



Jacob L. Steenwyk

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CURRENT POSITIONS

Since 2022 Postdoctoral Scholar, Laboratory of Dr. Nicole King (starting Sept.)
Dept. of Molecular & Cell Biology, University of California, Berkeley

Since 2022 Scientific consultant
Latch AI Inc., San Francisco, California

EDUCATION

2022	Ph.D., Biological Sciences Advisor: Dr. Antonis Rokas GPA: 3.97	Vanderbilt University
2016	M.S., Biochemistry and Molecular Biology Advisor: Dr. John G. Gibbons GPA: 3.98	Clark University
2015	B.A., Biochemistry and Molecular Biology Advisor: Dr. Denis Larochelle Cumulative GPA: 3.84; Science GPA: 3.84	Clark University

AWARDS

2022	Graduate Student Excellence Award Finalist, Society for Molecular Biology and Evolution
2022	Hanna H. Gray Fellows Finalist, Howard Hughes Medical Institute
2022	Edward Ferguson Jr. Graduate Award, Graduate School, Vanderbilt University
2022	James F. Crow Early Career Researcher Award Finalist, Genetics Society of America
2022	Harold M. Weintraub Graduate Student Award, Fred Hutchinson Cancer Research Center
2021	Sandler Fellows Finalist, University of California, San Francisco
2021	Honorable mention, Next Generation Faculty Symposium, Stanford.Berkeley.UCSF
2021	Presentation award, Canadian Fungal Research Network and Great Lakes Mycology Conference
2021	Graduate Research Excellence Award in Biological Sciences, Vanderbilt University
2021	Smriti Bardhan Scholarship, Vanderbilt University
2021	Registration award, Science Talk '21
2020	Favorite Artist Award, Catalyst: A Virtual Sci-Art Exhibition
2020	Oral presentation award, SACNAS – The National Diversity in STEM Virtual Conference
2020	Registration scholarship, SACNAS – The National Diversity in STEM Virtual Conference
2020	Best Talk Honorable Mention, Canadian Fungal Research Network Meeting
2020	Trainee-of-the-Year, Vanderbilt Institute for Infection, Immunology and Inflammation
2019	Gilliam Predoctoral Fellowship, Howard Hughes Medical Institute
2019	Ann Bernard Martin Award for Excellence in Graduate Research, Vanderbilt University
2019	Ruth L. Kirschstein National Research Service Award, National Institutes of Health
2019	Ford Foundation Predoctoral Fellowship, Ford Foundation
2019	Graduate student travel grant, Vanderbilt University

2019	Curb Center Fellow, ArtLab, Vanderbilt University
2018	<i>GENETICS</i> 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	Summer research scholar, Bridging the gaps, University of Southern California Keck School of Medicine
2013	Global environmental microbiology scholar, Center for dark energy biosphere investigations, University of Southern California
2011	Jonas Clark Scholar, Clark University

RESEARCH INTERESTS

- Evolution of technologically and medically significant fungi
- Evolution and function of DNA repair
- Genome and gene evolution
- Phylogenomics and phylogenetics
- Software development

TEN HIGHLIGHTED FIRST AUTHOR PUBLICATIONS

- (1) **Steenwyk, J.L.**, M.A. Phillips, F. Yang, S.S. Date, T. Graham, J. Berman, C.T. Hittinger, & A. Rokas (2022). An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function. *Science Advances*. DOI: 10.1126/sciadv.abn0105
- (2) **Steenwyk, J.L.**[^], 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
- (3) **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. *bioRxiv*. DOI: 10.1101/2021.10.30.466607
- (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*. PMID: 33560364; PMCID: PMC8388027; 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*. PMID: 33264284; PMCID: PMC7735675; DOI: 10.1371/journal.pbio.3001007
- (6) **Steenwyk, J.L.**^{*}, A.L. Lind^{*}, L.N.A. Ries, T.F. dos Reis, L.P. Silva, F. Almeida, R.W. Bastos, T.F. de Campos Fraga da Silva, V.L.D. Bonato, A.M. Pessoni, F. Rodrigues, H.A. Raja, S.L. Knowles, N.H. Oberlies, K. Lagrou, G.H. Goldman[^], A. Rokas[^] (2020). Pathogenic allodiploid hybrids of *Aspergillus* fungi. ^{*}Equal contributors; [^]Corresponding authors. *Current Biology*. PMID: 32502407; PMCID: PMC7343619; DOI: 10.1016/j.cub.2020.04.071
- (7) **Steenwyk, J.L.**, M.E. Mead^{*}, S.L. Knowles^{*}, H.A. Raja, C.D. Roberts, O. Bader, J. houbraken,

G.H. Goldman, N.H. Oberlies, & A. Rokas (2020). Biosynthetic gene clusters, secondary metabolite profiles, and cards of virulence in the closest nonpathogenic relatives of *Aspergillus fumigatus*.

*Equal contributors. *Genetics*. PMID: 32817009; PMCID: PMC7536862; DOI:

10.1534/genetics.120.303549

- (8) **Steenwyk, J.L.**, D. Opulente, J. Kominek, X.-X. Shen, X. Zhou, A.L. LaBella, N.P. Bradley, B.F. Eichman, N. Čadež, D. Libkind, J. DeVirgilio, A.B. Hulfachor, C.P. Kurtzman, C.T. Hittinger[^], & A. Rokas[^] (2019). Extensive loss of cell cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. [^]Corresponding authors. *PLOS Biology*. PMID: 31112549; PMCID: PMC6528967; DOI: 10.1371/journal.pbio.3000255
- (9) **Steenwyk, J.L.**, X.-X. Shen, A.L. Lind, G.H. Goldman, & A. Rokas (2019). A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera *Aspergillus* and *Penicillium*. *mBio*. PMID: 31289177; PMCID: PMC6747717; DOI: 10.1128/mBio.00925-19
- (10) **Steenwyk, J.** & A. Rokas (2017). Extensive Copy number variation in fermentation-related genes among *Saccharomyces cerevisiae* wine strains. *G3 Genes/Genomes/Genetics*. PMID: 28292787; PMCID: PMC5427499; DOI: 10.1534/g3.117.040105

FUNDING

Howard Hughes Medical Institute	Principal co-investigator (shared with Antonis Rokas), 09/19-09/22, Examining the loss of diverse DNA repair genes and long-term hypermutation in a lineage of budding yeasts, Gilliam Fellowship, Individual Predoctoral Fellowship, \$150,000
National Institutes of Health	Principal investigator, 08/19-08/22, Examining the loss of diverse DNA repair genes and long-term hypermutation in a lineage of budding yeasts, Ruth L. Kirschstein National Research Service Award, Individual Predoctoral Fellowship (Parent F31), \$88,128 (declined)
Ford Foundation Predoctoral Fellow	Principal investigator, 08/19-08/22, The consequences of aberrant cell cycle and DNA repair processes in budding yeast, Individual Predoctoral Fellowship, \$72,000 (declined)
Curb Center ArtLab Fellow	Principal investigator, 12/18-04/19, Bridging the gap between artist and scientist, ArtLab, Vanderbilt University, \$300

SOFTWARE

ClipKIT: a multiple sequence alignment-trimming software for accurate phylogenomic inference.

[Publication PDF](#); [Documentation](#); [Source code](#)

PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data. [Publication PDF](#);

[Documentation](#); [Source code](#)

BioKIT: a versatile toolkit for processing and analyzing diverse types of sequence data. [Publication PDF](#);

[Documentation](#); [Source code](#)

orthoSNAP: a tree splitting and pruning algorithm for retrieving single-copy orthologs from gene family trees. [Publication PDF](#); [Documentation](#); [Source code](#)

orthofisher: a broadly applicable tool for automated gene identification and retrieval. [Publication PDF](#); [Documentation](#); [Source code](#)

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

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

INVITED TALKS

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

2021	Students' Mycology Colloquium, Mycological Society of America
2020	Evolution Seminar Series, Vanderbilt University (Link)
2019	DNA Damage and Response Journal Club, Vanderbilt University, Nashville, TN
2019	Research in Progress Seminar, Vanderbilt University, Nashville, TN
2019	Biological Sciences Annual Retreat, Vanderbilt University, Nashville, TN
2019	Science club at the library, Nashville Public Library, Nashville, TN
2018	Nashville Science Club, Jackalope Brewing Company, Nashville, TN

2017 Mycological Society of America, University of Georgia, Athens, GA
 2016 Mycological Society of America, University of California Berkeley, Berkeley, CA
 2016 Graduate Student Multidisciplinary Conference, Clark University, Worcester, MA

ADVISING

Undergraduates

2022-Pres. Charu Balamurugan
 2019-2022 Qianhui (Olivia) Zheng
 2018-2021 Megan A. Phillips

WORKSHOP TEACHING

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

TEACHING EXPERIENCE

2020 Guest lecture, Science Communication Tools and Techniques, Vanderbilt University, Nashville, TN
 2017-2019 Teaching Assistant, Introductory Biology Lab, Vanderbilt University, Nashville, TN
 2016 Teaching Assistant, Introduction to Biostatistics, Clark University, Worcester, MA
 2014-2015 Teaching Assistant, Cell Biology, Clark University, Worcester, MA

POSTER PRESENTATIONS

2022 Decoding the Genome, Howard Hughes Medical Institute
 2021 Gilliam Fellows Meeting, Howard Hughes Medical Institute
 2021 Biology of Genomes, Cold Spring Harbor Laboratories
 2021 Science Talk '21, Science Talk
 2020 Gilliam Fellows Meeting, Howard Hughes Medical Institute
 2020 Vanderbilt Institute for Infection, Immunology and Inflammation Annual Symposium, Virtual Conference
 2020 The Allied Genetics Conference, Virtual Conference
 2019 Investigators Science Meeting, Howard Hughes Medical Institute, Bethesda, MD
 2019 Gilliam Fellows Annual Meeting, Howard Hughes Medical Institute, Bethesda, MD
 2019 Molecular Mechanisms in Evolution, Gordon Research Conference, Easton, MA
 2019 Molecular Mechanisms in Evolution, Gordon Research Seminar, Easton, MA
 2019 30th Fungal Genetics Conference at Asilomar, Pacific Grove, CA
 2019 Asperfest pre-meeting at 30th Fungal Genetics Conference at Asilomar, Pacific Grove, CA
 2018 Cellular and Molecular Fungal Biology, Gordon Research Conference, Holderness, NH
 2018 Cellular and Molecular Fungal Biology, Gordon Research Seminar, Holderness, NH
 2018 Department of Biological Sciences Annual Retreat, Vanderbilt University, Nashville, TN
 2015 Bumpus Symposium, Clark University, Worcester, MA
 2015 Traina Scholars Presentation, Clark University, Worcester, MA
 2015 Summer Research Presentation, Clark University, Worcester, MA

RESEARCH EXPERIENCE

- 2022-Pres.** Nicole King Lab at University of California, Berkeley, and Howard Hughes Medical Institute, Berkeley, CA. Post-doctoral Research. Evolution of the metazoan DNA damage response.
- 2016-2022** Antonis Rokas Lab at Vanderbilt University, Nashville, TN. Doctoral Research. Evolution of medically and technologically significant fungi.
- 2015-2016** John Gibbons Lab at Clark University, Worcester, MA. Undergraduate and Master's Research. Copy number variation in the human pathogen, *Cryptococcus gattii*.
- 2015-2016** Robert Drewell Lab at Clark University, Worcester, MA. Undergraduate and Master's Research. Genome-wide methylation patterns in the social amoeba, *Dictyostelium discoideum*.
- 2014** Ite A. Laird-Offringa Lab at University of Southern California, Los Angeles, CA. Bridging the Gaps Summer Scholar. Mapping the autoimmune triggering epitope of *ELAVL4* in small cell lung cancer.
- 2013** John Heidelberg and Eric Webb Labs at University of Southern California, Los Angeles, CA. Global Environmental Microbiology Summer Scholar. Fresh and marine water microbial diversity.

SERVICE

- 2022** Panelist at the Diversity, Equity, and Inclusion Discussion, Yeast Genetics Conference, Genetics Society of America
- 2022** Scientist-Artist: Embracing Duality, ArtLab, Vanderbilt University
- 2020-Pres.** Founder and Chief Officer, SciArt with Purpose, <https://jlsteenwyk.com/sciart.html>
- 2019-Pres.** Member, Steering Committee, Early Career Leadership Program, Genetics Society of America
- 2019-Pres.** Inclusion Coordinator, The Evolutionary Studies Initiative at Vanderbilt, Vanderbilt University, Nashville, TN
- 2019-Pres.** 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
- 2017-2018** Scientific consultant, Little Harpeth Brewing, Nashville, TN
- 2017** Vanderbilt Student Volunteers for Science, Volunteer Science Teacher, West End Middle School, Nashville, TN
- 2014-2015** Undergraduate Subcommittee for Department of Chemistry, Biochemistry and Molecular Biology Faculty Search Committee, Clark University, Worcester, MA
- 2014-2015** Science Education Outreach Blogger, C-DEBI Sci-Curious Blog

SOCIETIES

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

MANUSCRIPT REVIEWER

Nature Communications; Molecular Biology and Evolution; Systematic Biology; Methods in Ecology and Evolution; Genome Biology and Evolution; Genetics; Microbial Genomics; G3 Genes/Genomes/Genetics; FEMS Yeast Research; Fungal Biology and Biotechnology; BMC Genomics; Nature Communications Biology; PLOS One; Molecular Genetics and Genomics; and others

ART SHOWS

- 2021** Science Talk '21, Science Talk
- 2020** Catalyst: A Virtual Sci-Art Exhibition, Michigan State University
- 2020** Day of Wond'ry, Vanderbilt University, Nashville, TN
- 2020** Fire-Exhibition, Kefi Collective at Vanderbilt University, Nashville, TN
- 2019** Biomedical Sciences Winter Show, Vanderbilt University, Nashville, TN
- 2019** Focal point, ArtLab, Vanderbilt University, Nashville, TN
- 2019** Connecting the Dots, ArtLab, Vanderbilt University, Nashville, TN
- 2018** ArtLab opening reception, ArtLab, Vanderbilt University, Nashville, TN
- 2018** The Intersection between Art and Science, ArtLab, Vanderbilt University, Nashville, TN

POPULAR SCIENCE ARTICLES

- (6) **Steenwyk, J.L.** & K. Giffin. The silver lining of bioinformatics. *Genes to Genomes*. September 12, 2022
- (5) Simopoulos, M.A.C., A.F. Cisneros, A.D. Mendoza, C. Bautista, **J.L. Steenwyk**, N. Ahmad. Hurdles and advances to making science gender-neutral, *ecrLife*. November 26, 2020
- (4) Mendoza, A.D., C. Bautista, E.A. Marnik, C.M.A. Simopoulos, & **J.L. Steenwyk**. Navigating fake news as a scientist, *ecrLife*. October 8, 2020
- (3) **Steenwyk, J.L.** & M. Jonika. How to get started in science communication, *ecrLife*. August 21, 2020
- (2) **Steenwyk, J.L.** & A. Rokas. A new hybrid fungus is found in hospitals and linked to lung disease, *The Conversation*. June 4, 2020
- (1) **Steenwyk, J.L.** & A. Rokas. An outlaw yeast thrives with genetic chaos – and could provide

PUBLICATIONS

Preprints/Submitted

- (4) Sierra-Patev, Sean, B. Min, M. Naranjo-Ortiz, B. Looney, Z. Konkel, J.C. Slot, Y. Sakamoto, **J.L. Steenwyk**, A. Rokas, J. Carro, S. Camarero, P. Ferreira, G. Molpeceres, F.J. Ruiz-Dueñas, A. Serrano, B. Henrissat, E. Drula, K.W. Hughes, J.L. Mata, N.K. Ishikawa, R. Vargas-Isla, S. Ushijima, C.A. Smith, S. Ahrendt, W. Andreopoulos, G. He, K. LaButti, A. Lipzen, V. Ng, R. Riley, L. Sandor, K. Barry, A.T. Martínez, Y. Xiao, J.G. Gibbons, K. Terashima, I.V. Grigoriev, & D. Hibbett (2022). A Global Phylogenomic Analysis of the Shiitake Genus *Lentinula*. Submitted.
- (3) Li, Y., **J.L. Steenwyk**, A.L. LaBella, M.C. Harrison, M. Groenewald, X. Zhou, X.-X. Shen, T. Zhao, C.T. Hittinger, & A. Rokas (2022). Contrasting modes of macro- and micro-synteny evolution in a eukaryotic subphylum. Submitted.
- (2) Zheng, Q., **J.L. Steenwyk**[^], & A. Rokas[^] (2022). Lack of universal mutational biases in a fungal phylum. [^]Corresponding authors. bioRxiv. DOI: 10.1101/2022.03.29.486229
- (1) **Steenwyk, J.**, J. St. Denis, J. Dresch, D. Larochelle, & R. Drewell (2017). Whole genome bisulfite sequencing reveals a sparse, but robust pattern of DNA methylation in the *Dictyostelium discoideum* genome. bioRxiv. DOI: 10.1101/166033

Peer Review Published

- (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: *in press*.
- (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. PMID: 35536198; DOI: 10.1093/genetics/iyac079
- (46) **Steenwyk, J.L.**, M.A. Phillips, F. Yang, S.S. Date, T. Graham, J. Berman, C.T. Hittinger, & A. Rokas (2022). An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function. Science Advances. PMID: 35507651; DOI: 10.1126/sciadv.abn0105
- (45) Bradley, N.P.* , K.L. Wahl*, **J.L. Steenwyk**, A. Rokas, & B.F. Eichman (2022). Resistance-guided mining of bacterial genotoxins defines a family of DNA glycosylases. *Equal contributors. mBio. PMID: 35311535; PMCID: PMC9040887; DOI: 10.1128/mbio.03297-21

- (44) de Castro, P.A., A. Moraes, A.C. Colabardini, M.A.C. Horta, S.L. Knowles, H.A. Raja, N.H. Oberlies, Y. Koyama, M. Ogawa, K. Gomi, **J.L. Steenwyk**, A. Rokas, L.N.A. Ries, & G.H. Goldman (2022). Regulation of gliotoxin biosynthesis and protection in *Aspergillus* species. PLOS Genetics. PMID: 35041649; PMCID: PMC8797188; DOI: 10.1371/journal.pgen.1009965
- (43) **Steenwyk, J.L.**^ & A. Rokas^ (2021). ggpubfigs: colorblind friendly color palettes and ggplot2 graphic system extensions for publication-quality scientific figures. ^Corresponding authors. Microbiology Resource Announcements. PMID: 34734767; PMCID: PMC8567791; DOI: 10.1128/MRA.00871-21
- (42) Phillips, M.A., **J.L. Steenwyk**^, X.-X. Shen, & A. Rokas^ (2021). Examination of gene loss in the DNA mismatch repair pathway and its mutational consequences in a fungal phylum. ^Corresponding authors. Genome Biology and Evolution. PMID: 34554246; PMCID: PMC8597960; DOI: 10.1093/gbe/evab219
- (41) Santos, R.A.C., M.E. Mead, **J.L. Steenwyk**, O. Rivero-Menéndez, A. Alastruey-Izquierdo, G.H. Goldman^, & A. Rokas^ (2021). Examining signatures of natural selection in antifungal resistance genes across *Aspergillus* fungi. ^Corresponding authors. Frontiers in Fungal Biology. DOI: 10.3389/ffunb.2021.723051
- (40) **Steenwyk, J.L.** & A. Rokas (2021). orthofisher: a broadly applicable tool for automated gene identification and retrieval. G3 Genes|Genomes|Genetics. PMID: 34544141; PMCID: PMC8496211; DOI: 10.1093/g3journal/jkab250
- (39) Ries, L., P. de Castro, L. Silva, C. Valero, T. dos Reis, R. Saborano, I. Duarte, G. Persinoti, **J.L. Steenwyk**, A. Rokas, F. Almeida, J. Costa, T. Fill, S.S.W. Wong, V. Aimanianda, F. Rodrigues, R. Gonçalves, C. Duarte-Oliveira, A. Carvalho, & G.H. Goldman (2021). *Aspergillus fumigatus* acetate utilization impacts virulence traits and pathogenicity. mBio. PMID: 34311583; PMCID: PMC8406206; DOI: 10.1128/mBio.01682-21
- (38) Mead, M.E.*, **J.L. Steenwyk***, L.P. Silva, P.A. de Castro, N. Saeed, F. Hillmann, G.H. Goldman, & A. Rokas (2021). An evolutionary genomic approach reveals both conserved and species-specific genetic elements related to human disease in closely related *Aspergillus* fungi. *Equal contributors. Genetics. PMID: 33944921; PMCID: PMC8225353; DOI: 10.1093/genetics/iyab066
- (37) **Steenwyk, J.L.**, M.E. Mead, P.A. Castro, C. Valero, A. Damasio, R.A.C. Santos, A.L. LaBella, Y. Li, S.L. Knowles, H.A. Raja, N.H. Oberlies, X. Zhou, O.A. Cornely, F. Fuchs, P. Koehler^, G.H. Goldman^, A. Rokas^ (2021). Genomic and phenotypic analysis of COVID-19-associated pulmonary aspergillosis isolates of *Aspergillus fumigatus*. ^Corresponding authors. Microbiology Spectrum. PMID: 34106569; PMCID: PMC7654854; DOI: 10.1128/Spectrum.00010-21
- (36) LaBella, A.L., D. Opulente, **J.L. Steenwyk**, C.T. Hittinger, & A. Rokas (2021). Signatures of optimal codon usage in metabolic genes inform budding yeast ecology. PLOS Biology. PMID: 33872297; PMCID: PMC8084343; DOI: 10.1371/journal.pbio.3001185
- (35) **Steenwyk, J.L.** (2021). Evolutionary divergence in the DNA damage response among fungi. mBio. PMID: 33727357; PMCID: PMC8092291; DOI: 10.1128/mBio.03348-20
- (34) Shen, Xing-Xing, **J.L. Steenwyk**, & A. Rokas (2021). Dissecting incongruence between concatenation- and quartet-based approaches in phylogenomic data. Systematic Biology. PMID: 33616672; DOI: 10.1093/sysbio/syab011

- (33) **Steenwyk, J.L.**[^], T.J. Buida III, A.L. LaBella, Y. Li, X.-X. Shen, & A. Rokas[^] (2020). PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data. [^]Corresponding authors. Bioinformatics. PMID: 33560364; PMCID: PMC8388027; DOI: 10.1093/bioinformatics/btab096
- (32) Li, Y., **J.L. Steenwyk**, Y. Chang, Y. Wang, T.Y. James, J.E. Stajich, J.W. Spatafora, M. Groenewald, C. Dunn, C.T. Hittinger, X.-X. Shen[^], A. Rokas[^] (2020). A genome-scale phylogeny of the kingdom Fungi. [^]Corresponding authors. Current Biology. PMID: 33607033; PMCID: PMC8347878; DOI: 10.1016/j.cub.2021.01.074
- (31) **Steenwyk, J.L.** (2021). A portrait of budding yeasts: A symbol of the arts, sciences and a whole greater than the sum of its parts. Yeast. PMID: 32869892; DOI: 10.1002/yea.3518
- (30) **Steenwyk, J.L.**[^], T.J. Buida III, Y. Li, X.-X. Shen, & A. Rokas[^] (2020). ClipKIT: a multiple sequence alignment-trimming software for accurate phylogenomic inference. [^]Corresponding authors. PLOS Biology. PMID: 33264284; PMCID: PMC7735675; DOI: 10.1371/journal.pbio.3001007
- (29) Li, Y., K.T. David, X.-X. Shen, **J.L. Steenwyk**, K.M. Halanych, & A. Rokas (2020). Feature Frequency Profile-based phylogenies are inaccurate. Proceedings of the National Academy of Sciences of the United States of America. PMID: 33234569; PMCID: PMC7749326; DOI: 10.1073/pnas.2013143117
- (28) Shen, X.-X.[^], **J.L. Steenwyk**, A.L. LaBella, D.A. Ofulente, X. Zhou, J. Kominek, Y. Li, M. Groenewald, C.T. Hittinger, & A. Rokas[^] (2020). Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. [^]Corresponding authors. Science Advances. PMID: 33148650; PMCID: PMC7673691; DOI: 10.1126/sciadv.abd0079
- (27) Santos, R.A.C., O. Rivero-Menendez, **J.L. Steenwyk**, M.E. Mead, G.H. Goldman[^], A. Alastruey-Izquierdo, & A. Rokas[^] (2020). Draft genome sequences of four *Aspergillus* section *Fumigati* clinical strains. [^]Corresponding authors. Microbiology Resource Announcements. PMID: 33004453; PMCID: PMC7530925; DOI: 10.1128/MRA.00856-20
- (26) Filho, A.P.C., G.T.P. Brancini, P.A. de Castro, J.A. Ferreira, L.P. Silva, M.C. Rocha, I. Malavazi, J.G.M. Pontes, T. Fill, R. Silva, F. Almeida, **J.L. Steenwyk**, A. Rokas, T.F. dos Reis, L.N.A. Ries, & G.H. Goldman (2020). *Aspergillus fumigatus* G-protein coupled receptors GprM and GprJ are important for the regulation of the cell wall integrity pathway, secondary metabolite production, and virulence. mBio. PMID: 33051372; PMCID: PMC7554674; DOI: 10.1128/mBio.02458-20
- (25) **Steenwyk, J.L.**, M.E. Mead*, S.L. Knowles*, H.A. Raja, C.D. Roberts, O. Bader, J. houbraken, G.H. Goldman, N.H. Oberlies, & A. Rokas (2020). Biosynthetic gene clusters, secondary metabolite profiles, and cards of virulence in the closest nonpathogenic relatives of *Aspergillus fumigatus*. *Equal contributors. Genetics. PMID: 32817009; PMCID: PMC7536862; DOI: 10.1534/genetics.120.303549
- (24) Ries, L.N.A., L. Pardeshi, Z. Dong, K. Tan, **J.L. Steenwyk**, A.C. Colabardini, J.A.F. Filho, P.A. de Castro, L.P. Silva, N.W. Preite, F. Almeida, L.J. de Assis, R.A.C. dos Santos, P. Bowyer, M. Bromley, R.A. Owens, S. Doyle, M. Demasi, D.C.R. Hernández, L.E.S. Netto, M.T. Pupo, A. Rokas, F.V. Loures, K.H. Wong, & G.H. Goldman (2020). The *Aspergillus fumigatus* transcription factor RglT is important for gliotoxin biosynthesis and self-protection, and virulence. PLOS Pathogens. PMID: 32667960; PMCID: PMC7384679; DOI: 10.1371/journal.ppat.1008645
- (23) **Steenwyk, J.L.***, A.L. Lind*, L.N.A. Ries, T.F. dos Reis, L.P. Silva, F. Almeida, R.W.

Bastos, T.F. de Campos Fraga da Silva, V.L.D. Bonato, A.M. Pessoni, F. Rodrigues, H.A. Raja, S.L. Knowles, N.H. Oberlies, K. Lagrou, G.H. Goldman[^], A. Rokas[^] (2020). Pathogenic allodiploid hybrids of *Aspergillus* fungi. *Equal contributors; [^]Corresponding authors. Current Biology. PMID: 32502407; PMCID: PMC7343619; DOI: 10.1016/j.cub.2020.04.071

- (22) Mead, M.E.*, A.T. Borowsky*, B. Joehnk, **J.L. Steenwyk**, X.-X. Shen, A. Sil, & A. Rokas (2020). Recurrent loss of *abaA*, a master regulator of asexual development in filamentous fungi, correlates with changes in genomic and morphological traits. *Equal contributors. Genome Biology and Evolution. PMID: 32442273; PMCID: PMC7531577; DOI: 10.1093/gbe/evaa107
- (21) Santos, R.A.C., **J.L. Steenwyk**, O. Rivero-Menendez, M.E. Mead, L.P. Silva, R.W. Bastos, A. Alastruey-Izquierdo, G.H. Goldman[^], & A. Rokas[^] (2020). Genomic and phenotypic heterogeneity of clinical isolates of the human pathogens *Aspergillus fumigatus*, *Aspergillus lentulus* and *Aspergillus fumigati*affinis. [^]Corresponding contributors. Frontiers in Genetics. PMID: 32477406; PMCID: PMC7236307; DOI: 10.3389/fgene.2020.00459
- (20) Bastos, R.W., C. Valero, L.P. Silva, T. Schoen, M. Drott, V. Brauer, R. Silva-Rocha, A. Lind, **J.L. Steenwyk**, A. Rokas, F. Rodrigues, A. Resendiz-Sharpe, K. Lagrou, M. Marcet-Houben, T. Gabaldon, E. McDonnell, I. Reid, A. Tsang, B.R. Oakley, F. Loures, F. Almeida, A. Huttenlocher, N.P. Keller, L. Ries, G.H. Goldman (2020). Functional characterization of clinical isolates of the opportunistic fungal pathogen *Aspergillus nidulans*. mSphere. PMID: 32269156; PMCID: PMC7142298; DOI: 10.1128/mSphere.00153-20
- (19) Rokas, A., M.E. Mead, **J.L. Steenwyk**, N.H. Oberlies, & G.H. Goldman (2020). Evolving moldy murderers: *Aspergillus* section *Fumigati* as a model for studying the repeated evolution of fungal pathogenicity. PLOS Pathogens. PMID: 32106242; PMCID: PMC7046185; DOI: 10.1371/journal.ppat.1008315
- (18) Knowles, S.L., M.E. Mead, L.P. Silva, H.A. Raja, **J.L. Steenwyk**, G.H. Gustavo, A. Rokas, & N.H. Oberlies (2020). Gliotoxin, a known virulence factor in the major human pathogen *Aspergillus fumigatus*, is also biosynthesized by the non-pathogenic relative *A. fischeri*. mBio. PMID: 32047138; PMCID: PMC7018655; DOI: 10.1128/mBio.03361-19
- (17) Libkind, D., D. Peris, F.A. Cubillos, **J.L. Steenwyk**, D.A. Opulente, Q.K. Langdon, N. Bellora, A. Rokas, & C.T. Hittinger (2020). Into the wild: new yeast genomes from natural environments and new tools for their analysis. FEMS Yeast Research. PMID: 32009143; PMCID: PMC7067299; DOI: 10.1093/femsyr/foaa008
- (16) Rokas, A., M.E. Mead, **J.L. Steenwyk**, H.A. Raja, & N.H., Oberlies (2020). Biosynthetic gene clusters and the evolution of fungal chemodiversity. Natural Product Reports. PMID: 31898704; PMCID: PMC7332410; DOI: 10.1039/c9np00045c
- (15) Bodinakku, I., J. Shaffer, A.B. Connors, **J.L. Steenwyk**, E. Kastman, A. Rokas, A. Robbat, B. Wolfe (2019). Rapid phenotypic and metabolomics domestication of wild *Penicillium* molds on cheese. mBio. PMID: 31615965; PMCID: PMC6794487; DOI: 10.1128/mBio.02445-19
- (14) Mead, M.E.*, H.A. Raja*, **J.L. Steenwyk**, S.L. Knowles, N.H. Oberlies[^], & A. Rokas[^] (2019). Draft genome sequence of the griseofulvin-producing fungus *Xylaria flabelliformis* strain G536. *Equal contributors; [^]Corresponding authors. Microbiology Resource Announcements. PMID: 31537670; PMCID: PMC6753274; DOI: 10.1128/MRA.00890-19

- (13) **Steenwyk, J.L.** & A. Rokas (2019). treehouse: a user-friendly application to obtain subtrees from large phylogenies. BMC Research Notes. PMID: 31455362; PMCID: PMC6712805; DOI: 10.1186/s13104-019-4577-5
- (12) Labella, A.L., D.A. Ofulente, **J.L. Steenwyk**, C.T. Hittinger, & A. Rokas (2019). Variation and selection on codon usage bias across an entire subphylum. PLOS Genetics. PMID: 31365533; PMCID: PMC6701816; DOI: 10.1371/journal.pgen.1008304
- (11) **Steenwyk, J.L.**, X.-X. Shen, A.L. Lind, G.H. Goldman, & A. Rokas (2019). A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera *Aspergillus* and *Penicillium*. mBio. PMID: 31289177; PMCID: PMC6747717; DOI: 10.1128/mBio.00925-19
- (10) **Steenwyk, J.L.**, D. Ofulente, J. Kominek, X.-X. Shen, X. Zhou, A.L. LaBella, N.P. Bradley, B.F. Eichman, N. Čadež, D. Libkind, J. DeVirgilio, A.B. Hulfachor, C.P. Kurtzman, C.T. Hittinger[^], & A. Rokas[^] (2019). Extensive loss of cell cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. [^]Corresponding authors. PLOS Biology. PMID: 31112549; PMCID: PMC6528967; DOI: 10.1371/journal.pbio.3000255
- (9) Ries, L.N.A., **J.L. Steenwyk**, P.A. de Castro, P.B.A. de Lima, F. Almeida, L.J. de Assis, A.O. Manfiolli, A. Takahashi-Nakaguchi, Y. Kusuya, D. Hagiwara, H. Takahashi, X. Wang, J. Obar, A. Rokas, & G.H. Goldman (2019). Nutritional heterogeneity among *Aspergillus fumigatus* strains has consequences for virulence in a strain- and host-dependent manner. Frontiers in Microbiology. PMID: 31105662; PMCID: PMC6492530; DOI: 10.3389/fmicb.2019.00854
- (8) Mead M.E., S.L. Knowles, H.A. Raja, S.R. Beattie, C.H. Kowalski, **J.L. Steenwyk**, L.P. Silva, J. Chiaratto, L.N.A. Ries, G.G. Goldman, R.A. Cramer, N.H. Oberlies, & A. Rokas (2019). Characterizing the pathogenic, genomic, and chemical traits of *Aspergillus fischeri*, the closest sequenced relative of the major human fungal pathogen *Aspergillus fumigatus*. mSphere. PMID: 30787113; PMCID: PMC6382966; DOI: 10.1128/mSphere.00018-19
- (7) Knowles, S.L., H.A. Raja, A.J. Wright, A.M.L. Lee, L.K. Caesar, N.B. Cech, M.E. Mead, **J.L. Steenwyk**, L.N.A. Ries, G.H. Goldman, A. Rokas, & N.H. Oberlies (2019). Mapping the Fungal Battlefield: Using *in situ* Chemistry and Deletion Mutants to Monitor Interspecific Chemical Interactions between Fungi. Frontiers in Microbiology. PMID: 30837981; PMCID: PMC6389630; DOI: 10.3389/fmicb.2019.00285
- (6) Eidem, H.R., **J.L. Steenwyk**, J. Wisecaver, J.A. Capra, P. Abbot, & A. Rokas (2018). integRATE: a desirability-based data integration framework for the prioritization of candidate genes across heterogeneous 'omics and its application to preterm birth. BMC Medical Genomics. PMID: 30453955; PMCID: PMC6245874; DOI: 10.1186/s12920-018-0426-y
- (5) Shen, X.-X.* , D.A. Ofulente*, J. Kominek*, X. Zhou*, **J.L. Steenwyk**, K.V. Buh, M.A.B. Haase, J.H. Wisecaver, M. Wang, D.T. Doering, J.T. Boudouris, R.M. Schneider, Q.K. Langdon, M. Ohkuma, R. Endoh, M. Takashima, R. Manabe, N. Čadež, D. Libkind, C.A. Rosa, J. DeVirgilio, A.B. Hulfachor, M. Groenewald, C.P. Kurtzman[^], C.T. Hittinger[^] & A. Rokas[^] (2018). *Equal contributors; [^]Corresponding authors. Tempo and mode of genome evolution in the budding yeast subphylum. Cell. PMID: 30415838; PMCID: PMC6291210; DOI: 10.1016/j.cell.2018.10.023
- (4) Segal, E.S., V. Gritsenko, A. Levitan, B. Yadav, N. Dror, **J.L. Steenwyk**, Y. Silberberg, K. Mielich, A. Rokas, N.A.R. Gow, R. Kunze, R. Sharan, & J. Berman (2018). Gene

Essentiality Analyzed by In Vivo Transposon Mutagenesis and Machine Learning in a Stable Haploid Isolate of *Candida albicans*. mBio. PMID: 30377286; PMCID: PMC6212825; DOI: 10.1128/mBio.02048-18

- (3) **Steenwyk, J.L.** & A. Rokas (2018). Copy number variation in fungi and its implications for wine yeast genetic diversity and adaptation. *Frontiers in Microbiology*. PMID: 29520259; PMCID: PMC5826948; DOI: 10.3389/fmicb.2018.00288
- (2) **Steenwyk, J.** & A. Rokas (2017). Extensive Copy number variation in fermentation-related genes among *Saccharomyces cerevisiae* wine strains. *G3 Genes|Genomes|Genetics*. PMID: 28292787; PMCID: PMC5427499; DOI: 10.1534/g3.117.040105
- (1) **Steenwyk J.L.,** J.S. Soghigian, J.R. Perfect, & J.G. Gibbons (2016). Copy number variation contributes to cryptic genetic variation in outbreak lineages of *Cryptococcus gattii* from the North American Pacific Northwest. *BMC Genomics*. PMID: 27590805; PMCID: PMC5009542; DOI: 10.1186/s12864-016-3044-0