

ANTONIS ROKAS, Ph.D. – Brief Curriculum Vitae

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BRIEF BIOGRAPHY:

I am the holder of the Cornelius Vanderbilt Chair in Biological Sciences and Professor in the Departments of Biological Sciences and of Biomedical Informatics at Vanderbilt University. I also serve as the Director of the Vanderbilt Evolutionary Studies Initiative (<http://www.vanderbilt.edu/evolution>), an interdisciplinary center that aims to unite a remarkably diverse array of scholars from diverse disciplines with broad interests and expertise in evolution-related fields. I received my undergraduate degree in Biology from the University of Crete, Greece (1998) and my PhD from Edinburgh University, Scotland (2001). Prior to joining Vanderbilt in the summer of 2007, I was a postdoctoral fellow at the University of Wisconsin-Madison (2002 – 2005) and a research scientist at the Broad Institute (2005 – 2007).

Research in my laboratory focuses on the study of the DNA record to gain insight into the patterns and processes of evolution. Through a combination of computational and experimental approaches, my laboratory's current research aims to understand the molecular foundations of the fungal lifestyle, the reconstruction of the tree of life, and the evolution of human pregnancy.

My team's research has been recognized by many awards, including a Searle Scholarship (2008), an NSF CAREER award (2009), and an endowed chair (2013). Most recently, I was named Blavatnik National Awards for Young Scientists Finalist (2017), Guggenheim Fellow (2018), Fellow of the American Academy of Microbiology (2019), and American Association for the Advancement of Science (AAAS) Fellow (2020).

CURRENT POSITIONS:

Vanderbilt University, USA	Director, Evolutionary Studies Initiative	2019–present
Vanderbilt University, USA	Professor of Biological Sciences	2015–present
Vanderbilt University, USA	Professor of Biomedical Informatics	2015–present
Vanderbilt University, USA	Cornelius Vanderbilt Chair in Biological Sciences	2013–present

EDUCATION AND TRAINING:

University of Crete, Greece	Biology	BS	1998
University of Edinburgh, UK	Evolutionary Biology	PhD	2001
University of Wisconsin, USA	Evolutionary Genomics	Postdoc	2002–2005

SELECT NATIONAL/INTERNATIONAL HONORS AND AWARDS:

- 2020, Fellow of the American Association for the Advancement of Science
- 2019, Fellow of the American Academy of Microbiology
- 2018, Guggenheim Fellow in Molecular and Cellular Biology
- 2018, Chair, Cellular & Molecular Fungal Biology, Gordon Research Conference
- 2017, National Award Finalist, Blavatnik Awards for Young Scientists (US Competition)
- 2009, CAREER Award, National Science Foundation
- 2008, Searle Scholar Award, The Kinship Foundation
- 2002, Human Frontier Science Program Long-Term Fellowship
- 1998, Natural Environment Research Council Graduate Research Fellowship, UK

SELECT SERVICE:

2016–present, Board of Reviewing Editors, *eLife*
2018–present, Advisory Board, *Current Biology*
2018–present, Senior Editor, *Microbiology Resource Announcements*
2011–present, Associate Editor, *G3:Genes|Genomes|Genetics*
2015–present, Associate Editor, *BMC Genomics*

TEN REPRESENTATIVE RECENT PUBLICATIONS (Rokas lab members in bold):

1. **Li, Y., J. L. Steenwyk**, Y. Chang, Y. Wang, T. Y. James, J. E. Stajich, J. W. Spatafora, M. Groenewald, C. W. Dunn, C. T. Hittinger, **X.-X. Shen[^]**, & **A. Rokas[^]** (2021). A genome-scale phylogeny of the kingdom Fungi. (^Senior authors) ***Current Biology***: 31: 1653-1655
2. **Shen, X.-X.[^]**, Y Li, C. T. Hittinger, X. Chen, & **A. Rokas[^]** (2020). An investigation of irreproducibility in maximum likelihood phylogenetic inference. (^Senior authors) ***Nature Communications*** 11: 6096
3. **Steenwyk, J. L.***, **A. L. Lind***, L. N. A. Ries, T. F. dos Reis, L. P. Silva, F. Almeida, R. W. Bastos, T. F. C. F. 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 allo diploid hybrids of *Aspergillus* fungi. (*Equal contributors; ^senior authors) ***Current Biology*** 30: 2495-2507
4. **LaBella, A. L.***, A. Abraham*, Y. Pichkar, S. L. Fong, G. Zhang, L. J. Muglia, P. Abbot, **A. Rokas[^]**, & J. A. Capra[^] (2020). Accounting for diverse evolutionary forces reveals mosaic patterns of selection on human preterm birth loci. (*Equal contributors; ^senior authors) ***Nature Communications*** 11: 3731
5. **Steenwyk, J. L.**, D. A. 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. Hittinger[^], & **A. Rokas[^]** (2019). Extensive loss of cell cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. ***PLoS Biology*** 17: e3000255
6. **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). Tempo and mode of genome evolution in the budding yeast subphylum. ***Cell*** 175: 1533-1545
7. **Rokas, A., J. H. Wisecaver, & A. L. Lind** (2018). The birth, evolution and death of metabolic gene clusters in fungi. ***Nature Reviews Microbiology*** 16: 731–744
8. **Shen, X.-X.**, C. T. Hittinger, & **A. Rokas** (2017). Contentious relationships in phylogenomic studies can be driven by a handful of genes. ***Nature Ecology and Evolution*** 1: 0126
9. **Lind, A. L., J. H. Wisecaver**, C. Lameiras, Wiemann P, Palmer JM, Keller NP, F. Rodrigues, G. H. Goldman, & **A. Rokas** (2017). Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. ***PLoS Biology*** 15: e2003583
10. **Wisecaver, J. H., A. T. Borowsky**, V. Tzin, G. Jander, D. J. Kliebenstein, & **A. Rokas** (2017). A global co-expression network approach for connecting genes to specialized metabolic pathways in plants. ***The Plant Cell*** 29: 944–959

ANTONIS ROKAS, Ph.D. – Full Curriculum Vitae

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CURRENT POSITIONS

- 2019–present** Director, Vanderbilt Evolutionary Studies Initiative
2015–present Professor of Biological Sciences, Vanderbilt University
2015–present Professor of Biomedical Informatics, Vanderbilt University
2013–present Cornelius Vanderbilt Chair in Biological Sciences, Vanderbilt University

PAST POSITIONS

- 2013–2015** Associate Professor of Biological Sciences, Vanderbilt University
2013–2015 Associate Professor of Biomedical Informatics, Vanderbilt University
2007–2012 Assistant Professor of Biological Sciences, Vanderbilt University
2005–2007 Research Scientist, The Broad Institute of MIT & Harvard
2002–2005 Post-doctoral Fellow, University of Wisconsin-Madison, Advisor: S. B. Carroll
1998–2001 Doctoral Student, University of Edinburgh, Advisor: G. N. Stone
1997–1998 Undergraduate Exchange Student, Reading University, Advisor: P. W. H. Holland
1996–1997 Undergraduate Thesis Student, University of Crete, Advisor: E. Zouros

EDUCATION

- 2001** **Ph.D., Evolutionary Biology** University of Edinburgh, United Kingdom
1998 **B.Sc., Biology** University of Crete, Greece

AWARDS, FELLOWSHIPS, AND PROFESSIONAL HONORS

- 2020** Fellowship, American Association for the Advancement of Science
2019 Fellowship, American Academy of Microbiology
2018 Guggenheim Fellowship
2018 Biological Sciences Excellence in Research Award
2018 Chair (elected), Cellular and Molecular Fungal Biology Gordon Research Conference
2017 National Finalist, Blavatnik Awards for Young Scientists
2017 Biological Sciences Excellence in Research Award
2017 Littlejohn Faculty Fellow
2016 Vice-chair (elected), Cellular and Molecular Fungal Biology Gordon Research Conference
2015 Guest Editor for *Genomes and Evolution* special issue of *Current Opinion in Genetics and Development*
2015 Biological Sciences Excellence in Research Award
2013–present Cornelius Vanderbilt Chair of Biological Sciences
2013 Biological Sciences Excellence in Research Award
2011 Chancellor's Award for Research
2009 NSF CAREER Award
2008 Searle Scholar
2002–2005 Human Frontier Science Program Long-Term Fellowship

1998–2001	Natural Environment Research Council Studentship
1997–1998	Greek Foundation of State Scholarships for Undergraduate Study Abroad

RESEARCH INTERESTS

- ❖ The evolution of fungal specialized metabolic pathways and chemodiversity
- ❖ The repeated evolution of fungal pathogens of humans
- ❖ The evolution of human pregnancy
- ❖ Phylogenetics and phylogenomics of fungi and animals

FUNDING

National Institutes of Health	PI, 12/21-11/26, Deciphering the phenotypic and genomic traits that underlie the evolution of pathogenicity differences among <i>Aspergillus fumigatus</i> and its close relatives, \$3,723,728
National Science Foundation	PI (with C. T. Hittinger, PI), 07/21-07/26, Collaborative Research: RoL: The Evolution of the Genotype-Phenotype Map across Budding Yeasts, \$949,985
Burroughs Wellcome Trust	PI, 06/21-05/26, A Community Resource to Reveal Mechanisms for Mammalian Birth Timing, \$375,000
National Institutes of Health	PI, 09/20-08/22, Deciphering the phenotypic and genomic traits that underlie the evolution of pathogenicity differences among <i>Aspergillus fumigatus</i> and its close relatives, \$592,432
Howard Hughes Medical Institute	Advisor, 09/19-08/22, Gilliam Fellowship for Advanced Study to Jacob L. Steenwyk, Examining the loss of diverse DNA repair genes and long-term hypermutation in a lineage of budding yeasts, \$150,000
Burroughs Wellcome Trust	PI (with J. A. Capra, PI), 06/17-05/22, Integrating 'omics and electronic health records to elucidate the genetic architecture of preterm birth, \$300,000
March of Dimes	PI / Theme Leader (with P. Abbot, PI; K. Petren, PI), 7/13-12/22, The March of Dimes Prematurity Research Collaborative of Ohio (Director L. J. Muglia), Theme 1: Evolutionary Synthesis of Human Pregnancy, ~\$2,000,000
National Science Foundation	PI (with C. T. Hittinger, PI; C. P. Kurtzman, Co-PI), 02/15-01/22, DIMENSIONS: Collaborative Research: The making of biodiversity across the yeast subphylum, \$851,102
National Science Foundation	Advisor, 09/14-08/17, National Plant Genome Initiative Postdoctoral Research Fellowship to Jennifer H. Wisecaver, The evolution of secondary metabolic gene clusters in plants, \$207,000
National Institutes of Health	Co-PI (PI R. R. Dinglasan), 07/14-06/16, Midgut transcriptome and proteome analysis of non-model anopheline malaria vectors, \$180,175
National Institutes of Health	Co-Advisor (with L. J. Zwiebel), 12/12-11/15, F31 Pre-doctoral Research Fellowship Award to David C. Rinker, Chemosensory signatures of hematophagy in mosquitoes, \$81,708

National Science Foundation	PI, 09/09-08/14, CAREER: A genomics approach to identifying the factors influencing phylogenetic accuracy, \$688,129
National Institutes of Health	Advisor, 08/10-07/12, F31 Pre-doctoral Research Fellowship Award to John G. Gibbons, Characterizing the genomic patterns of variation in the fungal pathogen <i>Aspergillus fumigatus</i> , \$50,352
Searle Scholars Program	PI, 07/08-06/11, Deciphering the origins and assembly of the genetic toolkit for animal development, \$300,000
National Science Foundation	Advisor, 09/08-08/10, Postdoctoral Fellowship in Biological Informatics to Jason C. Slot, Dynamics and ecological significance of the origins, order and inheritance of fungal gene clusters, \$120,000

UNDERGRADUATE TEACHING

BSCI1511	<i>Introduction to Biological Sciences</i> , Vanderbilt Univ., 2015–present
BSCI3333	<i>Contagion</i> , Vanderbilt Univ., 2021
BSCI6320	<i>Graduate Seminar in Biological Sciences</i> , Vanderbilt Univ., 2018–2021
BSCI2205	<i>Evolution</i> , Vanderbilt Univ., 2010–2017
BSCI2272	<i>Computational Genomics</i> , Vanderbilt Univ., 2010–2013
BSCI3861-BSCI4999	<i>Research for Academic Credit Courses</i> , Vanderbilt Univ., every semester

INVITED ADVANCED TEACHING (LAST FEW YEARS)

Workshop on Phylogenomics – Europe, 2017, 2019 (co-director)
 Workshop on Genomics – Europe, 2011–2016, 2018, 2019
 Workshop on Molecular Evolution – MBL, USA, 2010–2015
 EMBO/Wellcome Trust Computational Molecular Evolution Workshop, 2010–2014
 Workshop on Molecular Evolution – Europe, 2010–2013

ADVISING

Postdoctoral fellows

Jason C. Slot (2008–2013; now Associate Professor, The Ohio State Univ., USA)
 Ioannis Stergiopoulos (2011; now Associate Professor, Univ. of California, Davis, USA)
 Padmanabhan Mahadevan (2009–2010; now Associate Professor, Tampa Univ., USA)
 Xiaofan Zhou (2011–2016; now Professor, South China Agricultural Univ., China)
 Kriston L. McGary (2009–2016; now Consultant, Genetic Networks)
 Jennifer H. Wisecaver (2013–2017; now Assistant Professor, Purdue Univ., USA)
 Julie B. Phillips (2014–2017; now Assistant Professor, Cumberland Univ., USA)
 Mingshuang Wang (2017–2018; now Assistant Prof., Hangzhou Normal Univ., China)
 Youhuang Bai (2017–2018; now postdoc, Vanderbilt Univ., USA)
 Xing-Xing Shen (2014–2019; now Assistant Professor, Zhejiang Univ., China)
 Yuanning Li (2019–2021; now Professor, Ocean University of China)
 Matthew E. Mead (current)
 Abigail L. LaBella (current)
 Carla Gonçalves (from 2022 onward)
 Kyle David (from 2022 onward)

Graduate students

John G. Gibbons (2012; postdoc, Harvard Univ.; now Assistant Professor, Univ. Massachusetts-Amherst, USA)

Leonidas Salichos (2014; postdoc, Yale Univ., USA; now Assistant Professor, New York Inst. of Technology)
David C. Rinker (co-advisor with L. J. Zwiebel, 2015; now Research Assistant Professor, Vanderbilt Univ., USA)
Yuyu Wang (visiting graduate student; now Associate Professor, Hebei Agricultural University, USA)
Abigail Lind (2017; now postdoc, Gladstone Institutes, Univ. California San Francisco, USA)
Haley Eidem (2018; now Quantitative UX Researcher, Google, USA)
Mara Kim (2018; now Senior Software Engineer, Microsoft, USA)
Juan F. Ortiz (2019; now postdoc, RIKEN, Japan)
Michelle Moon (2019; now Data Visualization Specialist, Tennessee Dept. Education, USA)
Jacob L. Steenwyk (current)
E. Anne Hatmaker (current)
Alec Brown (current)
Marie-Claire Harrison (current)
Christina Chavez (current)
Thodoris Danis (current)

Masters students

Patricia Soria (2014; now graduate student, Univ. of Florida, USA)
Kenneth Polzin (2014; now independent consultant, biodiversity informatics)

Undergraduate students

Matthew E. Campbell (2012; PhD from Univ. Montana; now postdoc, New England Biolabs, USA)
Mara Kim (2012; PhD from Vanderbilt Univ.; now Senior Software Engineer, Microsoft, USA)
Martha H. Elmore (2013; PhD from Harvard Univ.; now Researcher, Rethink Priorities, USA)
George H. Greene (2014; PhD from Duke Univ.; now Chief Scientific Officer at Upstream Biotechnology, USA)
Brian A. Cooper (2015; now Software Engineer at Opentrons Labworks, USA)
Sean B. King (2016; PhD from Princeton Univ.; now Consultant at Bain & Company, USA)
Samuel A. Smith (2017; now graduate student, Brown Univ. USA)
Rebecca Burke-Aguero (2017; now software developer, Microsoft, USA)
Alexander T. Borowsky (2018; now graduate student, Univ. of California, Riverside, USA)
Zackery Ely (2018; now graduate student, MIT, USA)
Maddison Johnson (2018; now Doctor of Veterinary Medicine candidate, Midwestern University College of Veterinary Medicine, USA)
Megan A. Phillips (2020; now graduate student, Emory University, USA)
Olivia Zheng (current)
Miya Hugaboom (current)

PROFESSIONAL AFFILIATIONS

Society for Molecular Biology and Evolution, Society for the Study of Evolution, Society of Systematic Biologists, Mycological Society of America, Genetics Society of America, American Association for the Advancement of Science, American Society of Microbiology.

CONSULTING

2020 – present LifeMine Therapeutics, Cambridge, MA

EDITED VOLUMES

2015 Rokas, A., & P. S. Soltis, Editors. Special issue on Genomes and Evolution. *Curr. Op. Genet. Dev.*, volume **35**: 1-126.

PEER-REVIEWED PUBLICATIONS (Rokas Lab Members in Bold)



Google Scholar publication statistics

Number of publications: 200

Number of citations: ~19,900

h-index: 69

2021 Steenwyk, J. L.[▲] & A. Rokas[▲]. ggpubfigs: colorblind friendly color palettes and ggplot2 graphic system extensions for publication-quality scientific figures. (^Senior authors) *Microbiol. Resour. Announc.* **10**: e00871-21.

Colabardini, A. C., F. Wang, Z. Dong, L. Pardeshi, M. C. Rocha, J. H. Costa, T.F. dos Reis, **A. Brown**, Q. Z. Jaber, M. Fridman, T. Fill, **A. Rokas**, I. Malavazi, K. H. Wong, & G. H. Goldman. Heterogeneity in the transcriptional response of the human pathogen *Aspergillus fumigatus* to the antifungal agent caspofungin. *Genetics*: iyab183.

Phillips, M. A., J. L. Steenwyk[▲], X.-X. Shen, & A. Rokas[▲]. Examination of gene loss in the DNA mismatch repair pathway and its mutational consequences in a fungal phylum. (^Senior authors) *Genome Biol. Evol.* **13**: evab219.

Prattes, J., J. Wauters, D. R. Giacobbe, J. Salmanton-García, J. Maertens, M. Bourgeois, M. Reynders, L. Rutsaert, N. Van Regenmortel, P. Lormans, S. Feys, A. C. Reisinger, O. A. Cornely, T. Lahmer, M. Valerio, L. Delhaes, K. Jabeen, J. Steinmann, M. Chamula, M. Bassetti, S. Hatzl, R. Rautemaa-Richardson, P. Koehler, K. Lagrou, M. Hoenigl; ECMM-CAPA Study Group*. Risk factors and outcome of pulmonary aspergillosis in critically ill coronavirus disease 2019 patients- a multinational observational study by the European Confederation of Medical Mycology. (ECMM-CAPA Study Group*: Y. Debaveye, M. H. Miceli, J.-J. Tudesq, G. Paul, R. Krause, M. Linhofer, J. Frost, P. Zechner, M. Kochanek, P. Eller, J. D. Jenks, S. Volpi, A.-P. Bellanger, P. L. White, G. H. Goldman, P. Bowyer, **A. Rokas**, S. Gago, P. Pelosi, C. Robba, J.-P. Gangneux, C. Lass-Floerl, M. Machado, P. Muñoz). *Clin Microbiol Infect.*: in press.

Harrison, M. C., A. L. LaBella, C. T. Hittinger[▲], & A. Rokas[▲]. The evolution of the GALactose utilization pathway in budding yeasts. (^Senior authors) *Trends Genet.*: in press.

Santos, R. A. C., M. E. Mead, J. L. Steenwyk, O. Rivero-Menendez, A. Alastruey-Izquierdo, G. H. Goldman[▲], & **A. Rokas[▲]**. Examining signatures of natural selection in antifungal resistance genes across *Aspergillus* fungi. (^Senior authors) *Front. Fungal Biol.* **2**: 723051.

Kwon, M. J., C. Steiniger, T. C. Cairns, **J. H. Wisecaver, A. Lind**, C. Pohl, C. Regner, **A. Rokas**, & V. Meyer. Beyond the biosynthetic gene cluster paradigm: Genome-wide co-expression networks connect clustered and unclustered transcription factors to secondary metabolic pathways. *Microbiol. Spectr.* **9**: e00898-21.

Tice, A. K., D. Žihala, T. Pánek, R. E. Jones, E. Salomaki, S. Nenarokov, F. Burki, M. Eliáš, L. Eme, A. J. Roger, **A. Rokas, X.-X. Shen**, J. F. H. Strassert, M. Kolísko, & M. W. Brown. PhyloFisher: A phylogenomic package for resolving eukaryotic relationships. *PLoS Biol.* **19**: e3001365.

Steenwyk, J. L.^ & A. Rokas^. orthofisher: a broadly applicable tool for automated gene identification and retrieval. (^Senior authors) *G3* **11**: jkab250.

Ries, L. N. A., P. A. Castro, L. P. Silva, C. Valero, T. F. Reis, R. Saborano, I. F. Duarte, G. F. Persinoti, **J. L. Steenwyk, A. Rokas**, F. Almeida, J. H. Costa, T. P. Fill, S. S. W. Wong, V. Aimanianda, F. Rodrigues, R. A. Gonçales, C. Duarte-Oliveira, A. Carvalho, & G. H. Goldman. *Aspergillus fumigatus* acetate utilisation impacts virulence traits and pathogenicity. *mBio* **12**: e01682-21.

Li, Y., X.-X. Shen, B. Evans, C. W. Dunn^, & **A. Rokas^**. Rooting the animal tree of life. (^Senior authors) *Mol. Biol. Evol.* **38**: 4322–4333.

Mead, M. E.*, **J. L. Steenwyk***, L. P. Silva, P. A. de Castro, N. Saeed, F. Hillmann, G. H. Goldman, & **A. Rokas**. An evolutionary genomic approach reveals both conserved and species-specific genetic elements related to human disease in closely related *Aspergillus* fungi. (*Equal contributors) *Genetics* **218**: iyab066.

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^**. Genomic and phenotypic analysis of COVID-19-associated pulmonary aspergillosis isolates of *Aspergillus fumigatus*. (^Senior authors) *Microbiol. Spectr.* **9**: e00010-21.

LaBella, A. L., D. Opulente, **J. L. Steenwyk**, C. T. Hittinger, & **A. Rokas**. Signatures of optimal codon usage in metabolic genes inform budding yeast ecology. *PLoS Biol.* **19**: e3001185.

Shen, X.-X., J. L. Steenwyk, & A. Rokas. Dissecting incongruence between concatenation- and quartet-based approaches in phylogenomic data. *Syst. Biol.* **70**: 997–1014.

Li, Y., J. L. Steenwyk, Y. Chang, Y. Wang, T. Y. James, J. E. Stajich, J. W. Spatafora, M. Groenewald, C. W. Dunn, C. T. Hittinger, **X.-X. Shen^, & A Rokas^**. A genome-scale phylogeny of the kingdom Fungi. (^Senior authors) *Curr. Biol.* **31**: 1653-1665.

Benton, M. L., A. Abraham, **A. L. LaBella**, P. Abbot, **A. Rokas**, & J. A. Capra. The influence of evolutionary history on human health and disease. *Nature Rev. Genet.* **22**: 269–283.

Steenwyk, J. L.^, T. J. Buida III, **A. L. LaBella**, Y. Li, X.-X. Shen, & **A. Rokas^**. PhyKIT: a broadly applicable UNIX shell toolkit for processing and analyzing phylogenomic data. (^Senior authors) *Bioinformatics* **37**: 2325–2331.

Haase, M. A. B., J. Kominek, D. Opulente, **X.-X. Shen**, **A. L. LaBella**, **X. Zhou**, J. DeVirgilio, A. Hulfachor, C. P. Kurtzman, **A. Rokas^**, & C. T. Hittinger^ . Repeated

horizontal gene transfer of *GAL*actose metabolism genes violates Dollo's law of irreversible loss. (^Senior authors) *Genetics* **217**: iyaa012.

Wu, M.-Y.* **M. E. Mead***, M.-K. Lee, G. F. Neuhaus, D. A. Adpressa, J. I. Martien, Y.-E. Son, H. Moon, D. Amador-Noguez, K.-H. Han, **A. Rokas**, S. Loesgen, J.-H. Yu, H.-S. Park (2021). Transcriptomic, protein-DNA interaction, and metabolomic studies of VosA, VelB, and WetA in *Aspergillus nidulans* asexual spores. (*Equal contributors) *mBio* **12**: e03128-20.

2020 Rokas, A., S. Mesiano, O. Tamam, **A. L. LaBella**, G. Zhang, & L. J. Muglia. Developing a theoretical evolutionary framework to solve the mystery of parturition initiation. *eLife* **9**: e58343.

Hatmaker, E. A.*, X. Zhou*, **M. E. Mead**, H. Moon, J.-H. Yu, & **A. Rokas**. A revised transcriptome-based gene annotation for *Aspergillus flavus* strain NRRL 3357. (*Equal contributors) *Microbiol. Resour. Announc.* **9**: e01155-20.

Steenwyk, J. L.^, T. J. Buida III, Y. Li, X.-X. Shen, & **A. Rokas^**. ClipKIT: a multiple sequence alignment-trimming algorithm for accurate phylogenomic inference. (^Senior authors) *PLoS Biol.* **18**: e3001007.

Shen, X.-X.^, Y Li, C. T. Hittinger, X. Chen, & **A. Rokas^**. An investigation of irreproducibility in maximum likelihood phylogenetic inference. (^Senior authors) *Nature Comm.* **11**: 6096.

Li, Y., K. T. David, **X.-X. Shen**, **J. L. Steenwyk**, K. M. Halanych, & **A. Rokas**. Feature Frequency Profile-based phylogenies are inaccurate. *Proc. Natl. Acad. Sci. USA* **117**: 31580-31581.

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^**. Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. (^Senior authors) *Sci. Adv.* **6**: eabd0079.

Santos, R. A. C., O. Rivero-Menendez, **J. L. Steenwyk**, **M. E. Mead**, G. H. Goldman^, A. Alastruey-Izquierdo, & **A. Rokas^**. Draft genome sequences of four *Aspergillus* section *Fumigati* clinical strains. (^Senior authors) *Microbiol. Resour. Announc.* **9**: e00856-20.

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. *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* **11**: e02458-20.

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**. Variation among biosynthetic gene clusters, secondary metabolite profiles, and cards of virulence across *Aspergillus* species. (*Equal contributors) *Genetics*: **216**: 481-497.

LaBella, A. L.*, A. Abraham*, Y. Pichkar, S. L. Fong, G. Zhang, L. J. Muglia, P. Abbot, **A. Rokas^**, & J. A. Capra^*. Accounting for diverse evolutionary forces reveals mosaic patterns of selection on human preterm birth loci. (*Equal contributors; ^senior authors) *Nature Comm.* **11**: 3731.

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. 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. The *Aspergillus fumigatus* transcription factor RglT is important for gliotoxin biosynthesis and self-protection, and virulence. *PLoS Path.* **16**: e1008645.

James, T. Y., J. E. Stajich, C. T. Hittinger, & **A. Rokas**. Toward a fully resolved fungal tree of life. *Ann. Rev. Microbiol.* **74**: 291–313.

Steenwyk, J. L.*, **A. L. Lind***, L. N. A. Ries, T. F. dos Reis, L. P. Silva, F. Almeida, R. W. Bastos, T. F. C. F. 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[^]**. Pathogenic allo diploid hybrids of *Aspergillus* fungi. (*Equal contributors; [^]senior authors) *Curr. Biol.* **30**: 2495-2507.

Mead, M. E.*, **A. T. Borowsky***, B. Joehnk, **J. L. Steenwyk**, **X.-X. Shen**, A. Sil, & **A. Rokas**. Recurrent loss of *abaA*, a master regulator of asexual development in filamentous fungi, correlates with changes in genomic and morphological traits. (*Equal contributors) *Genome Biol. Evol.* **12**: 1119–1130.

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*. (^Senior authors) *Front. Genet.* **11**: 459.

Drott, M. T., R. W. Bastos, **A. Rokas**, L.N.A. Ries, T. Gabaldon, G. H. Goldman, N. P. Keller, & C. Greco. Diversity of secondary metabolism in *Aspergillus nidulans* clinical isolates. *mSphere* **5**: e00156-20.

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. Functional characterization of clinical isolates of the opportunistic fungal pathogen *Aspergillus nidulans*. *mSphere* **5**: e00153-20.

Rokas, A., **M. E. Mead**, **J. L. Steenwyk**, N. H. Oberlies, & G. H. Goldman. Evolving moldy murderers: *Aspergillus* section *Fumigati* as a model for studying the repeated evolution of fungal pathogenicity. *PLoS Path.* **16**: e1008315.

Knowles, S. L., H. A. Raja, I. H. Isawi, L. C. Flores Bocanegra, P. H. Reggio, C. J. Pearce, J. E. Burdette, **A. Rokas**, & N. H. Oberlies. Wheldone: Characterization of a unique scaffold from the co-culture of *Aspergillus fischeri* and *Xylaria flabelliformis*. *Org. Lett.* **22**: 1878-1882.

Libkind, D., D. Peris Navarro, F. Cubillos, **J. L. Steenwyk**, D. Opulente, Q. Langdon, **A. Rokas**, & C. T. Hittinger. Into the wild: new yeast genomes from natural environments and new tools for their analysis. *FEMS Yeast Res.* **20**: foaa008.

Knowles, S. J., **M. E. Mead**, L. Pereira Silva, H. A. Raja, **J. L. Steenwyk**, G. H. Goldman[^], N. H. Oberlies[^], & **A. Rokas[^]**. Gliotoxin, a known virulence factor in the major human pathogen *Aspergillus fumigatus*, is also biosynthesized by the non-pathogenic relative *A. fischeri*. (^Senior authors) *mBio* **11**: e03361-19.

- Rokas, A., M. E. Mead, J. L. Steenwyk**, H. A. Raja, & N. H. Oberlies. Biosynthetic gene clusters and the evolution of fungal chemodiversity. *Natural Product Rep.* **37**: 868–878.
- Zhou, X.**, S. Lutteropp, L. Czech, A. Stamatakis, M. von Looz, & **A. Rokas**. Quartet-based computations of internode certainty provide accurate and robust measures of phylogenetic incongruence. *Syst. Biol.* **69**: 308-324.
- 2019** Knowles, S. L., N. Vu, D. A. Todd, H. A. Raja, **A. Rokas**, Q. Zhang, & N. H. Oberlies. Orthogonal method for double bond placement via ozone-induced dissociation mass spectrometry (OzID-MS). *J. Nat. Prod.* **82**: 3421-3431.
- Bodinaku, I., J. Shaffer, A. B. Connors, **J. L. Steenwyk**, E. Kastman, **A. Rokas**, A. Robbat, & B. Wolfe. Rapid phenotypic and metabolomic domestication of wild *Penicillium* molds on cheese. *mBio* **10**: e02445-19.
- Mead, M. E.***, H. A. Raja*, **J. L. Steenwyk**, S. L. Knowles, N. H. Oberlies^, & **A. Rokas^**. Draft genome sequence of the griseofulvin-producing fungus *Xylaria flabelliformis* strain G536. (*Equal contributors; ^senior authors) *Microbiol. Resour. Announc.* **8**: e00890-19.
- Steenwyk, J. L. & A. Rokas**. treehouse: a user-friendly application to obtain subtrees from large phylogenies. *BMC Res. Notes* **12**: 541.
- Ely, Z. A., J. M. Moon**, G. R. Sliwoski, A. K. Sangha, **X.-X. Shen**, **A. L. LaBella**, J. Meiler, J. A. Capra, & **A. Rokas**. The impact of natural selection on the evolution and function of placentally expressed galectins. *Genome Biol. Evol.* **11**: 2574–2592.
- Krassowski, T., J. Kominek, **X.-X. Shen**, D. A. Opulente, **X. Zhou**, **A. Rokas**, C. T. Hittinger, & K. H. Wolfe. Multiple reinventions of mating-type switching during budding yeast evolution. *Curr. Biol.* **29**: 2555–2562.
- Labella, A. L.**, D. A. Opulente, **J. L. Steenwyk**, C. T. Hittinger, & **A. Rokas**. Variation and selection on codon usage bias across an entire subphylum. *PLoS Genet.* **15**: e1008304.
- dos Reis, T. F., L. P. Silva, P. A. de Castro, R. A. do Carmo, M. M. Marini, J. F. da Silveira, B. H. Ferreira, F. Rodrigues, **A. L. Lind**, **A. Rokas**, & G. H. Goldman. The *Aspergillus fumigatus* mismatch repair MSH2 homologue is important for virulence and azole resistance. *mSphere* **4**: e00416-19.
- Moon, J. M.**, J. A. Capra, P. Abbot, & **A. Rokas**. Immune regulation in eutherian pregnancy: Live birth co-evolved with novel immune genes and gene regulation. *BioEssays* **41**: 1900072.
- Moon, J. M.**, J. A. Capra, P. Abbot, & **A. Rokas**. Signatures of recent positive selection in enhancers across 41 human tissues. *G3* **9**: 2671-2774.
- Steenwyk, J. L., X.-X. Shen, A. L. Lind**, G. G. Goldman, & **A. Rokas**. A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera *Aspergillus* and *Penicillium*. *mBio* **10**: e00925-19.
- Wang, M.**, H. Fu, **X.-X. Shen**, R. Ruan, N. Pun, J. Xu, **A. Rokas**, & H. Li. Genomic features and evolution of the conditionally dispensable chromosome in the tangerine pathotype of *Alternaria alternata*. *Mol. Plant Pathol.* **20**: 1425–1438.
- Steenwyk, J. L.**, D. A. 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. Hittinger^, & **A. Rokas^**. Extensive loss of cell cycle and DNA repair genes

in an ancient lineage of bipolar budding yeasts. (^Senior authors) *PLoS Biol.* **17**: e3000255.

Smith, S. P.*, J. B. Phillips*, M. L. Johnson, P. Abbot, J. A Capra, & **A. Rokas**. Genome wide association analysis identifies genetic variants associated with reproductive variation across domestic dog breeds and uncovers links to domestication. (*Equal contributors) *Evol. Med. Public Health* 2019: 93-103.

Greco, C., N. P. Keller^, & **A. Rokas**^. Unearthing fungal chemodiversity and prospects for drug discovery. (^Senior authors) *Curr. Opin. Microbiol.* **51**: 22-29.

Ries, L. N. A., **J. L. Steenwyk**, P. A. Castro, P. B. A. Lima, F. Almeida, L. J. Assis, A. O. Manfiolli, A. Takahashi-Nakaguchi, Y. Kusuya, D. Hagiwara, H. Takahashi, X. Wang, J. J. Obar, **A. Rokas**, & G. H. Goldman. Nutritional heterogeneity among *Aspergillus fumigatus* strains has consequences for virulence in a strain- and host-dependent manner. *Front. Microbiol.* **10**: 854.

Gao, S., S. E. Gold, **J. H. Wisecaver**, Y. Zhang, L. Guo, L.-J. Ma, **A. Rokas**, & A. E. Glenn. Genome-wide analysis of *Fusarium verticillioides* reveals inter-kingdom contribution of horizontal gene transfer to the expansion of metabolism. *Fungal Genet. Biol.* **128**: 60-73.

Kominek, J., D. T. Doering, D. A. Opulente, **X.-X. Shen**, **X. Zhou**, J. DeVirgilio, A. B. Hulfachor, M. Groenewald, M. A. Mcgee, S. D. Karlen, C. P. Kurtzman, **A. Rokas**, & C. T. Hittinger. Eukaryotic acquisition of a bacterial operon. *Cell* **176**: 1356-1366.

Wang, Y., X. Zhou, L. Wang, X. Liu, D. Yang, & **A. Rokas**. Gene selection and evolutionary modeling affect phylogenomic inference of Neuroptera based on transcriptome data. *Int. J. Mol. Sci.* **20**: 1072.

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. H. Goldman, R. A. Cramer, N. H. Oberlies, & **A. Rokas**. Characterizing the pathogenic, genomic, and chemical traits of *Aspergillus fischeri*, the closest sequenced relative of the major human fungal pathogen *Aspergillus fumigatus*. *mSphere* **4**: e00018-19.

Knowles, S. L., H. A. Raja, A. J. Wright, A. M. L. Lee, L. K. Caesar, N. B. Cech, **M. E. Mead**, **J. L. Steenwyk**, L. Ries, G. H. Goldman, **A. Rokas**, N. H. Oberlies. Mapping the fungal battlefield: using *in situ* chemistry and deletion mutants to monitor interspecific chemical interactions between fungi. *Front. Microbiol.* **10**: 285.

2018 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). Tempo and mode of genome evolution in the budding yeast subphylum. (*Equal contributors) *Cell* **175**: 1533-1545.

Eidem, H. R., J. L. Steenwyk, J H. Wisecaver, J. A. Capra, P. Abbot, & **A. Rokas**. 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* **11**: 107.

Segal, E. S., V. Gritsenko, A. Levitan, B. Yadav, B. N. Dror, J. L. Steenwyk, Y. Silberberg, K. Mielich, **A. Rokas**, N. A. R. Gow, R. Kunze, R. Sharan & J. Berman. Gene essentiality

analyzed by in vivo transposon mutagenesis and machine learning in a stable haploid isolate of *Candida albicans*. *mBio* **9**: e02048-18.

Krause, D. J., J. Kominek, D. A. Opulente, **X.-X. Shen, X. Zhou**, Q. K. Langdon, J. DeVirgilio, A. B. Hulfachor, C. P. Kurtzman, **A. Rokas** & C. T. Hittinger. Functional and evolutionary characterization of a secondary metabolite gene cluster in budding yeasts. *Proc. Natl. Acad. Sci. USA* **115**: 11030-11035.

Rokas, A., J. H. Wisecaver, & A. L. Lind. The birth, evolution, and death of metabolic gene clusters in fungi. *Nature Rev. Microbiol.* **16**: 731-744.

Sirota, M., C. G. Thomas, R. Liu, M. Zuhl, P. Banerjee, R. J. Wong, C. C. Quaintance, R. Leite, J. Chubiz, R. Anderson, J. Chappelle, **M. Kim**, W. Grobman, G. Zhang, **A. Rokas**, L. Muglia, C. Ober, S. K. England, G. Marcones, S. Parry, G. M. Shaw, D. K. Stevenson, J. L. Simpson, E. Thomson & A. J. Butte. Enabling precision medicine in neonatology, an integrated repository for preterm birth research. *Scientific Data* **5**: 180219.

Shi, R., **X.-X. Shen, A. Rokas** & B. F. Eichman. Structural biology of the HEAT-like repeat family of DNA glycosylases. *BioEssays* **40**: 1800133.

Wu, M.-Y.* **M. E. Mead***, M.-K. Lee, S. C. Kim, **A. Rokas** & J.-H. Yu. Conservation and divergence in the asexual sporulation gene regulatory network across a genus of filamentous fungi. (*Equal contributors) *mBio* **9**: e01130-18.

Huusko, J. M., M. K. Karjalainen, B. E. Graham, G. Zhang, E. G. Farrow, N. A. Miller, B. Jacobsson, **H. R. Eidem**, J. C. Murray, B. Bedell, F. L. Bødker, N. K. Litterman, P.-P. Jiang, L. Russell, D. A. Hinds, Y. Hu, the 23andMe Research Team, **A. Rokas**, K. Teramo, K. Christensen, S. M. Williams, M. Rämet, S. F. Kingsmore, K. K. Ryckman, M. Hallman, & L. J. Muglia. Whole exome sequencing reveals HSPA1L as a genetic risk factor for spontaneous preterm birth. *PLoS Genet.* **14**: e1007394.

Lim, F. Y., T. H. Won, N. Raffa, J. A. Baccile, **J. H. Wisecaver, A. Rokas**, F. Schroeder & N. P. Keller. Fungal isocyanide synthases and xanthocillin biosynthesis in *Aspergillus fumigatus*. *mBio* **9**: e00785-18.

Krassowski, T., A. Y. Coughlan, **X.-X. Shen, X. Zhou**, J. Kominek, D. A. Opulente, R. Riley, I. V. Grigoriev, N. Maheshwari, D. C. Shields, C. P. Kurtzman, C. T. Hittinger, **A. Rokas** & K. H. Wolfe. Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. *Nature Comm.* **9**: 1887.

Gonçalves, C., **J. H. Wisecaver**, J. Kominek, M. Salema-Oom, M. J. Leandro, **X.-X. Shen**, D. Opulente, **X. Zhou**, D. Peris, C. P. Kurtzman, C. T. Hittinger, **A. Rokas** & P. Gonçalves. Evidence for loss and reacquisition of alcoholic fermentation in a fructophilic yeast lineage. *eLife* **7**: e33034.

Lind, A. L., F. Y. Lim, A. Soukup, N. P. Keller & A. Rokas. A LaeA- and BrlA-dependent cellular network governs tissue-specific secondary metabolism in the human pathogen *Aspergillus fumigatus*. *mSphere* **3**: e00050-18.

Moon, J. M., D. M. Aronoff, J. A. Capra, P. Abbot & A. Rokas. Genes involved in human sialic acid biology do not harbor signatures of recent positive selection. *G3* **8**: 1315-1325.

Opulente, D. A., E. J. Rollinson, C. Bernick-Roehr, A. B. Hulfachor, **A. Rokas**, C. P. Kurtzman & C. T. Hittinger. Factors driving metabolic diversity in the budding yeast subphylum. *BMC Biol.* **16**: 26.

Fidler, A. L., S. P. Boudko, **A. Rokas** & B. G. Hudson. The triple helix of collagens: an ancient protein structure that enabled animal multicellularity and tissue evolution. *J. Cell Sci.* **131**: jcs203950.

Steenwyk, J. L. & A. Rokas. Copy number variation in fungi and its implications for wine yeast genetic diversity and adaptation. *Front. Microbiol.* **9**: 288.

K. Y. B. Lamm, **M. L. Johnson, J. B. Phillips**, M. B. Muntifering, J. M. James, H. N. Jones, R. W. Redline, **A. Rokas** & L. J. Muglia (2018). Inverted formin 2 regulates intracellular trafficking, placentation, and pregnancy outcome. *eLife* **7**: e31150.

Zhou, X., X.-X. Shen, C. T. Hittinger & **A. Rokas**. Evaluating fast maximum likelihood-based phylogenetic programs using empirical phylogenomic data sets. *Mol. Biol. Evol.* **35**: 486-503.

Shi, R., E. A. Mullins, **X.-X. Shen**, K. T. Lay, P. K. Yuen, S. S. David, **A. Rokas** & B. F. Eichman. Selective base excision repair of DNA damage by the non-base-flipping DNA glycosylase AlkC. *EMBO J.* **37**: 63-74.

2017 Lind, A. L., J. H. Wisecaver, C. Lameiras, F. Rodrigues, G. H. Goldman & **A. Rokas**. Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. *PLoS Biol.* **15**: e2003583.

King, N. & **A. Rokas**. Embracing uncertainty in early animal evolution. *Curr. Biol.* **27**: R1081–R1088.

Lojek, L. J., A. J. Farrand, **J. H. Wisecaver**, C. E. Blaby-Haas, S. S. Merchant, **A. Rokas** & E. P. Skaar. *Chlamydomonas reinhardtii* cMO is an IsdG family heme oxygenase. *mSphere* **2**: e00176-17.

Eidem, H. R.*, **K. L. McGary***, J. A. Capra, P. Abbot & A. Rokas. The transformative potential of an integrative approach to pregnancy. (*Equal contributors) *Placenta* **57**: 204–215.

Valsecchi, I., O. Sarikayabayram, J. Wong Sak Hoi, L. Muszkieta, **J. Gibbons**, M.-C. Prevost, A. Mallet, J. Krijnse-Locker, O. Granet, I. Mouyna, P. Carr, M. Bromley, V. K. Aimanianda, vishu kumar; J.-H. Yu, **A. Rokas**, G. Braus, C. Saveanu, O. Bayram & J.-P. Latgé. MybAp, a transcription factor involved in conidiation and conidial viability of the human pathogen *Aspergillus fumigatus*. *Mol. Microbiol.* **105**: 880-900.

Wu, M.-Y., **M. E. Mead**, S.-C. Kim, **A. Rokas** & J.-H. Yu. *WetA* bridges cellular and chemical development in *Aspergillus flavus*. *PLoS ONE* **12**: e0179571.

Zhao, L., **X. Zhou, A. Rokas** & R. D. Cone (2017). Functional variants of the melanocortin-4 receptor associated with the Odontoceti and Mysticeti suborders of cetaceans. *Sci. Rep.* **7**: 5684.

Fidler, A. L., C. E. Darris, S. V. Chetyrkin, V. K. Pedchenko, S. P. Boudko, K. L. Brown, W. G. Jerome, J. K. Hudson, **A. Rokas** & B. G. Hudson. Collagen IV and basement membrane at the evolutionary dawn of metazoan tissues. *eLife* **6**: e24176.

Wisecaver, J. H., A. T. Borowsky, V. Tzin, G. Jander, D. J. Kliebenstein & **A. Rokas**. A global co-expression network approach for connecting genes to specialized metabolic pathways in plants. *The Plant Cell* **29**: 944–959.

Shen, X.-X., C. T. Hittinger & **A. Rokas**. Contentious relationships in phylogenomic studies can be driven by a handful of genes. *Nature Ecol. Evol.* **1**: 0126.

- Steenwyk, J. & A. Rokas.** Extensive copy number variation in fermentation-related genes among *Saccharomyces cerevisiae* wine strains. *G3* **7**: 1475-1485.
- Ortiz, J. F. & A. Rokas.** CTDGFinder: A novel homology-based algorithm for identifying closely spaced clusters of tandemly duplicated genes. *Mol. Biol. Evol.* **34**: 215-229.
- 2016 Lind, A. L., T. Satterlee, T. D. Smith, A. M. Calvo, & A. Rokas.** Regulation of secondary metabolism by the Velvet complex is temperature-responsive in *Aspergillus*. *G3* **6**: 4023-4033.
- Shen, X.-X., X. Zhou, J. Kominek, C. P. Kurtzman, C. T. Hittinger & A. Rokas.** Reconstructing the backbone of the Saccharomycotina yeast phylogeny using genome-scale data. *G3* **6**: 3927-3939.
- Zhou, X., D. Peris, C. T. Hittinger & A. Rokas.** *in silico* Whole Genome Sequencer & Analyzer (iWGS): a computational pipeline to guide the design and analysis of *de novo* genome sequencing studies. *G3* **6**: 3655-3662.
- Shen, X.-X., L. Salichos & A. Rokas.** A genome-scale investigation of how sequence-, function-, and tree-based gene properties influence phylogenetic inference. *Genome Biol. Evol.* **8**: 2565-2580.
- Riley, R., S. Haridas, K. H. Wolfe, M. R. Lopes, C. T. Hittinger, M. Göker, A. Salamov, **J. H. Wisecaver**, T. M. Long, C. H. Calvey, A. L. Aerts, K. Barry, C. Choi, A. Clum, A. Y. Coughlan, S. Deshpande, A. P. Douglass, S. J. Hanson, H.-P. Klenk, K. LaButti, A. Lapidus, E. Lindquist, A. Lipzen, J. P. Meier-Kolthoff, R. A. Ohm, R. P. O'Neill, J. Pangilinan, Y. Peng, **A. Rokas**, C. A. Rosa, C. Scheuner, A. A. Sibirny, J. C. Slot, J. B. Stielow, H. Sun, C. P. Kurtzman, M. Blackwell, I. V. Grigoriev & T. W. Jeffries. Comparative genomics of biotechnologically important yeasts. *Proc. Natl. Acad. Sci. USA* **113**: 9882-9887.
- Ackerman IV, W. E., I. A. Buhimschi, **H. R. Eidem, D. C. Rinker, A. Rokas**, K. Rood, G. Zhao, T. L. Summerfield, M. B. Landon & C. S. Buhimschi. Comprehensive RNA profiling of villous trophoblast and decidua basalis in pregnancies complicated by preterm birth following intra-amniotic infection. *Placenta* **44**: 23-33.
- Wisecaver, J. H., W. G. Alexander, S. B. King, C. T. Hittinger & A. Rokas.** Dynamic evolution of nitric oxide detoxifying flavohemoglobins, a family of single-protein metabolic modules in bacteria and eukaryotes. *Mol. Biol. Evol.* **33**: 1979-1987.
- Eidem, H. R., D. C. Rinker, W. E. Ackerman IV, I. A. Buhimschi, C. S. Buhimschi, C. Dunn-Fletcher, S. G. Kallapur, M. Pavlicev, L. J. Muglia, P. Abbot & A. Rokas.** Comparing human and macaque placental transcriptomes to disentangle preterm birth pathology from gestational age effects. *Placenta* **41**: 74-82.
- Alexander, W. G., **J. H. Wisecaver, A. Rokas** & C. T. Hittinger. Horizontally acquired genes in early-diverging pathogenic fungi enable the use of host nucleosides and nucleotides. *Proc. Natl. Acad. Sci. USA* **113**: 4116-4121.
- Kobert, K., **L. Salichos, A. Rokas**, & A. Stamatakis. Computing the Internode Certainty and related measures from partial gene trees. *Mol. Biol. Evol.* **33**: 1606-1617.
- Staehlin, B. M., **J. G. Gibbons, A. Rokas**, T. V. O'Halloran, & **J. C. Slot**. Evolution of a heavy metal homeostasis/resistance island reflects increasing copper stress in Enterobacteria. *Genome Biol. Evol.* **8**: 811-826.

Kim, M., B. A. Cooper, R. Venkat, J. B. Phillips, H. R. Eidem, J. Hirbo, S. Nutakki, S. M. Williams, L. J. Muglia, J. A. Capra, K. Petren, P. Abbot, A. Rokas, & K. L. McGary. GENEstation 1.0: a synthetic resource of diverse evolutionary and functional genomic data for studying the evolution of pregnancy-associated tissues and phenotypes. *Nucleic Acids Res.* **44**, Database issue: D908-916.

2015 Wang, Y., X. Zhou, D. Yang, & A. Rokas. A genome-scale investigation of incongruence in Culicidae mosquitoes. *Genome Biol. Evol.* **7**: 3463-3471.

Hirbo, J., H. R. Eidem, A. Rokas, & P. Abbot. Integrating diverse types of genomic data to identify genes that underlie adverse pregnancy phenotypes. *PLoS ONE* **10**: e0144155.

Hittinger, C. T., A. Rokas, F.-Y. Bai, T. Boekhout, P. Gonçalves, T. W. Jeffries, J. Kominek, M.-A. Lachance, D. Libkind, C. A. Rosa, J. P. Sampaio, & C. P. Kurtzman. Genomics and the making of yeast biodiversity. *Curr. Opin. Genet. Dev.* **35**: 100–109.

Zhou, X., A. Rokas, S. L. Berger, J. Liebig, A. Ray & L. J. Zwiebel. Chemoreceptor evolution in Hymenoptera and its implications for the evolution of eusociality. *Genome Biol. Evol.* **7**: 2407-2416.

Phillips, J. B., P. Abbot & A. Rokas. Is preterm birth a human-specific syndrome? *Evol. Med. Public Health* **2015**: 136-148.

Eidem, H. R., W. E. Ackerman IV, K. L. McGary, P. Abbot, & A. Rokas. Gestational tissue transcriptomics in term and preterm human pregnancies: A systematic review and meta-analysis. *BMC Med. Genomics* **8**: 27.

Lind, A. L., J. H. Wisecaver, T. D. Smith, X. Feng, A. M. Calvo, & A. Rokas. Examining the evolution of the regulatory circuit controlling secondary metabolism and development in the fungal genus *Aspergillus*. *PLoS Genet.* **11**: e1005096.

Eidem, H. R.* , K. L. McGary*, & A. Rokas. Shared selective pressures on fungal and human metabolic pathways lead to divergent yet analogous genetic responses. (*Equal contributors) *Mol. Biol. Evol.* **32**: 1449–1455.

Wisecaver, J. H. & A. Rokas. Fungal metabolic gene clusters – caravans traveling across genomes and environments. *Front. Microbiol.* **6**: 161.

Elmore, M. H.* , K. L. McGary*, J. H. Wisecaver, J. C. Slot, D. M. Geiser, S. Sink, K. O'Donnell, & A. Rokas. Clustering of two genes putatively involved in cyanate detoxification evolved recently and independently in multiple fungal lineages. (*Equal contributors) *Genome Biol. Evol.* **7**: 789-800.

Neafsey, D. E., R. M. Waterhouse, 117 other authors including **X. Zhou, D. C. Rinker, A. Rokas** and L. J. Zwiebel, & N. J. Besansky. Highly evolvable malaria vectors: the genomes of 16 *Anopheles* mosquitoes. *Science* **347**: 43.

2014 Wisecaver, J. H.* , J. C. Slot* & A. Rokas. The evolution of fungal metabolic pathways. (*Equal contributors) *PLoS Genet.* **10**: e1004816.

Zhou, X.* , D. C. Rinker*, R. J. Pitts, A. Rokas & L. J. Zwiebel. Divergent and conserved elements comprise the chemoreceptive repertoire of the non-blood feeding mosquito *Toxorhynchites amboinensis*. (*Equal contributors) *Genome Biol. Evol.* **6**: 2883-2896.

Polzin, K. & A. Rokas. Evaluating rare amino acid substitutions (RGC_CAMs) in a yeast model clade. *PLoS ONE* **9**: e92213.

- Salichos, L., A. Stamatakis, & A. Rokas.** Novel information theory-based measures for quantifying incongruence among phylogenetic trees. *Mol. Biol. Evol.* **31**: 1261-1271.
- Zhou, X. & A. Rokas.** Prevention, diagnosis, and treatment of high throughput sequencing data pathologies. *Mol. Ecol.* **23**: 1679-1700.
- Soria, P. S.*, K. L. McGary*, & A. Rokas.** Functional divergence for every paralog. (*Equal contributors) *Mol. Biol. Evol.* **31**: 984-992.
- Greene, G. H., K. L. McGary, A. Rokas, & J. C. Slot.** Ecology drives the distribution of specialized tyrosine metabolism modules in fungi. *Genome Biol. Evol.* **6**: 121-132.
- 2013** Samuels, D. C., C. Li, B. Li, Z. Song, E. Torstenson, H. B. Clay, **A. Rokas**, T. Thornton-Wells, J. H. Moore, T. Hughes, R. Hoffman, J. L. Haines, D. G. Murdock, D. P. Mortlock & S. M. Williams. Recurrent tissue-specific mtDNA mutations are common in humans. *PLoS Genetics* **9**: e1003929.
- Rinker, D. C.*, X. Zhou***, R. J. Pitts, The AGC Consortium, **A. Rokas**, & L. J. Zwiebel. Antennal transcriptome profiles of anopheline mosquitoes reveal human host olfactory specialization in *Anopheles gambiae*. (*Equal contributors) *BMC Genomics* **14**: 749.
- Dhingra, S., **A. L. Lind**, H-C. Lin, Y. Tang, **A. Rokas** & A. M. Calvo. The fumagillin gene cluster, an example of hundreds of genes under veA control in *Aspergillus fumigatus*. *PLoS ONE* **8**: e77147.
- Campbell, M. A., M. Staats, J. L. A. van Kan, A. Rokas, & J. C. Slot.** Repeated loss of an anciently horizontally transferred gene cluster in *Botrytis*. *Mycologia* **105**: 1126–1134.
- McGary, K. L., J. C. Slot & A. Rokas.** The physical linkage of metabolic genes in fungi is an adaptation against the accumulation of toxic intermediate compounds. *Proc. Natl. Acad. Sci. USA* **110**: 11481-11486.
- Salichos, L. & A. Rokas.** Accurately inferring ancient divergences requires genes with strong phylogenetic signal. *Nature* **497**: 327-331.
- Predazzi, I. M., **A. Rokas**, A. Deinard, N. Schnetz-Boutaud, N. D. Williams, W. S. Bush, A. Tacconelli, K. Friedrich, S. Fazio, G. Novelli, J. L. Haines, G. Sirugo & S. M. Williams. Putting pleiotropy and selection into context defines a new paradigm for interpreting genetic data. *Circ. Cardiovasc. Genet.* **6**: 299-307.
- Rinker, D. C., R. J. Pitts, X. Zhou, E. Suh, A. Rokas & L. J. Zwiebel.** Blood meal-induced changes to antennal transcriptome profiles reveal shifts in odor sensitivities in the malaria vector mosquito *Anopheles gambiae*. *Proc. Natl. Acad. Sci. USA* **110**: 8260-8265.
- Bradshaw, R. E., **J. C. Slot**, G. G. Moore, P. Chettri, P. J. G. M. de Wit, K. C. Ehrlich, A. R. D. Ganley, M. A. Olson, **A. Rokas**, I. Carbone & M. P. Cox. Fragmentation of an aflatoxin-like gene cluster in a forest pathogen. *New Phytol.* **198**: 525–535.
- Xu, Y., P. Ma, P. Shah, **A. Rokas**, Y. Liu & C. H. Johnson. Non-optimal codon usage is a post-transcriptional mechanism to achieve conditionality of circadian clock function. *Nature* **495**: 116-120.
- Adhikary, S., M. C. Cato, **K. L. McGary, A. Rokas** & B. F. Eichman. Non-productive DNA damage binding by DNA glycosylase-like protein Mag2 from *Schizosaccharomyces pombe*. *DNA Repair* **12**: 196-204.

Muszkieta, L., A. Beauvais, V. Pähzt, **J. G. Gibbons**, V. A. Leberre, R. Beau, K. Shibuya, **A. Rokas**, J. M. Francois, O. Kniemeyer, A. A. Brakhage & J. P. Latge. Investigation of *Aspergillus fumigatus* biofilm formation by various “omics” approaches. *Front. Microbiol.* **4**: 13.

Ubaida Mohien, C., D. R. Colquhoun, D. K. Mathias, **J. G. Gibbons**, J. S. Armistead, M. del Carmen-Rodriguez, M. H. Rodriguez, N. J. Edwards, J. Hartler, G. G. Thallinger, D. R. Graham, J. Martinez-Barnetche, **A. Rokas**, & R. R. Dinglasan. A bioinformatics approach for integrated transcriptomic and proteomic comparative analyses of model and non-sequenced anopheline vectors of human malaria parasites. *Mol. Cell. Proteomics* **12**: 120-131.

Gibbons, J. G. & A. Rokas. The function and evolution of the *Aspergillus* genome. *Trends Microbiol.* **21**: 14-22.

2012 Elmore, M. H.* , J. G. Gibbons* & A. Rokas. Assessing the genome-wide effect of promoter region tandem repeat natural variation on gene expression. (*Equal contributors) *G3* **2**: 1643-1649.

Rokas, A., J. G. Gibbons, X. Zhou, A. Beauvais & J. P. Latge. The diverse applications of RNA-Seq for functional genomics studies in *Aspergillus fumigatus*. *Ann. N.Y. Acad. Sci.* **1273**: 25-34.

Zhou, X.* , J. D. Slone*, A. Rokas, S. L. Berger, J. Liebig, A. Ray, D. Reinberg & L. J. Zwiebel. Phylogenetic and transcriptomic analysis of chemosensory receptors in a pair of divergent ant species reveals sex-specific signatures of odor coding. (*Equal contributors) *PLoS Genet.* **8**: e1002930.

League, G. P., J. C. Slot & A. Rokas. The ASP3 locus in *Saccharomyces cerevisiae* originated by horizontal gene transfer from *Wickerhamomyces*. *FEMS Yeast Res.* **12**: 859-863.

Zhang, H., A. Rokas & J. C. Slot. Two different secondary metabolism gene clusters occupied the same ancestral locus in fungal dermatophytes of the Arthrodermataceae. *PLoS ONE* **7**: e41903.

Gibbons, J. G., L. Salichos, J. C. Slot, D. C. Rinker, K. L. McGary, J. G. King, M. A. Klich, D. L. Tabb, W. H. McDonald & **A. Rokas**. The evolutionary imprint of domestication on microbe genome variation and function. *Curr. Biol.* **22**: 1403-1409.

Stergiopoulos, I., Y. A. I. Kourmpetis, J. C. Slot, F. T. Bakker, P. J. G. M. De Wit & **A. Rokas**. *In silico* characterization and molecular evolutionary analysis of a novel superfamily of fungal effector proteins. *Mol. Biol. Evol.* **29**: 3371-3384.

Floudas, D., M. Binder, 68 other authors including **A. Rokas** and **J. C. Slot** & D. S. Hibbett. The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. *Science* **336**: 1715-1719.

Martinez-Barnetche, J., R. E. Gómez-Barreto, M. Ovilla-Muñoz, J. Téllez-Sosa, D. E. García-López, R. R. Dinglasan, C. Ubaida Mohien, R. M. MacCallum, S. N. Redmond, **J. G. Gibbons**, **A. Rokas**, C. M. Machado, F. Cazares-Raga, L. González-Cerón, S. Hernández-Martínez & M. H. Rodríguez-Lopez. Transcriptome of the adult female malaria mosquito vector *Anopheles albimanus*. *BMC Genomics* **13**: 207.

Wei, C., **L. Salichos**, C. M. Wittgrove, **A. Rokas** & J. G. Patton. Transcriptome-wide analysis of small RNA expression in early zebrafish development. *RNA* **18**: 915-929.

- Campbell, M. A., A. Rokas & J. C. Slot.** Horizontal transfer and death of a fungal secondary metabolic gene cluster. *Genome Biol. Evol.* **4**: 289-293.
- Gibbons, J. G., A. Beauvais, R. Beau, K. L. McGary, J.-P. Latge & A. Rokas.** Global transcriptome changes underlying colony growth in the opportunistic human pathogen *Aspergillus fumigatus*. *Euk. Cell* **11**: 68-78.
- Klaassen, C. H. W.* **J. G. Gibbons***, N. D. Fedorova, J. F. Meis & **A. Rokas**. Evidence for genetic differentiation and variable recombination rates among Dutch populations of the opportunistic human pathogen *Aspergillus fumigatus*. (*Equal contributors) *Mol. Ecol.* **21**: 57-70.
- 2011 Rokas, A.** Phylogenetic analysis of protein sequence data using the Randomized Axelerated Maximum Likelihood (RAxML) program. *Curr. Prot. Mol. Biol.*: **96**: 19.11.1-19.11.14.
- Pitts, R. J.* **D. C Rinker***, P. L. Jones*, **A. Rokas** & L. J. Zwiebel. Transcriptome profiling of chemosensory appendages in the malaria vector *Anopheles gambiae* reveals tissue- and sex-specific signatures of odor coding. (*Equal contributors) *BMC Genomics*: **12**: 271.
- Zill, O. A., D. R. Scannell, **A. Rokas**, C. Payen, M. J. Dunham, M. B. Eisen, J. Rine, M. Johnston & C. T. Hittinger. The awesome power of yeast evolutionary genetics: New genome sequences and strain resources for the *Saccharomyces sensu stricto* genus. *G3* **1**: 11-25.
- Salichos, L. & A. Rokas.** Evaluating ortholog prediction algorithms in a yeast model clade. *PLoS One* **6**: e18755.
- Kent, B. N., **L. Salichos, J. G. Gibbons, A. Rokas**, I. L.G. Newton, M. E. Clark & S. R. Bordenstein. Complete Bacteriophage Transfer in a Bacterial Endosymbiont (*Wolbachia*) Determined by Targeted Genome Capture. *Genome Biol. Evol.* **3**: 209-218.
- Slot, J. C. & A. Rokas.** Horizontal transfer of a large and highly toxic secondary metabolic gene cluster between fungi. *Curr. Biol.* **21**: 134-139.
- 2010 Carnahan, R. H.***, **A. Rokas***, E. A. Gaucher & A. B. Reynolds. The molecular evolution of the p120-catenin subfamily and its functional associations. (*Equal contributors) *PLoS One* **5**: e15747.
- Slot, J. C. & A. Rokas.** Multiple *GAL* pathway gene clusters evolved independently and by different mechanisms in fungi. *Proc. Natl. Acad. Sci. USA* **107**: 10136-10141.
- Hittinger, C. T., P. Gonçalves, J. P. Sampaio, J. Dover, M. Johnston & **A. Rokas**. Remarkably ancient balanced polymorphisms in a multi-locus gene network. *Nature*: **464**: 54-58.
- Salichos, L. & A. Rokas.** The diversity and evolution of circadian clock proteins in fungi. *Mycologia* **102**: 269-278.
- Gibbons, J. G., M. A. Klich & A. Rokas.** Developing highly conserved microsatellite markers: a case study in the filamentous fungal genus *Aspergillus*. *Mol. Ecol. Resources* **10**: 404-408.

Hittinger, C. T., M. Johnston, **J. T. Tossberg & A. Rokas**. Leveraging skewed transcript abundance by RNA-Seq to increase the genomic depth of the tree of life. *Proc. Natl. Acad. Sci. USA* **107**: 1476-1481.

- 2009 Gibbons, J. G.**, E. Janson, C. T. Hittinger, M. Johnston, P. Abbot & **A. Rokas**. Benchmarking next-generation transcriptome sequencing for functional and evolutionary genomics. *Mol. Biol. Evol.* **26**: 2731-2744.
- Rokas, A.** & P. Abbot. Harnessing genomics for evolutionary insights. *Trends Ecol. Evol.* **24**: 192-200.
- Gibbons, J. G. & A. Rokas**. Comparative and functional characterization of intragenic tandem repeats in ten *Aspergillus* genomes. *Mol. Biol. Evol.* **26**: 591-602.
- Rokas, A.** The effect of domestication on the fungal proteome. *Trends Genet.* **25**: 60-63.
- 2008 Rokas, A.** The origins of multicellularity and the early history of the genetic toolkit for animal development. *Ann. Rev. Genet.* **42**: 235-251.
- Rokas, A.** The molecular origins of multicellular transitions. *Curr. Opin. Genet. Dev.* **18**: 472-478.
- Rokas, A.**, & S. B. Carroll. Frequent and widespread parallel evolution of protein sequences. *Mol. Biol. Evol.* **25**: 1943-1953.
- Mathee, K. et al. (19 co-authors, including **A. Rokas**). Dynamics of *Pseudomonas aeruginosa* genome evolution. *Proc. Natl. Acad. Sci. USA* **105**: 3100-3105.
- King, N. et al. (34 co-authors, including **A. Rokas** and JGI Sequencing). The genome of the choanoflagellate *Monosiga brevicollis* and the origins of metazoan multicellularity. *Nature* **451**: 783-788.
- Stone, G. N., R. J. Atkinson, **A. Rokas**, J.-L. Nieves-Aldrey, G. Melika, Z. Acs, G. Csóka, A. Hayward, R. Bailey, C. Buckee & G. A. T. McVean. Evidence for widespread cryptic sexual generations in apparently purely asexual *Andricus* gallwasps. *Mol. Ecol.* **17**: 652-665.
- 2007 Rokas, A.** et al. (15 co-authors). What can comparative genomics tell us about species concepts in the genus *Aspergillus*? *Studies in Mycology* **59**: 11-17.
- Stone, G. N., R. J. Challis, R. J. Atkinson, G. Csóka, A. Hayward, G. Melika, S. Mutun, S. Preuss, **A. Rokas**, E. Sadeghi, & K. Schönrogge. The phylogeographic clade trade: Tracing the impact of human-mediated dispersal on the colonisation of northern Europe by the oak gallwasp *Andricus kollaris*. *Mol. Ecol.* **16**: 2768-2781.
- Stone, G. N., R. J. Challis, S. Mutun, J.-L. Nieves-Aldrey, S. Preuss, **A. Rokas**, A. Aebi, E. Sadeghi, & M. Tavakoli. Longitudinal range expansion and cryptic eastern species in the western Palaearctic oak gallwasp *Andricus coriarius*. *Mol. Ecol.* **16**: 2103-2114.
- Ane, C., B. Larget, D. A. Baum, S. D. Smith, & **A. Rokas**. Bayesian estimation of concordance among trees. *Mol. Biol. Evol.* **24**: 412-426.
- 2006 Rokas, A.** & Carroll, S. B. Bushes in the Tree of Life. *PLOS Biol.* **11**: e352.
- Jeong, S., **A. Rokas** & S. B. Carroll. Regulation of body pigmentation by the Abdominal-B Hox protein and its gain and loss in *Drosophila* evolution. *Cell* **125**: 1387-1399.

Prud'homme, B., N. Gompel, **A. Rokas**, V. A. Kassner, T. M. Williams, S.-D. Yeh, J. R. True & S. B. Carroll. Repeated morphological evolution through cis-regulatory changes in a pleiotropic gene. *Nature* **440**: 1050-1053.

2005 **Rokas, A.**, D. Krueger & S. B. Carroll. Animal evolution and the molecular signature of radiations compressed in time. *Science* **310**: 1933-1938.

Rokas, A. & S. B. Carroll. More genes or more taxa? The relative contribution of gene number and taxon number to phylogenetic accuracy. *Mol. Biol. Evol.* **22**: 1337-1344.

2004 Hittinger, C. T., **A. Rokas** & S. B. Carroll. Parallel inactivation of multiple *GAL* pathway genes and ecological diversification in yeasts. *Proc. Natl. Acad. Sci. USA* **101**: 14144-14149.

2003 **Rokas, A.***, B. L. Williams*, N. King & S. B. Carroll. Genome-scale approaches to resolving incongruence in molecular phylogenies. (*Equal contributors) *Nature* **425**: 798-804.

Rokas, A., E. Ladoukakis, & E. Zouros. Animal mitochondrial DNA recombination revisited. *Trends Ecol. Evol.* **18**: 411-417.

Rokas, A., R. J. Atkinson, L. W. I. Webster & G. N. Stone. Out of Anatolia: Longitudinal gradients in genetic diversity support a Turkish origin for a circum-Mediterranean oak gallwasp *Andricus quercustozae*. *Mol. Ecol.* **12**: 2153-2174.

Cummings, M. P., S. A. Handley, D. S. Myers, D. L. Reed, **A. Rokas** & K. Winka. Comparing bootstrap and posterior probability values in the four-taxon case. *Syst. Biol.* **52**: 477-487.

Rokas, A.*, N. King*, J. R. Finnerty & S. B. Carroll. Conflicting phylogenetic signals at the base of the metazoan tree. (*Equal contributors) *Evol. Devel.* **5**: 346-359.

Rokas, A., G. Melika, Y. Abe, J.-L. Nieves-Aldrey, J. M. Cook & G. N. Stone. Lifecycle closure, lineage sorting, and hybridization revealed in a phylogenetic analysis of European oak gallwasps (Hymenoptera: Cynipidae: Cynipini) using mitochondrial sequence data. *Mol. Phylog. Evol.* **26**: 36-45.

2002 Cook, J. M., **A. Rokas**, M. Pagel & G. N. Stone. Evolutionary shifts between host oak species and host plant organs in *Andricus* gallwasps. *Evolution* **56**: 1821-1830.

Stone, G. N., R. J. Atkinson, G. Brown, & **A. Rokas**. The population genetic consequences of range expansion: a review of pattern and process, and the value of oak gallwasps as a model system. *Biodiversity Science*, 10: 80-97.

Rokas, A., R. J. Atkinson, J.-L. Nieves-Aldrey, S. A. West & G. N. Stone. The incidence and diversity of *Wolbachia* in gallwasps (Hymenoptera; Cynipidae) on oak. *Mol. Ecol.* **11**: 1815-1829.

Rokas, A., J. A. A. Nylander, F. Ronquist & G. N. Stone. A maximum likelihood analysis of eight phylogenetic markers in gallwasps (Hymenoptera: Cynipidae); implications for insect phylogenetic studies. *Mol. Phylog. Evol.* **22**: 206-219.

2001 **Rokas, A.**, R. J. Atkinson, G. S. Brown, S. A. West & G. N. Stone. Understanding patterns of genetic variation in the oak gallwasp *Biorhiza pallida*: demographic history or a *Wolbachia* selective sweep? *Heredity* **87**: 294-304.

Stone, G. N., R. J. Atkinson, **A. Rokas**, G. Csóka & J.- L. Nieves-Aldrey. Differential success in northwards range expansion between ecotypes of the marble gallwasp *Andricus kollari*: a tale of two refugia. *Mol. Ecol.* **10**: 761-778.

- 2000** **Rokas, A.** & P. W. H. Holland. Rare genomic changes as a tool for phylogenetics. *Trends Ecol. Evol.* **15**: 454-459.

Averof, M., **A. Rokas**, K. H. Wolfe & P. M. Sharp. Evidence for a high frequency of simultaneous double-nucleotide substitutions. *Science* **287**: 1283-1286.

- 1999** **Rokas, A.**, J. Kathirithamby & P. W. H. Holland. Intron insertion as a phylogenetic character: the *engrailed* homeobox of Strepsiptera does not indicate affinity with Diptera. *Insect Mol. Biol.* **8**: 527-530.

BOOK CHAPTERS

- 2018** Abbot, P., **H. R. Eidem, & A. Rokas** (2018). Preterm birth. In “Encyclopedia of Evolutionary Psychological Science”, Shackelford T. & V. Weekes-Shackelford (Eds.), Springer, Cham.
- 2016** **Rokas, A.** Systematics in the age of genomics. In “Next Generation Systematics”, P. D. Olson, J. Hughes, & J. A. Cotton (Eds.), Cambridge University Press, pp. 219-228.
- 2008** **Rokas, A.** & S. Chatzimanolis. From gene-scale to genome-scale phylogenetics; the data flood in but the challenges remain. In “Phylogenomics” W. J. Murphy (Ed.), Methods in Molecular Biology series, Humana Press, Totowa, NJ, pp. 1-12.
- Geiser, D. M., R. A. Samson, J. Varga, **A. Rokas** and S. M. Witiak. A review of molecular phylogenetics in *Aspergillus*, and prospects for a robust genus-wide phylogeny. In “*Aspergillus* in the Genomics Era”, Varga, J., and R. A. Sampson (Eds.), Wageningen Academic Publishers, pp. 17-32.
- Rokas, A.** & J. E. Galagan. The *Aspergillus nidulans* genome and comparative analysis with other Aspergilli. In “The Aspergilli: Genomics, Medical Applications, Biotechnology, and Research Methods”, Osmani, S. A. and G. H. Goldman, CRC Press, pp. 43-55.
- 2006** Atkinson, R. J., **A. Rokas** & G. N. Stone. Longitudinal patterns in species richness and genetic diversity in European oaks and oak gallwasps. In: “Phylogeography in southern European refugia: Evolutionary Perspectives on the origins and conservation of European Biodiversity”, S. Weiss, N. Ferrand (Eds). Kluwer, The Netherlands.
- 2003** Stone, G. N., R. J. Atkinson, G. Brown, **A. Rokas** & G. Csóka. The population genetic consequences of range expansion: oak gallwasps as a model system. In: “Genes in the Environment”, R. S. Hails, J. E. Beringer and H. C. J. Godfray (Eds), Blackwell and the British Ecological Society, pp. 46-62.

SELECT RECENT COMMENTARIES

- 2018** Riquelme, M., M. C. Aime, S. Branco, A. Brand, A. Brown, L. N. Glass, R. Kahmann, M. Momany, **A. Rokas** & F. Trail. The power of discussion: support for women at the fungal Gordon Research Conference. *Fungal Genet. Biol.* **121**: 65-67.
- 2017** Shropshire, J. D. & **A. Rokas**. The gene family that cheats Mendel. *eLife* **6**: e28567.
- Abbot, P. & **A. Rokas**. Mammalian pregnancy. *Curr. Biol.* **27**: R127-R128.
- 2013** **Rokas, A.** My oldest sister is a sea walnut? *Science* **342**: 1327-1329.

Rokas, A. *Aspergillus. Curr. Biol.* **23**: R187-R188.

INVITED TALKS

- 2021** Guest Lecturer, St. Jude Graduate School of Biomedical Sciences (online)
Guest Lecturer, Mycology course in Swedish Agricultural University (online)
Invited Speaker, Microbial Resource Research Infrastructure (MIRRI) Consortium webinar (online)
March of Dimes Prematurity Research Centers Annual Symposium (online)
Invited Speaker, Organisms and Evolution Seminar Series, Department of Biology, Duke University, Durham, NC (online)
Invited Speaker, American Phytopathology Society, Denver, CO (online)
Invited Speaker, 2021 Women's Health Research Symposium, Vanderbilt Genetics Institute, Nashville, TN (online)
Centro de Investigación Científica y de Educación Superior de Ensenada CICESE, Baja California, México (online)
Stowers Institute for Medical Research, Kansas City, MO (online)
- 2020** Invited Panelist, ASAPBio: Accelerating Science and Publication in Biology Virtual Conversation on “The past, the present and the future of preprints” (online)
Invited Speaker, Seminar Series to Celebrate 50 Years from the Foundation of the Biology Department of the National Kapodistrian University of Athens, Greece (cancelled due to COVID-19)
Invited Speaker, Molecular Mechanisms in Evolution and Ecology EMBL Virtual Conference
Invited Panelist, Club EvMed — Virtual Evolutionary Medicine Conversations
Invited Speaker, American Phytopathology Society, Denver, CO (cancelled due to COVID-19)
Invited Speaker, Cellular and Molecular Fungal Biology Gordon Research Conference, Holderness, NH (cancelled due to COVID-19)
Mushroom Club of Georgia, Athens, GA (online)
South Carolina Upstate Mycological Society, Greenville, SC (online)
Plenary Speaker, 15TH European Conference on Fungal Genetics, Rome, Italy
Darwin Day Speaker, Cumberland University, Lebanon, TN
- 2019** Invited Speaker, 12th International Bioinformatics conference, Crete, Greece
Department of Plant and Microbial Biology, University of Minnesota, MN
Department of Botany and Plant Pathology, Purdue University, IN
Invited Speaker, “Fungal threats to animal, plant and ecosystem health” Symposium, Ribeirão Preto, São Paulo, Brazil
LifeMine Company, Cambridge, MA
PostDoc-Invited Seminar Speaker, University of Florida Whitney Lab, FL
Genetics/Genomics seminar series, North Carolina State University, NC
HudsonAlpha, Huntsville, AL
- 2018** Wellcome Sanger Institute, UK
University of Lausanne, Switzerland
University College London, UK
Keynote Speaker, 34th International Specialized Symposium on Yeasts, Cletus Kurtzman's Workshop on Taxonomy and Systematics of Yeasts, Bariloche, Argentina
Keynote Speaker, Auburn University Bioinformatics Bootcamp 2018, Auburn, AL
March of Dimes Prematurity Research Centers Annual Symposium, San Diego, CA

Invited Speaker, "Advances and Retreats in Molecular Evolution" Workshop, Nanyang Technological University, Singapore

- 2017** Keynote Speaker, iGenolevures Meeting on "The Future of Yeast Genomics", Paris, France
Invited Speaker, XIII International Meeting on Paracoccidioidomycosis 2017, Iguassu Falls, Brazil
Invited Speaker, no 29º Congresso Brasileiro de Microbiologia 2017, Iguassu Falls, Brazil
Department of Pathology, Microbiology, and Immunology, Vanderbilt University, Nashville, TN
Bridging Speaker, International Congress of Mycology and Eukaryotic Microbiology, Singapore
Heidelberg Institute for Theoretical Studies, Heidelberg, Germany
Plenary Speaker, 7th Advanced Lecture Course on Human Fungal Pathogens, Nice, France
Invited Speaker, Society for Reproductive Investigation Annual Meeting, Orlando, FL
March of Dimes Prematurity Research Centers Annual Symposium, Orlando, FL
- 2016** Plenary Speaker, Burroughs Wellcome-Fund/March of Dimes Biennial Preterm Birth Symposium, Research Triangle Park, NC
Graduate Student-Invited Speaker, Department of Organismal Biology, Uppsala University, Uppsala, Sweden
Distinguished Lectures in Microbiology, Department of Bacteriology, University of Wisconsin-Madison, WI
Division of Biological Sciences, University of Missouri, MO
Dimensions of Fungal Biodiversity Symposium, Mycological Society of America Meeting, Berkeley, CA
Department of Biology, Middle Tennessee State University, Murfreesboro, TN
March of Dimes Prematurity Research Centers Annual Symposium, Montreal, Canada
Department of Chemistry & Biochemistry, University of North Carolina Greensboro, Greensboro, NC
Plenary Speaker, "Evolution, of Cells, Genomes and Proteins" Workshop, Nanyang Technological University, Singapore
- 2015** Plenary Speaker, Society of Systematic Biologists Standalone Meeting, Ann Arbor, MI
Plenary Speaker, "Phylogeny meets genomics" workshop, Center for Advanced Studies (CAS), Ludwig-Maximilians-University, Munich, Germany
Plenary Speaker, "Genomes to Secondary Metabolites", GSC-17 Satellite Workshop, DOE Joint Genome Institute, Walnut Creek, CA
Plenary Speaker, "Genomics of Energy and the Environment" meeting, DOE Joint Genome Institute, Walnut Creek, CA
March of Dimes Prematurity Research Centers Annual Symposium, San Francisco, CA
- 2014** Plenary Speaker, Comparative and Functional Genomics of Fungal Pathogens, Current Trends in Biomedicine Series, International University of Andalusia, Baeza, Spain
Evolution Seminar Series, University of Wisconsin-Madison, WI
Department of Genetics, University of Wisconsin-Madison, WI
Center for Bioinformatics Research, Indiana University, IN
Session Chair and Discussion Leader, Cellular and Molecular Fungal Biology Gordon Research Conference, Holderness, NH
Plenary Speaker, XVI International Congress on Molecular Plant-Microbe Interactions, Rhodes, Greece

Plenary Speaker, Protein Structure and Protein Evolution Symposium, Royal Swedish Academy of Sciences
Organismic and Evolutionary Biology Seminar Series, Univ. Massachusetts–Amherst, MA
Plenary Speaker, 12th European Conference on Fungal Genetics, Seville, Spain

- 2013** Department of Plant Pathology, North Carolina State University, Raleigh, NC
American Museum of Natural History, New York, NY
Department of Plant Pathology, ETH Zurich, Switzerland
European Bioinformatics Institute, Hinxton, UK
Plenary Speaker, Italian Zoological Association Spring School on “Metazoan Phylogeny and Evolution”, Venice, Italy
Plenary Speaker, 27TH Fungal Genetics Meeting, Asilomar, CA
Plenary Speaker, 10TH International *Aspergillus* Meeting, Asilomar, CA
Cornell Center for Comparative and Population Genomics, Cornell University, NY
Department of Ecology and Evolutionary Biology, Yale University, CT

2007 – 2012 (Invited talks as Assistant Professor)

- (2012) Department of Genetics, University of Georgia, GA
(2012) Plenary Speaker, The 13th Annual Vanderbilt Genetics Symposium on “Evolution and the Genetic Basis for Human Disease”, Vanderbilt University, TN
(2012) Plenary Speaker, Graduate Research School in Genomic Ecology Summer Meeting, Lund, Sweden
(2012) Plenary Speaker, Cellular and Molecular Fungal Biology Gordon Research Conference, Holderness, NH
(2012) Plenary Speaker, HHMI Bioinformatics Workshop for Student-Scientist Partnerships, Chevy Chase, MD
(2012) Institute for Molecular Biology and Biotechnology, University of Crete, Greece
(2012) Plenary Speaker, 5TH Advances Against Aspergillosis Meeting, Istanbul, Turkey
(2012) Department of Biological Sciences, University of Alabama, AL
(2011) Department of Entomology, University of Maryland, MD
(2011) Department of Biological Science, University of Pittsburgh, PA
(2011) Plenary Speaker, Smithsonian Initiative in Biodiversity Genomics Lectures, Washington, DC
(2011) Plenary Speaker, 26TH Fungal Genetics Meeting, Asilomar, CA
(2010) Department of Ecology and Evolutionary Biology, University of Tennessee-Knoxville, TN
(2010) Department of Parasitology and Mycology, Institut Pasteur, Paris, France
(2010) Department of Biological and Environmental Sciences, University of Tennessee-Chattanooga, TN
(2010) Department of Ecology and Evolution, Michigan University, Ann Arbor, MI
(2009) Plenary Speaker, 100th International Titisee Conference on “Genome evolution and the origin of novel gene functions”, Lake Titisee, Germany
(2009) Plenary Speaker, IGERT Deep Genomics Symposium, Arizona University, Tucson, AZ
(2009) Plenary Speaker, “Evolutionary Biology: 150 Years After *The Origin*”, University of Michigan Life Sciences Institute Eighth Annual Symposium, Ann Arbor, MI
(2009) Department of Biology, IGERT Seminar Series, Indiana University, Bloomington, IN
(2009) Plenary Speaker, International Symposium on Deep Metazoan Phylogeny, Berlin, Germany
(2009) Department of Integrative Biology, University of Guelph, Ontario, Canada
(2008) Plenary Speaker, Entomological Society of America Annual Meeting, Reno, NV
(2008) Department of Genetics, Washington University in St. Louis, MO

- (2008) Plenary Speaker, XII International Congress of Mycology, Istanbul, Turkey
 (2008) Plenary Speaker, 33rd FEBS Congress / 11th IUBMB Conference, Athens, Greece
 (2008) Plenary Speaker, Society of Molecular Biology and Evolution Annual Meeting, Barcelona, Spain
 (2008) Infectious Disease Rounds, Vanderbilt University Medical Center, Nashville, TN
- 2000 – 2007 (Invited talks as graduate student, postdoc, or research scientist)**
- (2007) Plenary Speaker, Comparative Genomics of Eukaryotic Microorganisms ESF-EMBO Symposium, San Feliu de Guixols, Spain
 (2007) Department of Plant Pathology, Pennsylvania State University, PA
 (2007) Plenary Speaker, “*Aspergillus* systematics in the genomics era” Symposium, CBS Fungal Biodiversity Centre, Utrecht, The Netherlands
 (2007) Plenary Speaker, “Tree of Life” Symposium, University of Iowa, IA
 (2007) Department of Biology, Johns Hopkins University, MD
 (2007) Department of Biology, Boston College, MA
 (2007) Department of Biology, Georgetown University, DC
 (2006) Department of Earth & Planetary Sciences, Harvard University, MA
 (2006) Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, MA
 (2006) Department of Biological Sciences, Vanderbilt University, TN
 (2006) Department of Biology, Clark University, MA
 (2006) Department of Biology, Duke University, NC
 (2006) Plenary Speaker, IXTH International Fungal Biology Conference & 16TH New Phytopathologist Symposium on “Impact of Genomics on Fungal Biology”, Nancy, France
 (2006) Plenary Speaker, Joint meeting of American Phytopathological Society, Canadian Phytopathological Society & Mycological Society of America, Symposium on “Gene Clustering as a Mechanism for Microbial Innovation”, Quebec City, Canada
 (2006) Department of Earth, Atmospheric and Planetary Sciences, MIT, MA
 (2006) Darwin Day Speaker, Department of Biology, St. John’s University, NY
 (2005) Plenary Speaker, Phylogeography and Phylogenetics Workshop, Mathematical Biosciences Institute, Ohio State University, OH
 (2005) The Broad Institute of MIT & Harvard, MA
 (2004) Department of Biology, New York University, NY
 (2004) Department of Biology, Boston College, MA
 (2004) Plenary Speaker, Mycological Society of America, Symposium on “Phyloinformatics”, Ashville, NC
 (2004) Plenary Speaker, Royal Netherlands Academy of Arts and Sciences, Colloquium on “Fungal Phylogenomics”, Amsterdam, The Netherlands
 (2004) Plenary Speaker, Workshop Research School on “Phylogenomics of Fungi”, Utrecht, The Netherlands
 (2003) Department of Entomology, University of Wisconsin-Madison, WI
 (2002) Department of Ecology and Evolutionary Biology, University of Kansas, KS
 (2000) Department of Zoology, Reading University, U.K.

NATIONAL AND INTERNATIONAL ACADEMIC AND PUBLIC SERVICE ACTIVITIES

Editorial Board Member

- Journal of Fungi* (2019–)
Current Biology (2018–)
Microbiology Resource Announcements (2018–)
eLife (2016–)
BMC Genomics (2015–)

PLoS ONE (2014–)
BMC Microbiology (2013–)
G3:Genes|Genomes|Genetics (2011–)
Journal of Biological Research (2010–)
Genomics Insights (2009–)
Frontiers in Microbiology (2018–2020)
Evolution, Medicine, & Public Health (2014–2019)
Fungal Genetics and Biology (2014–2021)

Manuscript Reviewer

I review many manuscripts per year and have served as a reviewer for dozens of top-flight journals, including: *BioEssays*, *Bioinformatics*, *BMC Biology*, *BMC Evol. Biol.*, *BMC Genomics*, *BMC Microbiol.*, *Cell*, *Chem. & Biol.*, *Curr. Biol.*, *Development*, *Euk. Cell*, *Evolution*, *Evol. Med. Public Health*, *Fungal Genet. Biol.*, *Gene*, *Genetics*, *Genes Dev. Evol.*, *Genome Biol.*, *Genome Res.*, *Heredity*, *Integr. Comp. Biol.*, *J. Theor. Biol.*, *Mol. Biol. Evol.*, *Mol. Ecol.*, *J. Biol. Rhythms*, *J. Mol. Evol.*, *Mol. Phylog. Evol.*, *Mycologia*, *Nature*, *Nature Ecol. Evol.*, *Nature Comm.*, *New Phytol.*, *The Plant Cell*, *PLOS Biol.*, *PLOS Comp. Biol.*, *PLOS Genet.*, *PLOS One*, *PLoS Path.*, *Proc. Roy. Soc. Lond. Ser. B.*, *PNAS*, *Science*, *Science Signalling*, *Trends Ecol. Evol.*, *Trends Genet.*, and *Zoology*.

Book / Book Proposal Reviewer

W. W. Norton, Princeton University Press, Roberts & Company, W. H. Freeman.

Grant Reviewer

2021, NIH/NIAID Special Emphasis Panel on Coccidiomycosis Collaborative Research Centers
2021, HHMI Gilliam Fellowship Program, Stage 1 Reviewer
2015, NASA Panel
2012, NSF Panel
2010, NSF Panel
2007–present, Ad hoc grant reviewer for NIH (USA), NSF (USA), The Wellcome Trust (UK), NASA (USA), BBSRC (UK), Marsden Fund (New Zealand), ANR (France), FCT (Portugal), STW (The Netherlands)

Promotion / Tenure Evaluation Writer

Clark University, College of William & Mary, Cumberland University, Dalhousie University (Canada), Duke University, Emory University, Foundation for Research & Technology–Hellas (Greece), Max Planck Society (Germany), Michigan State University, Northern Illinois University, Ohio State University, Pontifical Catholic University of Chile (Chile), University of Alberta (Canada), University of California–Berkeley, University of Crete (Greece), University of Denver, University of Florida, University of Maryland, University of Massachusetts–Amherst, University of Michigan, University of Minnesota, University of Mississippi, University of North Carolina–Chapel Hill, University of Pittsburgh, University of Rochester, University of Southern California, University of Texas–Austin, University of Wisconsin–Madison, Vanderbilt University Medical Center, Washington Univ. St Louis.

Conference Organizer

- 2008**, Member of Program Committee, 6th RECOMB Comparative Genomics Satellite Workshop, October 13-15, 2008, Paris, France
- 2014**, Member, Scientific Board for the Congresses of the International Union of Microbiological Societies (IUMS 2014), Montréal, Canada
- 2016**, Vice Chair, Gordon Research Conference on Cellular and Molecular Fungal Biology
- 2018**, Chair, Gordon Research Conference on Cellular and Molecular Fungal Biology
- 2021–present**, Scientific Organizer, EMBO meeting in Molecular Mechanisms in Evolution and Ecology

Other Scientific Service

- 2013–2015**, Member, Aspergillus Genomes Research Policy Committee, Genetics Society of America
- 2015–present**, Aspergillus Scientific Advisory Team, *FungiDB*
- 2013–2016**, Member (2 years), Chair (1 year), and Former Chair (ex officio, 1 year), Karling Annual Lecture Committee, Mycological Society of America
- 2016–2019**, Member, External Scientific Consultant Panel, Placental Atlas Tool Project, NIH/NICHD
- 2017**, International Society for Evolution, Medicine & Public Health Omenn Prize Committee
- 2021–2023**, Councilor of Genetics/Cell Biology, Mycological Society of America

GRADUATE ADVISING

Graduate Thesis Committees

- Brian Robertson (2007 – 2009, member, Biological Sciences program)
- John G. Gibbons (2007 – 2012, advisor and member, Biological Sciences program)
- Leonidas Salichos (2008 – 2014, advisor and member, Biological Sciences program)
- Chunyao Wei (2009 – 2013, member, Biological Sciences program)
- Kamya Rajaram (2010 – 2014, member, Biological Sciences program)
- Robert Brucker (2010 – 2013, member, Biological Sciences program)
- Cassidy C. Cobbs (2011 – 2014, member, Biological Sciences program)
- Gregory Colby (2011 – 2012, member, Biological Sciences program)
- Sarah P. Lawson (2011 – 2014, member, Biological Sciences program)
- Lisa J. Funkhouser (2011 – 2016, member, Biological Sciences program)
- Mahesh Rao (2012 – 2016, member, Biological Sciences program)
- Diana Cha (2013 – 2017, member, Biological Sciences program)
- Garrett P. League (2013 – 2017, member, Biological Sciences program)
- Haley E. Eidem (2013 – 2018, advisor and member, Biological Sciences program)
- Mara Kim (2013 – 2018, advisor and member, Biological Sciences program)
- Abigail L. Lind (2014 – 2017, advisor and chair, Biomedical Informatics program)
- Andrew Brooks (2015 – 2019, member, Human Genetics program)
- Esther Epum (2015 – 2019, member, Biological Sciences program)
- Ling Chen (2016 – 2019, chair, Biological Sciences program)
- Stephanie Birnbaum (2016 – 2019, member, Biological Sciences program)
- Michelle Moon (2016 – 2019, co-advisor and member, Biological Sciences program)
- Juan F. Ortiz (2016 – 2019, advisor and member, Biological Sciences program)
- Michael Sivley (2017 – 2018, member, Biomedical Informatics program)
- Abigail Searfoss (2017 – 2020, member, Chemical & Physical Biology program)
- Dylan Shropshire (2017 – 2020, chair, Biological Sciences program)
- Abin Abraham (2018 – 2021, chair, Biomedical Informatics program)
- Mary Lauren Benton (2018 – 2020, member, Biomedical Informatics program)

Souhrid Mukherjee (2018 – present, chair, Biological Sciences program)
Nikita Tsyba (2018 – present, chair, Biological Sciences program)
Melanie Hurst (2018 – present, member, Microbe-Host Interactions program)
Jacob Steenwyk (2018 – present, advisor and member, Biological Sciences program)
Katrina Ngo (2019 – present, chair, Biological Sciences program)
Souradip Das (2019 – present, member, Biological Sciences program)
Parker Rundstrom (2019 – present, chair, Biological Sciences program)
Andrea Shiakolas (2019 – present, member, Microbe Host Interactions program)
Alec Brown (2020 – present, advisor and member, Biological Sciences program)
E. Anne Hatmaker (2020 – present, advisor and member, Biological Sciences program)
Adriana Norris (2020 – present, chair, Biological Sciences program)
Robert Markowitz (2020 – present, chair, Biological Sciences program)
Yakov Pichkar (2020 – present, chair, Biological Sciences program)
Keila Velazquez Arcelay (2020 – present, chair, Biological Sciences program)
Marie-Claire Harrison (2021 – present, advisor, Biological Sciences program)

Graduate Thesis Committees Outside Vanderbilt University

Jeremy Levy (2018, University College London, UK, external examiner)
Sonja Knowles (2018 – 2021, Univ. North Carolina, Greensboro, external member)

ADMINISTRATIVE, COMMITTEE, AND OTHER SERVICE

To Department

2007 – 2008, Member, Faculty Search Committee, Evolutionary Ecology
2008 – 2012, Co-Organizer, Departmental Seminar Series
2011 – 2013, Member, Departmental Graduate Program Committee
2013 – 2014, Chair, Faculty Search Committee
2013 – 2014, Leader of Biological Sciences faculty efforts to retain Dr. John Anthony Capra to Vanderbilt Univ. through his move from the School of Medicine to the School of Arts and Science
2014 – 2019, Member, Mentorship Committee of Assistant Professor John A. Capra
2014 – 2015, Member, Undergraduate Curriculum Committee
2014 – 2015, Member, Faculty Search Committee
2015 – 2016, Member, Faculty Search Committee
2016 – present, Member, Awards Committee
2017 – present, Member, Mentorship Committee of Assistant Professor Nicole Creanza
2019 – 2020, Member, Mentorship Committee of Associate Professor John A. Capra
2019 – present, Member, Mentorship Committee of Associate Professor Patrick Abbot
2019 – present, Member, Mentorship Committee of Associate Professor Larisa R. G. DeSantis
2019 – 2020, Chair, Faculty Search Committee, Evolutionary Anthropology
2019 – present, Member, Departmental Building / Space Committee
2020 – present, Member, Mentorship Committee of Assistant Professor Megan L. Behringer
2021 – 2022, Chair, Faculty Search Committee, Evolutionary Biochemistry

To College

2013 – 2014, Member, Junior Advisory Review Committee
2013 – present, Member, Advisory Committee for Scientific Computing
2015 – 2019, Member, Committee on Individual Programs
2019 – 2020, Chair, Ad Hoc Promotion Review Committee

2021 – 2022, Member, Faculty Search Committee, Biomedical Anthropology, Department of Anthropology

To University

- 2010 – 2012, Member, Provost's Graduate Fellowship Topping Up Award Selection Committee
- 2010 – 2015, Member, Graduate Faculty Delegate Assembly Representative for the Human Genetics Graduate Program
- 2013 – 2014, Member, Trans-institutional Programs Steering Committee
- 2013 – 2014, Member, Vanderbilt University Medical Center Faculty Search Committee for the chair of Vanderbilt Genetics Institute (hiring of Dr. Nancy J. Cox)
- 2014 – 2016, Member, Genetics Executive Council
- 2015 – 2016, Member, Biomedical Sciences Advisory Committee
- 2016 – 2017, Member, Graduate Education and Research Endowment Committee
- 2017, Member, Graduate School Master's Program Evaluation Committee
- 2018, Member, Goldwater Scholar Internal Selection Committee
- 2018, Member, University Faculty Research Awards Committee
- 2018 – 2019, Member, Trans-Institutional Capital Planning Committee
- 2020 – 2021, Member, Promotions and Tenure Review Committee
- 2021 – 2022, Co-Chair, Promotions and Tenure Review Committee