

Curriculum Vitae, 25th May 2023

CHRIS TODD HITTINGER, PhD

1552 University Avenue, Wisconsin Energy Institute 4129

Madison, WI 53726-4084, USA

<http://hittinger.genetics.wisc.edu>, @HittingerLab, cthittinger@wisc.edu

BIRTH AND CITIZENSHIP: Indiana, USA (details available on request)

EMPLOYMENT

2022-: Professor of Genetics, University of Wisconsin-Madison
2017-22: Associate Professor of Genetics, University of Wisconsin-Madison
2011-7: Assistant Professor of Genetics, University of Wisconsin-Madison

SECONDARY AFFILIATIONS

2019-: Director, J. F. Crow Institute for the Study of Evolution (Faculty Member 2011-)
2019-: Affiliate Professor, Department of Medical Genetics
2018-: Affiliate Professor, Department of Integrative Biology
2016-: Trainer, Biotechnology Training Program
2016-: Core Faculty Mentor, Integrated Biological Sciences-Summer Research Program
2014-: Affiliate Professor, Department of Botany
2013-: Trainer, Molecular Biosciences Training Grant Program
2012-: Core Faculty, Center for Genomic Science Innovation (formerly Genome Center of Wisconsin)
2012-: Team Lead, Co-Investigator, DOE Great Lakes Bioenergy Research Center
2011-: Trainer, Microbiology Doctoral Training Program
2011-: Trainer, Genomic Sciences Training Program
2011-: Trainer, Graduate Program in Cellular and Molecular Biology
2011-: Investigator, Wisconsin Energy Institute

EDUCATION

2007-11: Postdoctoral Fellow (Mentor: Mark Johnston), Washington University in St. Louis School of Medicine (Center for Genome Sciences, Department of Genetics), University of Colorado School of Medicine (Department of Biochemistry and Molecular Genetics)
2001-7: Doctor of Philosophy (Mentor: Sean B. Carroll), University of Wisconsin-Madison (Laboratory of Genetics, HHMI)
1997-2001: Bachelor of Science (Mentors: Allen C. Gathman, Walt W. Lilly), Southeast Missouri State University (Department of Biology, Department of Chemistry)

HONORS AND AWARDS

2023-: Sustainability Faculty Fellow (UW)
2019-: International Commission on Yeasts (USA Commissioner)
2019-24: H. I. Romnes Faculty Fellow (UW/WARF)
2019: Species epithet of *Kurtzmaniella hittingeri* Lopes et al. 2019
2017-9: Vilas Faculty Early Career Investigator (Vilas Trust Estate)
2017: 40 Under 40 Honoree (*Midwest Energy News*)
2015-6: Alfred Toepfer Faculty Fellow (Alexander von Humboldt Foundation)
2014-21: Pew Scholar in the Biomedical Sciences (Pew Charitable Trusts)
2013-9: Faculty Early Career Development Award (NSF-CAREER)
2008-11: Helen Hay Whitney Fellow, Maclyn McCarty Fellow (HHWF)
2007-8: NIH-NHGRI NRSA Trainee (2T32HG00045), James S. McDonnell Genetics Fellow (WUSTL)
2007: Schlimgen Award (top graduate, Genetics)
2001-6: Howard Hughes Medical Institute Predoctoral Fellow in the Biological Sciences
2001: Provost's Award (top graduate, College of Science and Mathematics), Honors Scholar, Deimund National Merit Scholar, *summa cum laude* (Southeast)
2000: NSF-Research Experiences for Undergraduates Participant (UW)
1997-2001: Governor's Scholar (Southeast), Robert C. Byrd Scholar (Indiana)
1997: Academic All-Star (top 40 Indiana graduates), Valedictorian (Southport, Indianapolis, IN)

REVIEWS/COMMENTARY (&equal, @corresponding, citations=8573, i10-index=82, h-index=47)

R18. Gabaldón T[@], **Hittinger CT[@]**. 2022. Editorial: genomic insights on fungal hybrids. *Front Fungal Biol* **3**: 1063609.
R17. Case NT, Berman J, Blehert DS, Cramer RA, Cuomo C, Currie CR, Ene IV, Fisher MC, Fritz-Laylin LK, Gerstein AC, Glass NL, Gow NAR, Gurr SJ, **Hittinger CT**, Hohl TM, Iliev ID, James TY, Jin H, Klein BS, Kronstad JW, Lorch JM, McGovern V, Mitchell AP, Segre JA, Shapiro RS, Sheppard DC, Sil A, Stajich JE, Stukenbrock EE, Taylor JW, Thompson D, Wright GD, Heitman J, Cowen LE. 2022. The future of fungi: threats and opportunities. *G3* **12**: jkac224.
R16. Mozzachiodi S, Bai FY, Baldrian P, Bell G, Boundy-Mills K, Buzzini P, Čadež N, Cubillos FA, Dashko S, Dimitrov R, **Fisher KJ**, Gibson B, Gouliamova D, Greig D, Heisteringer L, **Hittinger CT**, Jecmenica M, Koufopanou V, Landry CR, Mašínová T, Naumova ES, Oplente D, Peña JJ, Petrovič U, Tsai IJ, Turchetti B, Villarreal P, Yurkov A, Liti G, Boynton P. 2022. Yeasts from temperate forests. *Yeast* **39**: 4-24.

- R15. Harrison MC, LaBella AL, **Hittinger CT**[®], Rokas A[®]. 2022. The evolution of the GALactose utilization pathway in budding yeasts. *Trends Genet* **38**: 97-106.
- R14. Yurkov A, Alves A, Bai FY, Boundy-Mills K, Buzzini P, Čadež N, Cardinali G, Casaregola S, Chaturvedi V, Collin V, Fell JW, Girard V, Groenewald M, Hagen F, **Hittinger CT**, Kachalkin AV, Kostrzewa M, Kouvelis V, Libkind D, Liu X, Maier T, Meyer W, Péter G, Piątek M, Robert V, Rosa CA, Sampaio JP, Sipiczki M, Stadler M, Sugita T, Sugiyama J, Takagi H, Takashima M, Turchetti B, Wang QM, Boekhout T. 2021. Nomenclatural issues concerning cultured yeasts and other fungi: why it is important to avoid unneeded name changes. *IMA Fungus* **12**: 18.
- R13. Libkind D, Čadež N, **Opulente DA**, **Langdon QK**, Rosa CA, Sampaio JP, Gonçalves P, **Hittinger CT**, Lachance MA. 2020. Towards yeast taxogenomics: lessons from novel species descriptions based on complete genome sequences. *FEMS Yeast Res* **20**: foaa042.
- R12. James TY, Stajich JE, **Hittinger CT**, Rokas A. 2020. Toward a fully resolved fungal tree of life. *Annu Rev Microbiol* **74**: 291-313.
- R11. Libkind D, Peris D, Cubillos FA, Steenwyk JL, **Opulente DA**, **Langdon QK**, Rokas A, **Hittinger CT**. 2020. Into the wild: new yeast genomes from natural environments and new tools for their analysis. *FEMS Yeast Res* **20**: foaa008.
- R10. **Hittinger CT**[®]. 2020. Evaluation of Kuroda et al.: insight into yeast isobutanol tolerance with advances still needed. *Cell Syst* **10**: 124.
- R9. Lachance MA, **Hittinger CT**. 2018. Introducing 'ecoYeast': ecology and communities of yeasts. *Yeast* **35**: 313.
- R8. **Hittinger CT**[®], Steele JL, Ryder DS. 2018. Diverse yeasts for diverse fermented beverages and foods. *Curr Opin Biotechnol* **49**: 199-206.
- R7. **Peris D**[®], Pérez-Torrado R, **Hittinger CT**, Barrio E, Querol A. 2018. On the origins and industrial applications of *Saccharomyces cerevisiae* x *Saccharomyces kudriavzevii* hybrids. *Yeast* **35**: 51-69. (Yeast Top 20 Downloads 2018)
- R6. Gibson B, Geertman JA, **Hittinger CT**, Krogerus K, Libkind D, Louis EJ, Magalhães F, Sampaio JP. 2017. New yeasts-new brews: modern approaches to brewing yeast design and development. *FEMS Yeast Res* **17**: fox038.
- R5. **Hittinger CT**[®], Rokas A, Bai FY, Boekhout T, Gonçalves P, Jeffries TW, **Kominek J**, Lachance MA, Libkind D, Rosa CA, Sampaio JP, Kurtzman CP. 2015. Genomics and the making of yeast biodiversity. *Curr Opin Genet Dev* **35**: 100-9.
- R4. **Hittinger CT**[®]. 2013. *Saccharomyces* diversity and evolution: a budding model genus. *Trends Genet* **29**: 309-17. (COVER)
- R3. **Hittinger CT**[®]. 2012. Endless rots most beautiful. *Science* **336**: 1649-50.
- R2. **Hittinger CT**[®], Hesselberth JR. 2010. Nucleosome patterning evolution: steady aim despite moving targets. *Mol Syst Biol* **6**: 376.
- R1. Rokas A, **Hittinger CT**. 2007. Transcriptional rewiring: the proof is in the eating. *Curr Biol* **17**: R626-8.

RESEARCH PUBLICATIONS ([®]equal, [®]corresponding, citations=8573, i10-index=82, h-index=47)

83. **Schmitz JM**, **Wolters JF**, Murray NH, Guerra RM, Bingman CA, **Hittinger CT**, Pagliarini DJ. 2023. Aim18p and Aim46p are chalcone isomerase domain-containing mitochondrial hemoproteins in *Saccharomyces cerevisiae*. *J Biol Chem* **299**: 102981.
82. **Peris D**[®], **Ubbelohde EJ**, **Kuang MC**, **Kominek J**, **Langdon QK**, Adams M, Koshalek JA, **Hulfachor AB**, **Opulente DA**, Hall DJ, Hyma K, Fay JC, Leducq JB, Charron G, Landry CR, Libkind D, Gonçalves C, Gonçalves P, Sampaio JP, **Wang QM**, Bai FY, **Wrobel RL**, **Hittinger CT**[®]. 2023. Macroevolutionary diversity of traits and genomes in the model yeast genus *Saccharomyces*. *Nat Commun* **14**: 690.
81. **Liu L**, Ansari RU, Vang-Smith M, **Hittinger CT**[®], Sato TK[®]. 2023. A role for ion homeostasis in yeast ionic liquid tolerance. *microPubl Biol* **2023**: 10.17912/micropub.biology.000718.
80. **Barros KO**, Alvarenga FBM, Magni G, Souza GFL, Abegg MA, Palladino F, da Silva SS, Rodrigues RCLB, Sato TK, **Hittinger CT**, Rosa CA. 2023. The Brazilian Amazonian rainforest harbors a high diversity of yeasts associated with rotting wood, including many candidates for new yeast species. *Yeast* **40**: 84-101.
79. Li Y, Liu H, Steenwyk JL, LaBella AL, Harrison MC, Groenewald M, Zhou X, Shen XX, Zhao T, **Hittinger CT**, Rokas A. 2022. Contrasting modes of macro and microsynteny evolution in a eukaryotic subphylum. *Curr Biol* **32**: 5335-5343.e4.
78. **Krause DJ**, **Hittinger CT**[®]. 2022. Functional divergence in a multi-gene family is a key evolutionary innovation for anaerobic growth in *Saccharomyces cerevisiae*. *Mol Biol Evol* **39**: msac202.
77. Vanacloig-Pedros E, **Fisher KJ**, Liu L, Debrauske DJ, Young MKM, Place M, **Hittinger CT**, Sato TK, Gasch AP. 2022. Comparative chemical genomic profiling across plant-based hydrolysate toxins reveals widespread antagonism in fitness contributions. *FEMS Yeast Res* **21**: foac036.
76. Wadler CS[§], **Wolters JF**[§], Fortney NW[§], Throckmorton KO, Zhang Y, **Miller CR**, **Schneider RM**, Wendt-Pienkowski E, Currie CR, Donohue TJ, Noguera DR, **Hittinger CT**, Thomas MG. 2022. Utilization of lignocellulosic biofuel conversion residue by diverse microorganisms. *Biotechnol Biofuels Bioprod* **15**: 70.
75. Steenwyk JL, Phillips MA, Yang F, Date SS, Graham TR, Berlan J, **Hittinger CT**, Rokas A. 2022. An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function. *Sci Adv* **8**: eabn0105.
74. Gambacorta FV, Wagner ER, Jacobson TB, Tremaine M, Muehlbauer LK, McGee MA, Baerwald JJ, **Wrobel RL**, **Wolters JF**, Place M, Dietrich JJ, Xie D, Serate J, Gajbhiye S, **Liu L**, Vang-Smith M, Coon JJ, Zhang Y, Gasch AP, Amador-Noguez D, **Hittinger CT**, Sato TK, Pflieger BF. 2022. Comparative functional genomics identifies an iron-limited bottleneck in a *Saccharomyces cerevisiae* strain with a cytosolic-localized isobutanol pathway. *Synth Syst Biotechnol* **7**: 738-49.
73. **Spurley WJ**[§], **Fisher KJ**[§], **Langdon QK**[§], **Buh KV**, **Jarzyna M**, **Haase MAB**, **Sylvester K**, **Moriarty RV**, **Rodriguez D**, **Sheddan A**, **Wright S**, **Sorlie L**, **Hulfachor AB**, **Opulente DA**[§], **Hittinger CT**[®]. 2022. Substrate, temperature, and geographical patterns among nearly 2000 natural yeast isolates. *Yeast* **39**: 55-68.
72. **Lee SB**, Tremaine M, Place M, **Liu L**, Pier A, **Krause DJ**, Xie D, Zhang Y, Landick R, Gasch AP, **Hittinger CT**[®], Sato TK[®]. 2021. Crabtree/Warburg-like aerobic xylose fermentation by engineered *Saccharomyces cerevisiae*. *Metab Eng* **68**: 119-130.

71. Čadež N, Bellora N, Ulloa R, Tome M, Petković H, Groenewald M, **Hittinger CT**, Libkind D. 2021. *Hanseniaspora smithiae* sp. nov., a novel apiculate yeast species from Patagonian forests that lacks the typical genomic domestication signatures for fermentative environments. *Front Microbiol* **12**: 679894.
70. Li Y, Steenwyk JL, Chang Y, Wang Y, James TY, Stajich JE, Spatafora JW, Groenewald M, Dunn CW, **Hittinger CT**, Shen XX, Rokas A. 2021. A genome-scale phylogeny of the kingdom Fungi. *Curr Biol* **31**: 1653-65.
69. LaBella AL, **Opulente DA**, Steenwyk JL, **Hittinger CT**, Rokas A. 2021. Signatures of optimal codon usage in metabolic genes inform budding yeast ecology. *PLoS Biol* **19**: e3001185.
68. O'Brien CE, Oliveira-Pacheco J, Ó Cinnéide E, **Haase MAB**, **Hittinger CT**, Rogers TR, Zaragoza O, Bond U, Butler G. 2021. Population genomics of the pathogenic yeast *Candida tropicalis* identifies hybrid isolates in environmental samples. *PLoS Pathog* **17**: e1009138.
67. **Haase MAB**[§], **Kominek J**[§], **Opulente DA**, Shen XX, LaBella AL, Zhou X, DeVirgilio J, **Hulfachor AB**, Kurtzman CP, Rokas A[®], **Hittinger CT**[®]. 2021. Repeated horizontal gene transfer of *GAL*actose metabolism genes violates Dollo's law of irreversible loss. *Genetics* **217**: iyaa012.
66. Shen XX, Li Y, **Hittinger CT**, Chen XX, Rokas A. 2020. An investigation of irreproducibility in maximum likelihood phylogenetic inference. *Nat Commun* **11**: 6096.
65. Shen XX, Steenwyk JL, LaBella AL, **Opulente DA**, Zhou X, **Kominek J**, Li Y, Groenewald M, **Hittinger CT**, Rokas A. 2020. Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. *Sci Adv* **6**: eabd0079.
64. **Stoneman HR**, **Wrobel RL**, Place M, Graham M, **Krause DJ**, De Chiara M, Liti G, Schacherer J, Landick R, Gasch AP, Sato TK, **Hittinger CT**[®]. 2020. CRISpy-pop: a web tool for designing CRISPR/Cas9-driven genetic modifications in diverse populations. *G3* **10**: 4287-94.
63. **Peris D**[®], **Alexander WG**, **Fisher KJ**, **Moriarty RV**, Basuino MG, Ubbelohde EJ, **Wrobel RL**, **Hittinger CT**[®]. 2020. Synthetic hybrids of six yeast species. *Nat Commun* **11**: 2085.
62. Dharampal PS, Diaz-Garcia L, **Haase MAB**, Zalapa J, Currie CR, **Hittinger CT**, Steffan SA. 2020. Microbial diversity associated with the pollen stores of captive-bred bumble bee colonies. *Insects* **11**: 250.
61. **Langdon QK**, **Peris D**, Eizaguirre JI, **Opulente DA**, **Buh KV**, **Sylvester K**, **Jarzyna M**, Rodríguez ME, Lopes CA, Libkind D[®], **Hittinger CT**[®]. 2020. Postglacial migration shaped the genomic diversity and global distribution of the wild ancestor of lager-brewing hybrids. *PLoS Genet* **16**: e1008680.
60. **Langdon QK**, **Peris D**, **Baker EP**, **Opulente DA**, Nguyen HV, Bond U, Gonçalves P, Sampaio JP, Libkind D, **Hittinger CT**[®]. 2019. Fermentation innovation through complex hybridization of wild and domesticated yeasts. *Nat Ecol Evol* **3**: 1576-86.
59. LaBella AL, **Opulente DA**, Steenwyk JL, **Hittinger CT**, Rokas A. 2019. Variation and selection on codon usage bias across an entire subphylum. *PLoS Genet* **15**: e1008304.
58. **Krassowski T**, **Kominek J**, Shen XX, **Opulente DA**, Zhou X, Rokas A, **Hittinger CT**, Wolfe KH. 2019. Multiple reinventions of mating-type switching during budding yeast evolution. *Curr Biol* **29**: 2555-62.
57. Steenwyk JL, **Opulente DA**, **Kominek J**, Shen XX, Zhou X, LaBella AL, Bradley NP, Eichman BF, Čadež N, Libkind D, DeVirgilio J, **Hulfachor AB**, Kurtzman CP, **Hittinger CT**[®], Rokas A[®]. 2019. Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. *PLoS Biol* **17**: e3000255.
56. **Opulente DA**, **Langdon QK**, **Buh KV**, **Haase MAB**, **Sylvester K**, **Moriarty RV**, **Jarzyna M**, **Considine SL**, **Schneider RM**, **Hittinger CT**[®]. 2019. Pathogenic budding yeasts isolated outside of clinical settings. *FEMS Yeast Res* **19**: foz032.
55. **Baker EP**, **Hittinger CT**[®]. 2019. Evolution of a novel chimeric maltotriose transporter in *Saccharomyces eubayanus* from parent proteins unable to perform this function. *PLoS Genet* **15**: e1007786. (COVER)
54. **Kominek J**[§], **Doering DT**[§], **Opulente DA**, Shen XX, Zhou X, DeVirgilio J, **Hulfachor AB**, Groenewald M, Mcgee MA, Karlen SD, Kurtzman CP, Rokas A, **Hittinger CT**[®]. 2019. Eukaryotic acquisition of a bacterial operon. *Cell* **176**: 1356-66.
53. **Baker EP**, **Peris D**, **Moriarty RV**, Li XC, Fay JC, **Hittinger CT**[®]. 2019. Mitochondrial DNA and temperature tolerance in lager yeasts. *Sci Adv* **5**: eaav1869.
52. Li XC, **Peris D**, **Hittinger CT**, Sia EA, Fay JC. 2019. Mitochondria-encoded genes contribute to evolution of heat and cold tolerance in yeast. *Sci Adv* **5**: eaav1848.
51. Čadež N, Bellora N, Ulloa R, **Hittinger CT**, Libkind D. 2019. Genomic content of a novel yeast species *Hanseniaspora gamundiae* sp. nov. from fungal stromata (*Cyttaria*) associated with a unique fermented beverage in Andean Patagonia, Argentina. *PLoS One* **14**: e0210792.
50. Shen XX[§], **Opulente DA**[§], **Kominek J**[§], Zhou X[§], Steenwyk JL, **Buh KV**, **Haase MAB**, Wisecaver JH, Wang M, **Doering DT**, **Boudouris JT**, **Schneider RM**, **Langdon QK**, Ohkuma M, Endoh R, Takashima M, Manabe RI, Čadež N, Libkind D, Rosa CA, DeVirgilio J, **Hulfachor AB**, Groenewald M, Kurtzman CP, **Hittinger CT**[®], Rokas A[®]. 2018. Tempo and mode of genome evolution in the budding yeast subphylum. *Cell* **175**: 1533-45.
49. **Krause DJ**, **Kominek J**, **Opulente DA**, Shen XX, Zhou X, **Langdon QK**, DeVirgilio J, **Hulfachor AB**, Kurtzman CP, Rokas A, **Hittinger CT**[®]. 2018. Functional and evolutionary characterization of a secondary metabolite gene cluster in budding yeasts. *Proc Natl Acad Sci USA* **115**: 11030-5.
48. **Langdon QK**, **Peris D**, Kyle B, **Hittinger CT**[®]. 2018. sppIDer: a species identification tool to investigate hybrid genomes with high-throughput sequencing. *Mol Biol Evol* **35**: 2835-49.
47. Eizaguirre JI, **Peris D**, Rodríguez ME, Lopes CA, De Los Ríos P, **Hittinger CT**, Libkind D. 2018. Phylogeography of the wild Lager-brewing ancestor (*Saccharomyces eubayanus*) in Patagonia. *Environ Microbiol* **20**: 3732-43.
46. Higgins DA, Young MK, Tremaine M, Sardi M, Fletcher JM, Agnew M, Liu L, Dickinson Q, **Peris D**, **Wrobel RL**, **Hittinger CT**, Gasch AP, Singer SW, Simmons BA, Landick R, Thelen MP, Sato TK. 2018. Natural variation in the multidrug efflux pump *SGE1* underlies ionic liquid tolerance in yeast. *Genetics* **210**: 219-34.
45. **Kuang MC**, **Kominek J**, **Alexander WG**, Cheng JF, **Wrobel RL**, **Hittinger CT**[®]. 2018. Repeated cis-regulatory tuning of a metabolic bottleneck gene during evolution. *Mol Biol Evol* **35**: 1968-81. (COVER)

44. **Krassowski T**, Coughlan AY, Shen XX, Zhou X, **Kominek J**, **Opulente DA**, Riley R, Grigoriev IV, Maheshwari N, Shields DC, Kurtzman CP, **Hittinger CT**, Rokas A, Wolfe KH. 2018. Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. *Nat Commun* **9**: 1887.
43. **Gonçalves C**, Wisecaver JH, **Kominek J**, Oom MS, Leandro MJ, Shen XX, **Opulente DA**, Zhou X, **Peris D**, Kurtzman CP, **Hittinger CT**, Rokas A, Gonçalves P. 2018. Evidence for loss and reacquisition of alcoholic fermentation in a fructophilic yeast lineage. *eLife* **7**: e33034.
42. **Opulente DA**, Rollinson EJ, **Bernick-Roehr C**, **Hulfachor AB**, Rokas A[®], Kurtzman CP, **Hittinger CT**[®]. 2018. Factors driving metabolic diversity in the budding yeast subphylum. *BMC Biol* **16**: 26.
41. Vakirlis N, Hebert AS, **Opulente DA**, Achaz G, **Hittinger CT**, Fischer G, Coon JJ, Lafontaine I. 2018. A molecular portrait of de novo genes in yeasts. *Mol Biol Evol* **35**: 631-45.
40. Zhou X, Shen XX, **Hittinger CT**, Rokas A. 2018. Evaluating fast maximum likelihood-based phylogenetic programs using empirical phylogenomic data sets. *Mol Biol Evol* **35**: 486-503. (MBE Emerging Classics 2021)
39. Morais CG, Batista TM, **Kominek J**, Borelli BM, Furtado C, Moreira RG, Franco GR, Rosa LH, Fonseca C, **Hittinger CT**, Lachance MA, Rosa CA. 2017 *Spathaspora boniae* sp. nov., a D-xylose-fermenting species in the *Candida albicans/Lodderomyces* clade. *Int J Syst Evol Microbiol* **67**: 3798–805.
38. Steffan SA, Dharampal PS, Diaz-Garcia L, Currie CR, Zalapa J, **Hittinger CT**. 2017. Empirical, metagenomic, and computational techniques illuminate the mechanisms by which fungicides compromise bee health. *J Vis Exp* **128**: e54631.
37. **Haase MAB**, **Kominek J**, **Langdon QK**, Kurtzman CP, **Hittinger CT**[®]. 2017. Genome sequence and physiological analysis of *Yamadazyma laniorum* f.a. sp. nov. and a reevaluation of the apocryphal xylose fermentation of its sister species, *Candida tenuis*. *FEMS Yeast Res* **17**: fox019.
36. Shen XX, **Hittinger CT**, Rokas A. 2017. Contentious relationships in phylogenomic studies can be driven by a handful of genes. *Nat Ecol Evol* **1**: 0126.
35. **Peris D**, **Moriarty RV**, **Alexander WG**, **Baker E**, **Sylvester K**, **Sardi M**, **Langdon QK**, Libkind D, Wang QM, Bai FY, Leducq JB, Charron G, Landry CR, Sampaio JP, Gonçalves P, Hyma KE, Fay JC, Sato TK, **Hittinger CT**[®]. 2017. Hybridization and adaptive evolution of diverse *Saccharomyces* species for cellulosic biofuel production. *Biotechnol Biofuels* **10**: 78.
34. Shen XX, Zhou X, **Kominek J**, Kurtzman CP[®], **Hittinger CT**[®], Rokas A[®]. 2016. Reconstructing the backbone of the *Saccharomycotina* yeast phylogeny using genome-scale data. *G3* **6**: 3927-39.
33. Bellora N, Moliné M, David-Palma M, **Coelho MA**, **Hittinger CT**, Sampaio JP, Gonçalves P, Libkind D. 2016. Comparative genomics provides new insights into the diversity, physiology, and sexuality of the only industrially exploited tremellomycete: *Phaffia rhodozyma*. *BMC Genomics* **17**: 901.
32. Zhou X, **Peris D**, **Kominek J**, Kurtzman CP, **Hittinger CT**[®], Rokas A[®]. 2016. *in silico* Whole Genome Sequencer & Analyzer (iWGS): a computational pipeline to guide the design and analysis of *de novo* genome sequencing studies. *G3* **6**: 3655-62.
31. Sato TK, Tremaine M, Parreiras LS, Hebert AS, Myers KS, Higbee AJ, Sardi M, **Mcllwain SJ**, Ong IM, Breuer RJ, Narasimhan RA, McGee MA, Dickinson Q, La Reau A, Xie D, Tian M, Piotrowski JS, Reed JL, Zhang Y, Coon JJ, **Hittinger CT**, Gasch AP, Landick R. 2016. Directed evolution reveals unexpected epistatic interactions that alter metabolic regulation and enable anaerobic xylose use by *Saccharomyces cerevisiae*. *PLoS Genet* **12**: e1006372.
30. **Kuang MC**, Hutchins PD, Russell JD, Coon JJ, **Hittinger CT**[®]. 2016. Ongoing resolution of duplicate gene functions shapes the diversification of a metabolic network. *eLife* **5**: e19027.
29. Riley R, Haridas S, Wolfe KH, **Lopes MR**, **Hittinger CT**, Göker M, Salamov AA, Wisecaver JH, Long TM, Calvey CH, Aerts AL, Barry KW, Choi C, Clum A, Coughlan AY, Deshpande S, Douglass AP, Hanson SJ, Klenk HP, LaButti KM, Lapidus A, Lindquist EA, Lipzen AM, Meier-Kolthoff JP, Ohm RA, Otilar RP, Pangilinan JL, Peng Y, Rokas A, Rosa CA, Scheuner C, Sibirny AA, Slot JC, Stielow JB, Sun H, Kurtzman CP, Blackwell M, Grigoriev IV, Jeffries TW. 2016. Comparative genomics of biotechnologically important yeasts. *Proc Natl Acad Sci USA* **113**: 9882-7.
28. Wisecaver JH, **Alexander WG**, King SB, **Hittinger CT**, Rokas A. 2016. Dynamic evolution of nitric oxide detoxifying flavohemoglobins, a family of single-protein metabolic modules in bacteria and eukaryotes. *Mol Biol Evol* **33**: 1979-87.
27. **Peris D**[®], **Langdon QK**[®], **Moriarty RV**, **Sylvester K**, **Bontrager M**, Charron G, Leducq JB, Landry CR, Libkind D, **Hittinger CT**[®]. 2016. Complex ancestries of lager-brewing hybrids were shaped by standing variation in the wild yeast *Saccharomyces eubayanus*. *PLoS Genet* **12**: e1006155. (COVER)
26. **Lopes MR**[®], Morais CG[®], **Kominek J**, Cadete RM, Soares MA, Uetanabaro AP, Fonseca C, Lachance MA, **Hittinger CT**, Rosa CA. 2016. Genomic analysis and D-xylose fermentation of three novel *Spathaspora* species: *Spathaspora girioi* sp. nov., *Spathaspora hagerdaliae* f. a., sp. nov., and *Spathaspora gorwiae* f. a., sp. nov. *FEMS Yeast Res* **16**: fow044.
25. **Mcllwain SJ**, **Peris D**, Sardi M, Moskvina OV, Zhan F, Myers KS, Riley NM, Buzzell A, Parreiras L, Ong IM, Landick R, Coon JJ, Gasch AP, Sato TK, **Hittinger CT**[®]. 2016. Genome sequence and analysis of a stress-tolerant, wild-derived strain of *Saccharomyces cerevisiae* used in biofuels research. *G3* **6**: 1757-66.
24. **Alexander WG**, Wisecaver JH, Rokas A, **Hittinger CT**[®]. 2016. Horizontally acquired genes in early-diverging pathogenic fungi enable the use of host nucleosides and nucleotides. *Proc Natl Acad Sci USA* **113**: 4116-21.
23. **Alexander WG**, **Peris D**, **Pfannenstiel BT**, **Opulente DA**, **Kuang M**, **Hittinger CT**[®]. 2016. Efficient engineering of marker-free synthetic allotetraploids of *Saccharomyces*. *Fungal Genet Biol* **89**: 10-7.
22. Leducq JB, Nielly-Thibault L, Charron G, Eberlein C, Verta JP, Samani P, **Sylvester K**, **Hittinger CT**, Bell G, Landry CR. 2016. Speciation driven by hybridization and chromosomal plasticity in a wild yeast. *Nat Microbiol* **1**: 15003.
21. **Baker E**, **Wang B**, Bellora N, **Peris D**, **Hulfachor AB**, **Koshalek JA**, Adams M, Libkind D, **Hittinger CT**[®]. 2015. The genome sequence of *Saccharomyces eubayanus* and the domestication of lager-brewing yeasts. *Mol Biol Evol* **32**: 2818-31. (MBE Best Graduate Student Paper of 2015, MBE Citation Classic 2017-9)
20. **Coelho MA**, Almeida JM, **Hittinger CT**, Gonçalves P. 2015. Draft genome sequence of *Sporidiobolus salmonicolor* CBS 6832, a red-pigmented basidiomycetous yeast. *Genome Announc* **3**: e00444-15.

19. **Sylvester K, Wang QM, James B, Mendez R, Hulfachor AB, Hittinger CT**[®]. 2015. Temperature and host preferences drive the diversification of *Saccharomyces* and other yeasts: a survey and the discovery of eight new yeast species. *FEMS Yeast Res* **15**: fov002.
18. **Alexander WG, Doering DT, Hittinger CT**[®]. 2014. High-efficiency genome editing and allele replacement in prototrophic and wild strains of *Saccharomyces*. *Genetics* **198**: 859-66.
17. Almeida P, Gonçalves C, Teixeira S, Libkind D, **Bontrager M**, Masneuf-Pomarède I, Albertin W, Durrens P, Sherman DJ, Marullo P, **Hittinger CT**, Gonçalves P, Sampaio JP. 2014. A Gondwanan imprint on global diversity and domestication of wine and cider yeast *Saccharomyces uvarum*. *Nat Commun* **5**: 4044.
16. **Peris D, Sylvester K**, Libkind D, Gonçalves P, Sampaio JP, **Alexander WG, Hittinger CT**[®]. 2014. Population structure and reticulate evolution of *Saccharomyces eubayanus* and its lager-brewing hybrids. *Mol Ecol* **23**: 2031-45. (COVER)
15. Leducq JB, Charron G, Samani P, Dubé AK, **Sylvester K, James B**, Almeida P, Sampaio JP, **Hittinger CT**, Bell G, Landry CR. 2014. Local climatic adaptation in a widespread microorganism. *Proc Biol Sci* **281**: 20132472.
14. Libkind D[‡], **Hittinger CT**[‡], Valério E, Gonçalves C, Dover J, Johnston M, Gonçalves P, Sampaio JP. 2011. Microbe domestication and the identification of the wild genetic stock of lager-brewing yeast. *Proc Natl Acad Sci USA* **108**: 14539-44. (COVER)
13. Scannell DR, Zill OA[®], Rokas A, Payen C, Dunham MJ, Eisen MB, Rine J, Johnston M, **Hittinger CT**[®]. 2011. The awesome power of yeast evolutionary genetics: New genome sequences and strain resources for the *Saccharomyces sensu stricto* genus. *G3* **1**: 11-25.
12. **Hittinger CT**, Gonçalves P, Sampaio JP, Dover J, Johnston M, Rokas A. 2010. Remarkably ancient balanced polymorphisms in a multi-locus gene network. *Nature* **464**: 54-8.
11. **Hittinger CT**, Johnston M, Tossberg JT, Rokas A. 2010. Leveraging skewed transcript abundance by RNA-Seq to increase the genomic depth of the tree of life. *Proc Natl Acad Sci USA* **107**: 1476-81.
10. Gibbons JG, Janson EM, **Hittinger CT**, Johnston M, Abbot P, Rokas A. 2009. Benchmarking next-generation transcriptome sequencing for functional and evolutionary genomics. *Mol Biol Evol* **26**: 2731-44.
9. **Hittinger CT**, Carroll SB. 2008. Evolution of an insect-specific GROUCHO-interaction motif in the ENGRAILED selector protein. *Evol Dev* **10**: 537-45.
8. **Hittinger CT**[®], Carroll SB[®]. 2007. Gene duplication and the adaptive evolution of a classic genetic switch. *Nature* **449**: 677-81.
7. Tour E, **Hittinger CT**, McGinnis W. 2005. Evolutionarily conserved domains required for activation and repression functions of the *Drosophila* Ultrabithorax protein. *Development* **132**: 5271-81.
6. **Hittinger CT**, Stern DL, Carroll SB. 2005. Pleiotropic functions of a conserved insect-specific Hox peptide motif. *Development* **132**: 5261-70.
5. **Hittinger CT**, Rokas A, Carroll SB. 2004. Parallel inactivation of multiple GAL pathway genes and ecological diversification in yeasts. *Proc Natl Acad Sci USA* **101**: 14144-9.
4. Palangat M, **Hittinger CT**, Landick R. 2004. Downstream DNA selectively affects a paused conformation of human RNA polymerase II. *J Mol Biol* **341**: 429-42.
3. King N, **Hittinger CT**, Carroll SB. 2003. Evolution of key cell signaling and adhesion protein families predates animal origins. *Science* **301**: 361-3.
2. Guettler S, Jackson EN, Lucchese SA, Honaas L, Green A, **Hittinger CT**, Tian Y, Lilly WW, Gathman AC. 2003. ESTs from the basidiomycete *Schizophyllum commune* grown on nitrogen-replete and nitrogen-limited media. *Fungal Genet Biol* **39**: 191-8.
1. Vigouroux Y, McMullen M, **Hittinger CT**, Houchins K, Schulz L, Kresovich S, Matsuoka Y, Doebley J. 2002. Identifying genes of agronomic importance in maize by screening microsatellites for evidence of selection during domestication. *Proc Natl Acad Sci USA* **99**: 9650-5.

EXTRAMURAL RESEARCH TALKS

- T65. *International Symposium on Fungal Stress*. 2024 (scheduled). Brazil.
- T64. *Congreso Conjunto Sociedad de Genética de Chile y Sociedad Chilena de Evolución*. 2022. Punta Arenas, Chile.
- T63. *Reunión Anual de la Sociedad de la Bioquímica y Biología Molecular de Chile*. 2022. Cuncumén, Chile.
- T62. Pontificia Universidad Católica de Chile. 2022. Santiago, Chile.
- T61. Duke University. 2022. Virtual Durham, NC: Fungal Supergroup.
- T60. *International Specialised Symposium on Yeasts*. 2022. Vancouver, Canada: ICY.
- T59. *International Workshop on Brewing Yeasts*. 2021. Virtual Bariloche, Argentina: Universidad Nacional del Comahue.
- T58. *International Congress on Yeasts*. 2021. Virtual Vienna, Austria: ICY.
- T57. *The Allied Genetics Conference*. 2020. Virtual Washington, DC: GSA.
- T56. Oregon State University. 2020. Corvallis, OR: Center for Genome Research and Biocomputing.
- T55. Universidad Nacional Autónoma de México. 2019. Querétaro, México: Laboratorio Internacional de Investigación sobre el Genoma Humano.
- T54. *Molecular Mechanisms of Evolution*. 2019. North Easton, MA: Gordon Research Conference.
- T53. *Fungal Genetics Conference (Chairs' Choice Plenary)*. 2019. Pacific Grove, CA: GSA.
- T52. *MassMyco (Keynote)*. 2018. Cambridge, MA: Friends of the Farlow Herbarium, Harvard University.
- T51. *International Workshop on Brewing Yeasts*. 2018. Bariloche, Argentina: ICY.
- T50. *International Specialized Symposium on Yeasts*. 2018. Bariloche, Argentina: ICY.
- T49. *Cellular & Molecular Fungal Biology*. 2018. Holderness, NH: Gordon Research Conference.
- T48. *Population, Evolutionary, and Quantitative Genetics Conference*. 2018. Madison, WI: Genetics Society of America.
- T47. Stowers Institute for Medical Research. 2018. Kansas City, MO.
- T46. *Pew Scholars, Pew Fellows, and Pew-Stewart Scholars Annual Meeting*. 2018. Marana, AZ: Pew Charitable Trusts.
- T45. *Midwest Yeast Meeting*. 2017. Evanston, IL: Northwestern University.

- T44. University of Richmond. 2017. Richmond, VA: Department of Biology.
- T43. Chinese Academy of Sciences. 2017. Beijing, China.
- T42. China Center of Industrial Culture Collection. 2017. Beijing, China.
- T41. *The Genomics of Beer*. University of Minnesota-Twin Cities. 2016. Minneapolis, MN: Microbial and Plant Genome Institute.
- T40. *Yeast Genetics & Genomics Course*. 2016. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory.
- T39. *The Allied Genetics Conference*. 2016. Orlando, FL: GSA.
- T38. University at Buffalo-State University of New York. 2016. Buffalo, NY: Department of Biological Sciences.
- T37. University of Michigan-Ann Arbor. 2016. Ann Arbor, MI: Department of Ecology and Evolutionary Biology.
- T36. Northwestern University. 2015. Chicago, IL: Department of Molecular Biosciences.
- T35. Washington University in St. Louis. 2015. St. Louis, MO: McDonnell Department of Genetics.
- T34. West Virginia University. 2015. Morgantown, WV: Department of Biology.
- T33. *International Conference on Yeast Genetics and Molecular Biology*. 2015. Levico Terme, Italy: EMBO.
- T32. *Botany*. 2015. Edmonton, Canada: Canadian Phytopathological Society/Mycological Society of America/Botanical Society of America.
- T31. *Society for Molecular Biology and Evolution*. 2015. Vienna, Austria: SMBE.
- T30. Workshop on Yeast Population Genomics. 2015. Montpellier, France: *iGénolevures*.
- T29. *Fungal Genetics Conference*. 2015. Pacific Grove, CA: GSA.
- T28. *Pew Scholars and Fellows Annual Meeting*. 2015. Vieques, Puerto Rico, USA: Pew Charitable Trusts.
- T27. University of Wisconsin-Milwaukee. 2015. Milwaukee, WI: Department of Biological Sciences.
- T26. Vanderbilt University. 2015. Nashville, TN: Department of Biological Sciences.
- T25. *Yeast Genetics Meeting*. 2014. Seattle, WA: GSA.
- T24. *Cellular & Molecular Fungal Biology*. 2014. Holderness, NH: Gordon Research Conference.
- T23. University of Western Ontario. 2013. London, Canada: Department of Biology.
- T22. *International Congress on Yeasts*. 2012. Madison, WI: ICY.
- T21. *Yeast Genetics and Molecular Biology Meeting*. 2012. Princeton, NJ: GSA.
- T20. *Jornadas Portuguesas de Genética*. 2012. Lisboa, Portugal: Sociedade Portuguesa de Genética.
- T19. Université Laval. 2011. Québec, Canada: Institut de Biologie Intégrative et des Systèmes.
- T18. *Midwest Yeast Meeting*. 2011. Evanston, IL: Northwestern University.
- T17. *Annual Meeting of Research Fellows*. 2010. Dedham, MA: HHWF.
- T16. University of Colorado-Boulder. 2010. Boulder, CO: RNA Club.
- T15. *iEvoBio (Informatics for Phylogenetics, Evolution, and Biodiversity Conference)*. 2010. Portland, OR: NESCent, SSB, EOL.
- T14. *Evolution*. 2010. Portland, OR: SSE, SSB, ASN.
- T13. *Cellular & Molecular Fungal Biology*. 2010. Holderness, NH: Gordon Research Conference.
- T12. The University of Chicago. 2010. Chicago, IL: Department of Organismal Biology and Anatomy.
- T11. Yale University. 2010. New Haven, CT: Microbial Diversity Institute, Department of Ecology and Evolutionary Biology.
- T10. University of Wisconsin-Madison. 2010. Madison, WI: Wisconsin Bioenergy Initiative, Laboratory of Genetics.
- T9. University of Massachusetts-Amherst. 2010. Amherst, MA: Department of Microbiology.
- T8. University of Colorado School of Medicine. 2008. Aurora, CO: Department of Biochemistry and Molecular Genetics.
- T7. *Evolutionary and Environmental Genomics of Yeasts*. 2008. Heidelberg, Germany: EMBO.
- T6. *Comparative Genomics of Eukaryotic Microorganisms: Eukaryotic Genome Evolution*. 2007. Sant Feliu de Guixols, Spain: ESF, EMBO.
- T5. The University of Chicago. 2006. Chicago, IL: Department of Ecology and Evolution.
- T4. Washington University in St. Louis. 2006. St. Louis, MO: Center for Genome Sciences, Department of Genetics.
- T3. Princeton University. 2006. Princeton, NJ: Lewis-Sigler Institute for Integrative Genomics.
- T2. *Developmental Basis of Evolutionary Change*. 2005. Chicago, IL: The University of Chicago.
- T1. *Meeting of Predoctoral Fellows*. 2005. Chevy Chase, MD: HHMI.

GENERAL AUDIENCE TALKS

- O14. Science on Tap. 2018. Madison, WI: Mirus Bio, Great Dane Brewing Company.
- O13. *Wild Yeast: from Soil to Sourdough*. 2018. Madison, WI: Madison Mycological Society/Madison Fermentation Collective/Madison Sourdough Company.
- O12. *Wednesday Nite @ the Lab*. 2017. Madison, WI: UWBC, Wisconsin Public Television.
- O11. University Roundtable. 2017. Madison, WI: UW.
- O10. Future Farmers of America (FFA) Day. 2016. Madison, WI: Kiwanis Club.
- O9. *Science of Supper Clubs*. 2014. Madison, WI: Wisconsin Science Festival, UW CALS.
- O8. Food Research Institute. 2014. Madison, WI: UW.
- O7. *NextGeneration Sequencing and Array Workshop*. 2014. Madison, WI: Illumina, UWBC.
- O6. *Beer School*. 2012. Madison, WI: Madison Homebrewers and Tasters Guild, Wil-Mar Neighborhood Center.
- O5. Badger Brewing Association. 2012. Madison, WI: UW.
- O4. *Midwest Technical Conference*. 2012. Madison, WI: Master Brewers Association of the Americas.
- O3. *Wednesday Nite @ the Lab*. 2012. Madison, WI: UWBC, Wisconsin Public Television.
- O2. Madison Science Pub. 2011. Madison, WI: <http://sciencepub.us>, Brocach Irish Pub and Restaurant.
- O1. Fourth Tuesday Group. 2011. Madison, WI: UW.

FUNDING

- G12. Collaborative Research: RoL: The evolution of the genotype-phenotype map across budding yeasts (PI, co-PI Antonis Rokas). 15 Jul 2021 - 30 Jun 2026. NSF: DEB-2110403.
- G11. H. I. Romnes Faculty Fellow. 1 Jul 2019 - 30 Jun 2024. UW/WARF.
- G10. Genetic investigation of key traits driving the performance of synthetic and wild lager-brewing yeasts (PI). 1 Oct 2019 - 31 Sep 2023. USDA: Hatch-1020204.
- G9. DIMENSIONS: Collaborative Research: The making of biodiversity across the yeast subphylum (PI, co-PIs Antonis Rokas, Cletus P. Kurtzman). 1 Feb 2015 - 31 Jan 2023. NSF: DEB-1442148.
- G8. Primary Fuel Synthesis and Conversion Residue Valorization (Team Lead and Co-I, PI Timothy J. Donohue). 1 Dec 2017 - 30 Nov 2022. DOE-GLBRC: BER DE-SC0018409).
- G7. Reconstructing the evolutionary transition from respiration to aerobic fermentation (PI). 1 Aug 2014 - 31 Jul 2021. Pew Charitable Trusts: Pew Scholars Program in the Biomedical Sciences.
- G6. Vilas Faculty Early Career Investigator. 1 Jul 2017 - 30 Jun 2019. Vilas Trust Estate.
- G5. CAREER: *Saccharomyces* diversity and the rapid evolution of hybrid lager-brewing yeast (PI). 15 May 2013 - 30 Apr 2019. NSF: DEB-1253634.
- G4. Potential of yeast hybrids for the production of alcoholic beverages (co-PI, PI James L. Steele). 1 Jan 2017 - 31 Dec 2017. Wisconsin Alumni Research Foundation: Robert Draper Technology Innovation Fund.
- G3. Biodesign for fuel production by stress-resistant yeast (Project Lead, PI Timothy J. Donohue). 1 May 2012 - 30 Nov 2017. DOE-GLBRC: BER DE-FC02-08ER64494.
- G2. Genomic investigation of the *Saccharomyces eubayanus*-specific traits responsible for brewing lager, a major value-added barley product (PI). 1 Aug 2014 - 31 Sep 2017. USDA: Hatch-1003258.
- G1. Alfred Toepfer Faculty Fellow Award. 1 Jul 2015 - 30 Jun 2016. Alexander von Humboldt Foundation.

TEACHING AND OUTREACH

2012-16,21-:	Genetics 466: Principles of Genetics (1/4 every semester, 3 credits)
2012-:	Biology/Genetics 522: Communicating Evolutionary Biology (Spring 2-3 credits)
2016-9:	Genetics 467: General Genetics 1 (1/2 Fall, 3 credits)
2016:	<i>Yeast Genetics & Genomics Course</i> . Cold Spring Harbor, NY: Cold Spring Harbor Laboratory.
2016:	Genetics 702: Advanced Genetics 2 (1/3 Spring, 3 credits)
2012-14:	Genetics 701: Advanced Genetics 1 (1/4 Fall, 3 credits)
2006-13:	Ask A Scientist (HHMI)
2009:	Lecturer (NIH-NHLBI Genomics and Proteomics Hands-On Workshop)
2005-6:	Mentor (Interdisciplinary 151: Ways of Knowing Biology)
2003:	Teaching Assistant, Discussion Section Leader (Genetics 466: General Genetics, 3 credits)
1998-2001:	Substitute Teacher (Perry Township, Indianapolis, IN: grades 6-12)
1997:	Ecology Counselor (Camp Ransburg, Bloomington, IN)

STUDENTS AND SCIENTISTS TRAINED AND ADVISED (*former, @co-advisor)

Postdoctoral:	Harrison Moon, Jacek Kominek*, David J. Krause*, John F. Wolters, Kaitlin J. Fisher*, Liang Sun, Linda Horianopoulos, Katharina Barros@, Sae-Byuk Lee@*, William G. Alexander*, David Peris*, Dana A. Opulente*
PhD:	Jassim Al-Oboudi, Emily J. Ubbelohde, John Crandall, Jon Schmitz@*, EmilyClare P. Baker*, Meihua "Christina" Kuang*, Quinn K. Langdon*, Drew T. Doering*
MS:	Lisa Liu@*, Jin Kang*
Undergraduate:	Katarina Aranguiz, Reese Hanke, Molly Hardwick, Quaid Handy, Logan Elkin*, Hezekiah Gillies*, Paul Urban@, Will Spurley*, Taylor Meyer*, Rishitha Nalabothu*, Raymond Wang*, Yuren Sun*, Jenna VanDenAvond*, Hayley Stoneman*, Caroline Miller*, Napoleon Nosker*, James Boudouris*, Ritika Punathil*, Aaron Barton*, Samantha Considine*, Elise Austin*, Edward Cao*, Rachel Schneider*, Manuel Alvarez*, Damayanti Rodríguez Ramos*, Ryan Moriarty*, Daniel Rodríguez*, Kelly Buh*, Max Haase*, Kevin Chen*, Martin Jarzyna*, Cleome Bernick-Roehr*, Bowen Jia*, Siqi "Catherine" Huang*, Krystal Almazan*, Bing Wang*, Michael Price*, Russell Mendez*, Heidi Tessmer*, Brielle James*, Kayla Sylvester*
Staff Scientist:	Russell L. Wrobel, Amanda B. Hulfachor, Sean J. McIlwain@*
Teacher:	Joseph Hartley*, Yvonne Butterfield*, Lisa Sorlie*, Angela Sheddan*, Sarah Wright*
High School:	Thomas Silver*, Ashanti Rogers*
Visiting:	Laura Rusche*, Nicolas Bellora*, Marco António Dias Coelho@*, Carla Gonçalves@, Tadek Krassowski*, Qi-Ming Wang*, Mariana Lopes@*, Juan Ignacio Eizaguirre*, Clara Bruzone*

PROFESSIONAL MEMBERSHIPS AND SERVICE (excluding ad hoc committees)

International Leadership:	International Commission on Yeasts (USA Commissioner)
Member:	Genetics Society of America, Society for Molecular Biology and Evolution, Society for the Study of Evolution, Mycological Society of America, American Association for the Advancement of Science
Editor:	<i>mBio</i> (2022- Editor, 2021 Invited Editor), <i>Frontiers in Fungal Biology</i> (2020- Associate Editor, Fungal Genomics and Evolution), <i>Yeast</i> (2015- Editor, 2017- Founding Co-Lead Editor ecoYeast Series, 2015-21 Lead Editor Yeast Primers Series), <i>Trends in Genetics</i> (2014-, Editorial Board), <i>PLoS Genetics</i> (2017-9 Guest Associate Editor), <i>eLife</i> (2018 Guest Reviewing Editor), <i>Proc Natl Acad Sci USA</i> (2021 Guest Editor),

Grant Panelist: DOE-BER, NSF-DEB, NSF-IOS, NSF-DBI, NASA-SB
Grant Reviewer: NIH-NIGMS, DOE-BER, NSF-MCB, NSF-DEB, NSF-IOS, NSF-DBI, BBSRC-BBR (UK), RCUK-GCRF (UK), Academia Sinica, UW-Milwaukee, Office of the Vice Chancellor for Research and Graduate Education (OVCRGE), College of Agricultural and Life Sciences
Reviewer: *ACS Synth Biol, Appl Environ Microbiol, Appl Microbiol Biotechnol, Biol Rev, BMC Genomics, Biotechnol Biofuels, Cell Syst, eLife, EMBO Rep, Environ Microbiol, Environ Microbiol Rep, Eukaryot Cell, Evolution, Evol Dev, FEBS J, FEMS Yeast Res, G3, Genetics, Genetics (YeastBook), Genome Res, Genome Biol Evol, Genomics, J Ind Microbiol Biotechnol, J Mol Evol, mBio, Microbiol Mol Biol Rev, Mol Biol Evol, Mol Cell Biol, Mol Microbiol, Mol Phylogenet Evol, Mol Syst Biol, Nature, Nat Commun, Nat Microbiol, Nucleic Acids Res, PLoS Biol, PLoS Comput Biol, PLoS Genet, PLoS One, Proc Biol Sci, Proc Natl Acad Sci USA, Science, Sci Rep, Trends Genet, Yeast*
External Evaluator: Royal Society of Canada, Associate Professor with Tenure (3), PhD (2), MS (1)
Organizer: *LIFE: Leveraging Innovations From Evolution*. 2023 (scheduled). Indianapolis, IN/virtual: NSF (Leadership Team, PI Jennifer H. Wisecaver).
International Specialised Symposium on Yeasts. 2022. Vancouver, Canada: ICY (Organizing Committee).
The Allied Genetics Conference. 2020. Virtual Washington, DC: GSA (Cross-Community Workshop Committee).
Molecular Mechanisms of Evolution. 2019. North Easton, MA: Gordon Research Seminar (Mentor and Discussion Leader).
International Specialized Symposium on Yeasts. 2018. Bariloche, Argentina: ICY (International Scientific Committee).
Fungal evolutionary genomics: unravelling mysteries from the forgotten kingdom. 2015. Vienna, Austria: SMBE Symposium (Lead Organizer, Co-organizers Joseph Schacherer, Kenneth H. Wolfe).
2023-: Teaching Professor Appointment and Promotion Committee (Genetics)
2022-: Standing Post Tenure Review Committee (Genetics)
2020-: Diversity, Equity, and Inclusion Committee (Evolution)
2019-: WEI Executive Committee
2017-: GLBRC Bioinformatics and Data Council, Co-Chair; GLBRC Primary Fuel Synthesis Team Lead
2012-: Graduate Education Committee (Evolution), Chair (2013-8)
2005-6,12-: Evolution Coordinating Committee (Evolution), Director (2019-)
2002-7,13-: Evolution Seminar Series Committee (Evolution), Chair (2002-6)
2020-1: Chair's Support Committee (Genetics)
2019-20: Undergraduate Program Committee (Genetics)
2018-9: Chair's Advisory Committee (Genetics)
2017-9: Microbiology Doctoral Training Program Steering Committee
2004-6,12-5,8-9: Graduate Curriculum and Training Grant Committee (Genetics)
2017-8: Faculty Award Nominations Committee (Genetics)
2012-8: Computing Committee (Genetics), Chair (2016-8)
2012-6: Undergraduate Education Committee (Evolution), Chair (2012-3)
2003-4: Graduate Admissions Committee (Genetics)