, Y. Li, X.-X. Shen, & A. Rokas<sup>^</sup> (2020). ClipKIT: a multiple sequence alignment-trimming software for accurate phylogenomic inference. <sup>^</sup>Corresponding authors. ***PLOS Biology***. DOI: 10.1371/journal.pbio.3001007
5. **Steenwyk, J.L.**<sup>\*</sup>, A.L. Lind<sup>\*</sup>, 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<sup>^</sup>, A. Rokas<sup>^</sup> (2020). Pathogenic allodiploid hybrids of *Aspergillus* fungi. <sup>\*</sup>Equal contributors; <sup>^</sup>Corresponding authors. ***Current Biology***. DOI: 10.1016/j.cub.2020.04.071

## AWARDS

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| <b>2024</b> | Trailblazers of Tomorrow National Postdoctoral Symposium, The University of Texas at Austin                 |
| <b>2024</b> | Englund Emerging Scholar Award, Department of Biological Chemistry, John Hopkins Medicine                   |
| <b>2023</b> | JXTX + CSHL Genome Informatics Scholarship, Biology of Genomes, Cold Spring Harbor Laboratory               |
| <b>2023</b> | Honorable mention, Next Generation Faculty Symposium, Stanford.Berkeley.UCSF                                |
| <b>2023</b> | Howard Hughes Medical Institute Awardee, Life Sciences Research Foundation                                  |
| <b>2022</b> | Fifty 50 Community Fellow, Fifty Years Industries, LLC  |
| <b>2022</b> | Berkeley Science Fellow, Berkeley Postdoctoral Entrepreneurship Program, University of California, Berkeley |
| <b>2022</b> | Graduate Student Excellence Award Finalist, Society for Molecular Biology and Evolution                     |
| <b>2022</b> | Hanna H. Gray Fellows Finalist, Howard Hughes Medical Institute   |

<b>2022</b>	Edward Ferguson Jr. Graduate Award, Graduate School, Vanderbilt University
<b>2022</b>	James F. Crow Early Career Researcher Award Finalist, Genetics Society of America
<b>2022</b>	Harold M. Weintraub Graduate Student Award, Fred Hutchinson Cancer Research Center
<b>2021</b>	Sandler Fellows Finalist, University of California, San Francisco
<b>2021</b>	Honorable mention, Next Generation Faculty Symposium, Stanford.Berkeley.UCSF
<b>2021</b>	Presentation award, Canadian Fungal Research Network and Great Lakes Mycology Conference
<b>2021</b>	Graduate Research Excellence Award in Biological Sciences, Vanderbilt University
<b>2021</b>	Smriti Bardhan Scholarship, Vanderbilt University
<b>2021</b>	Registration award, Science Talk '21
<b>2020</b>	Favorite Artist Award, Catalyst: A Virtual Sci-Art Exhibition
<b>2020</b>	Oral presentation award, SACNAS – The National Diversity in STEM Virtual Conference
<b>2020</b>	Registration scholarship, SACNAS – The National Diversity in STEM Virtual Conference
<b>2020</b>	Best Talk Honorable Mention, Canadian Fungal Research Network Meeting
<b>2020</b>	Trainee-of-the-Year, Vanderbilt Institute for Infection, Immunology and Inflammation
<b>2019</b>	Gilliam Predoctoral Fellowship, Howard Hughes Medical Institute
<b>2019</b>	Ann Bernard Martin Award for Excellence in Graduate Research, Vanderbilt University
<b>2019</b>	Ruth L. Kirschstein National Research Service Award, National Institutes of Health
<b>2019</b>	Ford Foundation Predoctoral Fellowship, Ford Foundation
<b>2019</b>	Graduate student travel grant, Vanderbilt University
<b>2019</b>	Curb Center Fellow, ArtLab, Vanderbilt University
<b>2018</b>	<i>GENETICS</i> Peer Review Training Program, Genetics Society of America
<b>2018</b>	Best poster award, Cellular and Molecular Fungal Biology, Gordon Research Seminar
<b>2018</b>	Best poster award, Cellular and Molecular Fungal Biology, Gordon Research Conference
<b>2018</b>	Best poster award, Department of Biological Sciences, Vanderbilt University
<b>2018</b>	T-shirt design contest winner, Department of Biological Sciences, Vanderbilt University
<b>2017</b>	Graduate student travel grant, Vanderbilt University
<b>2016</b>	Graduate student council travel awards, Clark University
<b>2015</b>	Summa cum laude, Clark University
<b>2014</b>	Bridging the gaps scholar, University of Southern California Keck School of Medicine
<b>2013</b>	Global environmental microbiology scholar, Center for Dark Energy Biosphere Investigations, University of Southern California
<b>2011</b>	Jonas Clark Scholar, Clark University

## **FUNDING**

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<b>Life Sciences Research Foundation</b>	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.
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<b>Howard Hughes Medical Institute</b>	Principal investigator, 09/22, The evolution of pathways responsible for genome integrity in early animals and close relatives, Hanna H. Gray Finalist, \$10,000
<b>Howard Hughes Medical Institute</b>	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
<b>National Institutes of Health</b>	Principal investigator, 08/19-08/22, Examining the loss of diverse DNA repair genes and long-term hypermutation in a lineage of budding yeasts, Ruth L. Kirschstein National Research Service Award, Individual Predoctoral Fellowship (Parent F31), \$88,128 (declined)
<b>Ford Foundation Predoctoral Fellow</b>	Principal investigator, 08/19-08/22, The consequences of aberrant cell cycle and DNA repair processes in budding yeast, Individual Predoctoral Fellowship, \$72,000 (declined)
<b>Curb Center ArtLab Fellow</b>	Principal investigator, 12/18-04/19, Bridging the gap between artist and scientist, ArtLab, Vanderbilt University, \$300

## SOFTWARE

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- 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

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<b>2024</b>	Department of Computer Science, The University of Maryland
<b>2024</b>	Trailblazers of Tomorrow National Postdoctoral Symposium, The University of Texas at Austin
<b>2024</b>	Department of Biological Chemistry, John Hopkins Medicine
<b>2024</b>	32 <sup>st</sup> Fungal Genetics Conference at Asilomar, Pacific Grove, CA
<b>2023</b>	Seminar, Stowers Institute
<b>2023</b>	Innovative Genomics Institute and the Department of Electrical Engineering and Computer Sciences, University of California, Berkeley
<b>2023</b>	CanFunNet, Acadia University

**2023** Lightning 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<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 ([Link](#))  
**2021** Alliance for Diversity in Science and Engineering, Young Researchers Conference  
**2021** Andrew Murray Lab seminar, Harvard University, Cambridge  
**2020** Institute of Insect Sciences, Zhejiang University  
**2020** Evan Eichler Lab seminar, University of Washington, Seattle  
**2020** Genetics Society of America, Early Career Scientist Seminar Series  
**2020** Nicole King Lab seminar, University of California Berkeley  
**2020** The National Diversity in STEM Conference, SACNAS  
**2020** Canadian Fungal Research Network Meeting  
**2020** Trainee-of-the-year talk, Vanderbilt Institute for Infection, Immunology and Inflammation  
**2020** Day of Wond'ry, Vanderbilt University, Nashville, TN  
**2019** Genetics Society of America, Early Career Scientist Seminar Series  
**2019** Gordon Research Conference, Molecular Mechanisms in Evolution, Easton, MA  
**2019** Gordon Research Seminar, Molecular Mechanisms in Evolution, Easton, MA (declined)  
**2019** Focal Point, ArtLab, Vanderbilt University, Nashville, TN  
**2019** 30<sup>th</sup> Fungal Genetics Conference at Asilomar, Pacific Grove, CA  
**2019** Phylogenomics and Evolution Group, North Carolina State University, Raleigh, NC  
**2018** ArtLab Seminar Series, Vanderbilt University, Nashville, TN  
**2015** TedXClarkUniversity, Clark University, Worcester, MA

## CONTRIBUTED TALKS

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**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

<b>2019</b>	Research in Progress Seminar, Vanderbilt University, Nashville, TN
<b>2019</b>	Biological Sciences Annual Retreat, Vanderbilt University, Nashville, TN
<b>2019</b>	Science club at the library, Nashville Public Library, Nashville, TN
<b>2018</b>	Nashville Science Club, Jackalope Brewing Company, Nashville, TN
<b>2017</b>	Mycological Society of America, University of Georgia, Athens, GA
<b>2016</b>	Mycological Society of America, University of California Berkeley, Berkeley, CA
<b>2016</b>	Graduate Student Multidisciplinary Conference, Clark University, Worcester, MA

## TRAINEE ADVISING

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### Graduate Students

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

### Undergraduates

**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

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

**2022-2023** 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

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<b>2024</b>	Lead instructor, Workshop on Phylogenomics, Evolution and Genomics, Český Krumlov, Czech Republic
<b>2019</b>	Organizer and instructor, Values-based leadership, Vanderbilt University, Nashville, TN
<b>2019</b>	Founder and instructor, 'A beginner's guide to making figures in R,' Vanderbilt University, Nashville, TN
<b>2019</b>	Instructor, Workshop on Phylogenomics, Evolution and Genomics, Český Krumlov, Czech Republic
<b>2019</b>	Instructor, Workshop on Genomics, Evolution and Genomics, Český Krumlov, Czech Republic

## TEACHING EXPERIENCE

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**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

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<b>2023</b>	Genome Informatics, Cold Spring Harbor Laboratory
<b>2023</b>	The International Choanoflagellates & Friends Workshop
<b>2022</b>	Decoding the Genome, Howard Hughes Medical Institute
<b>2021</b>	Gilliam Fellows Meeting, Howard Hughes Medical Institute
<b>2021</b>	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<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

## 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.** Founder, Genomely Internship in Genome Sciences Program, Genomely  
**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.** Executive Board Member, Berkeley Postdoctoral Entrepreneurship Program, University of California, Berkeley  
**2023-Pres.** Chair, TAGC Undergraduate Travel Award Subcommittee, Genetics Society of America  
**2023-Pres.** Representative for Early Career Scientists, Allied Program Committee, The Allied Genetics Conference 2024, 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>  
**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, 30<sup>th</sup> Fungal Genetics Conference at Asilomar, Pacific Grove, CA
- 2018-2019** Vice President, Graduate Student Association, Department of Biological Sciences, Vanderbilt University, Nashville, TN
- 2018-2019** Vice co-chair, MEGAMicrobe, Vanderbilt Institute for Infections, Immunology and Inflammation, Nashville, TN
- 2017-2018** Secretary, Graduate Student Association, Department of Biological Sciences, Vanderbilt University, Nashville, TN
- 2017** 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**

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*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**

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*Nature Communications; Proceedings of the National Academy of Sciences, Molecular Biology and Evolution; Systematic 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

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- 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

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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.)

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### Preprints/Submitted

12. Brown, A., **J.L. Steenwyk**, & A. Rokas (2024). Genome-wide patterns of non-coding sequence variation in the major fungal pathogen *Aspergillus fumigatus*. bioRxiv. DOI: 10.1101/2024.01.08.574724.  
11. 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  
10. 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 (2023). Diverse signatures of convergent evolution in cacti-associated yeasts. bioRxiv. DOI: 10.1101/2023.09.14.557833.  
9. **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.  
8. **Steenwyk, J.L.** & N. King (2023). From Genes to Genomes: Opportunities, Challenges,



and a Roadmap for Synteny-based Phylogenomics. Preprints. DOI: 10.20944/preprints202309.0495.v2.

7. 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. bioRxiv. DOI: 10.1101/2023.09.20.556338
6. G.H. Goldman^, 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^ (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
5. **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.
4. 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.
3. **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.
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

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 (2022). 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^ (2023). ^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.<sup>^</sup>, **J.L. Steenwyk**, & J.D. Boeke (2023). <sup>^</sup>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.**<sup>^</sup>, A. Rokas, & G.H. Goldman (2023). <sup>^</sup>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. Hobbett (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.**<sup>^</sup> & A. Rokas<sup>^</sup> (2023). The dawn of relaxed phylogenetics. <sup>^</sup>Corresponding authors. PLOS Biology. DOI: 10.1371/journal.pbio.3001998
51. Li, Y.<sup>^</sup>, 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<sup>^</sup> (2022). <sup>^</sup>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.**<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. ^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. 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. 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