

Melissa A. Wilson

Associate Professor, Arizona State University
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FACULTY APPOINTMENTS

Associate Professor, Genomics, Evolution, and Bioinformatics, August 2020-present

School of Life Sciences

Computational Life Sciences Program, Co-Director, 2019-present

Evolutionary Biology Graduate Program, Chair, 2016-2020

Center for Evolution and Medicine (CEM)

Center for Mechanisms of Evolution (CME)

Biodiversity Knowledge Integration Center (BioKIC)

Barrett, The Honors College, Honors Faculty

Arizona State University, Tempe, AZ, USA

Adjunct Assistant Professor, Neurogenomics Division, August 2014-present

Translational Genomics Research Institute (TGen), Phoenix, Arizona 85004

Assistant Professor, Genomics, Evolution, and Bioinformatics, August 2014-August 2020

Arizona State University, Tempe, AZ, USA

EDUCATION AND TRAINING

Miller Postdoctoral Fellow, July 2011-July 2014

University of California, Berkeley

Advisor: Dr. Rasmus Nielsen

Ph. D. Integrative Biosciences, Bioinformatics & Genomics, NSF grad research fellow, Aug 2011

The Pennsylvania State University

Primary Advisor: Dr. Kateryna Makova; Co-advisors: Dr. Stephen Schaeffer and Dr. Webb Miller

B.S., Medical Mathematics, with Honors, Recipient of Outstanding Mathematician Award, May 2005

Creighton University

Advisor: Dr. Lance Nielsen

RESEARCH INTERESTS

I am an evolutionary and computational biologist, broadly interested in sex differences in genome evolution, mutation rate variation, and the consequences of population history. I use high performance computing, statistics, simulations, and comparative genomics to study questions relating to sex-biased mutational processes including, how sex chromosomes arise and evolve, why mutation rates differ between males and females, and how expression patterns vary between the sexes. Most recently, my lab is applying this fundamental understanding of evolutionary processes to understand why there are sex-differences in human health, including sex-specific gene expression in the liver cancer, sex differences in human placentas, and how sex-biased processes have affected patterns of genetic variation in human populations in Africa. I am part of an NIH collaborative effort through the Office of Research on Women's Health to develop and implement methodology to better assess variation on the sex chromosomes, and to incorporate sex as a biological variable in clinical and biological studies going forward.

HONORS & AWARDS

2019 *Invited participant*, NIH Workshop on Cloud-Based Platforms Interoperability

2019 *Invited participant*, Joint NIH NHGRI, National Institute of Food and Agriculture (NIFA) and NSF workshop, Perspectives in Comparative Genomics & Evolution

2019 *Awardee*, Mary Lyon Award, International Mammalian Genome Society

2019 NIH NIGMS Director's Early Career Investigator (ECI) Lecturer
 2019 *Invited participant*, NIH/OD ORWH Think Tank: Sex and Chromosomes
 2018 *Awardee*, SMBE Allan Wilson Junior Award for Independent Research
 2018 *Awardee*, Zebulon Pearce Distinguished Teaching Award, ASU, nominated 2015, 2016, 2017
 2017 *Nominee*, Badass Woman of ASU
 2016 *Invited participant*, Kavli Frontiers of Science, National Academy of Science
 2012 *Semifinalist* Charles J. Epstein Trainee Award for Excellence in Human Genetics Research
 2010 *Awardee* Mohnkern Scholarship, The Pennsylvania State University
 2010 Evolution 2010 Conference Travel Fellowship
 2010 *Second Place Award*, Grad Exhibition Poster Competition, Pennsylvania State University
 2010 *Awardee* Braddock Homer Research Award, The Pennsylvania State University
 2010 *First Place Award*, Genome Research poster competition at CSH: The Biology of Genomes
 2010 *Awardee* Institute of Molecular Evolutionary Genetics, Competitive Travel Grant
 2010 *Awardee* Women In the Sciences and Engineering, Travel Grant (\$250 each year)
 2009 *Awardee* Sex & Recombination: In Theory and Practice Conference, Travel Fellowship
 2009 *Selected participant*, NIH Graduate Student Research Festival
 2008 Women In Science and Engineering Outstanding Service Award
 2008 *Selected participant*, Munich Graduate Program EES Summer School: Evolution of Sex Chr
 2007 J. Ben and Helen D. Hill Memorial Award, The Pennsylvania State University
 2006 The Pennsylvania State University NSF GRFP Incentive Award
 2005 Graham Endowed Fellowship: University-wide recognition of highly recruited students
 2005 Huck Institute of the Life Sciences Fellowship
 2005 Huck Institute of the Life Sciences Supplemental Award: For academic excellence
 2005 Creighton University Outstanding Mathematician Award: One award per academic year

PUBLICATIONS

(Trainees: ^u undergraduate; ^g graduate; ^p postdoctoral; ^t technician/programmer/other)

Significance of the author list order: The "First Author" position in the case of primary research publications is reserved to the person most intimately connected with carrying out the experiments and drafting the manuscript. In review articles, the first author is usually the person who most substantially contributed to the writing of the manuscript. On occasions, equally contributing authors deserve to be recognized as "Co-First Authors" or "Co-Senior Authors" and are recognized by a star (*). Middle authors usually contributed to the research by carrying out some of the experiments or substantially assisting in the experiments, intellectual input, experimental design, and writing parts of the manuscripts. The last author position is, usually, reserved for the senior author of correspondence who is responsible for the research design and final version of the manuscript. Corresponding authorships are underlined. Journal impact factors are calculated from the number of citations per publication. Current citations for each article and author indices are from Google Scholar databases.

Wilson, MA - Total citations: 8782; h-index: 21; i10-index: 28

Google Scholar: <https://scholar.google.com/citations?user=IWqoF48AAAAJ&hl=en>

In Review (9 total with preprint where possible)

62. Castillo AI^g, Roos BH^u, Rosenberg MS, Cartwright R, and **Wilson MA**. Genie: An interactive real-time simulation for teaching genetic drift. (*in review*) <https://www.biorxiv.org/content/early/2018/02/22/268672>

61. Phung TN, Olney KC, Kliman HJ, **Wilson MA**. Patchy, incomplete, and heterogeneous X-inactivation in the human placenta. (*in review*) <https://www.biorxiv.org/content/10.1101/785105v1>

60. Fontenele, RS, Kraberger S, Hadfield J, Driver EM, Bowes D, Holland LA, Faleye TOC, Adhikari S, Kumar R, Inchausti R, Holmes WK, Deitrick S, Brown P, Duty D, Smith T, Bhatnagar A, Yeager RA, Holm RH, Hoogesteijn von Reitzenstein N, Wheeler E, Dixon K, Constantine T, Wilson MA, Lim ES, Jiang X, Halden RU, Scotch M and Varsani A. High-throughput sequencing of SARS-CoV-2 in wastewater provides insights into circulating variants. (*in review*)
<https://www.medrxiv.org/content/10.1101/2021.01.22.21250320v1>

59. Phung T, Tchoukalova Y, Grandjean D, Becquer E, Chen L, Steel J, Valentin Dinu, Wilson MA, David G. Lott DG. Gene expression in idiopathic subglottic stenosis (iSGS) suggests an important role for epithelial cells in iSGS pathogenesis (*in review*)
58. Malukiewicz J, Dergram J, Grativol AD, Igayara CS, Ruiz-Miranda CR, Nicola PA, Pereira LMC, Varsani A, Wilson MA, Stone AC, Silva DL, de Fátima Rodrigues da Silva F, Walter L, Zinner D, Roos C. Genomic Skimming and Nanopore Sequencing Uncover Cryptic Hybridization in One of World's Most Threatened Primates (*in review*)
57. Dolby GA^{*p}, Webster TH^{*p}, McCartney-Melstad E, Shaffer HB, DeNardo D, **Wilson M**, Kusumi K. Speciation by river vicariance and monsoon adaptation via low-coverage genome sequencing of desert tortoises (*in review*)
56. Olney KC, Gibson JD, Natri HM, Underwood A, Gadau J, **Wilson MA**. Lack of parent-of-origin effects in *Nasonia* jewel wasp: a replication and extension study (*in review*)
<https://www.biorxiv.org/content/10.1101/2021.02.11.430138v1>
55. Cotter DJ, Webster TH, and **Wilson MA**. Genomic and demographic processes differentially influence genetic variation across the X chromosome (*in review*)
<https://www.biorxiv.org/content/10.1101/2021.01.31.429027v1>
54. Phung T, Webster T, Lenkiewicz E, Malasi S, Andreozzi M, McCullough AE, Anderson KS, Pckaj BA, **Wilson MA**, Barrett MT. Unique evolutionary trajectories of breast cancers with distinct genomic and spatial heterogeneity. *Scientific Reports* (*in review*)

Published Peer-Reviewed Articles (53 total: 12 first authorships; 23 corresponding)

2021 (5)

53. Collins C, DeNardo D, Blake M, Norton J, Schmidlin K, Fontenele R, **Wilson MA**, Kraberger S, Varsani A. 2021. Genome sequences of microviruses identified in *Gila* monster feces. *Microbiology Resources Announcements* (*accepted*)
 Role: Collaborator, collected samples, writing
52. Hinde K, CEG. Amorim, AF Brokaw, N Burt, M Casillas, A Chen, T Chestnut, PK Connors, M Dasari, J Dietrick, CF Ditelberg, J Drew, L Durgavich, B Easterling, C Henning, A Hilborn, EK Karlsson, M Kissel, J Kobylecky, J Krell, DN Lee, KM Lesciotto, KL Lewton, JE Light, J Martin, A Murphy, W Nickley, A Núñez-de la Mora, O Pellicer, V Pellicer, AM Perry, SG Schuttler, AC Stone, B Tanis, J Weber, **M Wilson**, E Willcocks, CN Anderson. 2021. March Mammal Madness and the Power of Narrative in Science Outreach. *eLife* (*accepted*)
 Role: Collaborator, genetics summary, writing
51. Ozga AT, Webster TH^p, Gilby IC, **Wilson MA**, Nockerts RS, Wilson ML, Pusey AE, Li Y, Hahn BH and Stone AC. 2021. Urine as a high quality, abundant source of host genomic DNA from wild populations. *Molecular Ecology* (*accepted*)
 Role: Collaborator, genomics analysis, writing
50. Taravella Oill AM⁹, Deshpande AJ^u, Natri HM^p and **Wilson MA**. 2021. PopInf: An approach for reproducibly visualizing and assigning population affiliation in genomic samples of uncertain origin. *Journal of Computational Biology* (*accepted*) PMID: 33074720
 Role: Senior author, conception/design, writing
49. Massey SC, Whitmire P, Doyle TE, Ippolito J, Mrugala MM, Hu L, Canoll P, Anderson ARA, **Wilson MA**, Fitzpatrick SM, McCarthy MM, Rubin J, Swanson KR. 2021. Sex Differences in Health and Disease: a review of biological sex differences relevant to cancer with a spotlight on glioma. *Cancer Letters* 498:178-187. PMID: 33130315
 Role: Collaborator, analysis, writing

2020 (11)

48. **Wilson MA**. 2020. Searching for sex differences. *Science* 369(6509): 1298-1299.

Role: Sole contributor

47. Borden ES⁹, Kang P, Natri HM^P, Phung TN^P, **Wilson MA**, Buetow KH, Hastings KT. 2020. Neoantigen fitness model predicts lower immune recognition of cutaneous squamous cell carcinomas than actinic keratoses. *Frontiers in Immunology* 10:2799. PMID: 31849976

Role: Collaborator, neopeptide analysis, writing

46. Gemmell N,...**Wilson M**, Rupp S⁹.... Stone C, Ngatiwai Trust Board Ngatiwai Trust Board. 2020. The tuatara genome reveals ancient features of amniote evolution. *Nature* 584(7821): 403-409. PMID: 32760000

Role: Collaborator, sex chromosome comparative genomics and selection analyses, writing

45. Olney K⁹, Brotman SM^U, Valverde-Vesling V^U, Andrews J^U, **Wilson MA**. 2020. Reference genome and transcriptome informed by the sex chromosome complement of the sample increases ability to detect sex differences in gene expression from RNA-Seq data. *Biology of Sex Differences* 11(1): 42. PMCID: PMC7374973

Role: Senior author, conception/design, RNAseq analysis, writing

44. Phung TN^P, Lenkiewicz E, Malasi S, Sharma A, Anderson KS, **Wilson MA**, Pockaj BA, Barrett MT. 2020. Unique genomic and neopeptide landscapes across tumors: a study across time, tissues, and space within a single Lynch Syndrome patient. *Scientific Reports* 10(1):12190. PMCID: PMC7376229

Role: Collaborator, Neopeptide analysis, writing

43. Powell GL, Vannan A, Bastle RM, **Wilson MA**, Dell'Orco M, Perrone-Bizzozero NI, Neisewander JL. 2020. Environmental enrichment during forced abstinence from cocaine self-administration opposes gene network expression changes associated with the incubation effect. *Scientific Reports* 10(1):11291. PMCID: PMC7347882

Role: Collaborator, RNAseq analysis, writing

42. Dolby GA^P, Morales M, Webster TH^P, DeNardo D, **Wilson M**, Kusumi K. 2020. Discovery of a new TLR gene and gene expansion event through improved desert tortoise genome assembly with chromosome-scale scaffolds. *Genome Biology and Evolution* 12(2): 3817-3925 PMCID: PMC7058155

Role: Collaborator, comparative genomics, writing

41. Orton J, Morales M, Fontenele R, Schmidlin K, Kraberger S, Leavitt D, Webster T^P, **Wilson MA**, Kusumi K, Dolby G*, Varsani A*. 2020. Virus discovery in desert tortoise fecal samples: Novel circular single stranded DNA viruses. *Viruses* 12(2): 143. PMCID: PMC7077246

Role: Collaborator, sample collection, writing

40. **Wilson MA** and Buetow KH. 2020. Novel mechanisms of cancer emerge when accounting for sex as a biological variable. 2020. *Cancer Research*. 80(1) 27-29. PMCID: PMC6942614

Role: Co-corresponding author; developed idea, oversaw all components of writing and synthesis

39. Natri H^P, Garcia A, Buetow KH, Trumble B and **Wilson MA**. 2020. Endogenous retroviruses and the Pregnancy Compensation Hypothesis. *Trends in Genetics* 36(1):2-3. PMCID: PMC7357623

Role: Senior author; developed idea, oversaw all components of writing and synthesis

38. Garcia A, Natri H^P, Buetow KH, Trumble B and **Wilson MA**. 2020. Evolution of immune sexual dimorphism in response to placental invasiveness. *Trends in Genetics* 36(1):5-7. PMCID: PMC7373348

Role: Senior author; developed idea, oversaw all components of writing and synthesis

2019 (7)

37. **Wilson MA** 2019. Crowdfunding science *Genome Biology*. 20, 250 PMCID: PMC6876096

Role: Sole contributor

36. Williams JJ, Drew JC, Galindo-Gonzalez S, Robic S, Dinsdale E, Morgan W, Triplett EW, Burnette J, Donovan S, Elgin S, Fowlks ER, Goodman AL, Grandgenett NF, Goller C, Hauser C, Jungck JR, Newman JD, Pearson W, Ryder E, **Wilson MA**, Sierk M, Smith T, Tosado-Acevedo R, Tappich W, Tobin TC, Toroy A, Welch L, Wright R, Ebenbach D, McWilliams M, Rosenwald AG, Pauley MA. 2019. Barriers to integration of bioinformatics into undergraduate life sciences education: a national study of US life sciences

faculty uncover significant barriers to integrating bioinformatics into undergraduate instruction. *PLoS One* 14(11):e0224288. PMID: PMC6860448

Role: Study development

35. Natri HP, **Wilson MA***, and Buetow K*. 2019. Distinct molecular etiologies of male and female hepatocellular carcinoma. *BMC Cancer*. 19(951). PMID: PMC6794913

Role: Co-corresponding author; developed idea, oversaw all components of writing and synthesis

34. Natri HP, Garcia A, Buetow KH, Trumble B and **Wilson MA**. 2019. The Pregnancy Pickle: Evolved immune compensation due to pregnancy underlies sex differences in human diseases. *Trends in Genetics* 35(7):478-488. PMID: PMC6611699

Role: Senior author; developed idea, oversaw all components of writing and synthesis

33. Webster TH^P, Phung T, Grande B, Karlins E, Richmond P, Couse M, Whitford W, and **Wilson MA**. 2019. Identifying, understanding, and correcting technical artifacts on the sex chromosomes in next-generation sequencing data. *GigaScience* 8(7):giz074. PMID: PMC6615978

Role: Co-senior author; developed project idea, oversaw all sex chromosome analyses

32. Phung T, Wayne B, **Wilson MA*** and Lohmueller K*. 2019. Complex patterns of sex-biased demography in canines. *Proceedings of the Royal Society B* 286(1903): 20181976. PMID: PMC6545087

Role: Co-senior author; developed project idea, oversaw all sex chromosome analyses

31. Narang P^P, Chen M, Sharma AA, Anderson KS and **Wilson MA**. 2019. The neoepitope landscape of breast cancer: implications for immunotherapy. *BMC Cancer* 19(1):200. PMID: PMC6399957

Role: Developed and oversaw all computational aspects of the project

2018 (9)

30. Olney K^{C9}, Nyer DB, **Wilson Sayres MA**, and Haynes K. 2018. The synthetic histone-binding regulator protein PcTF activates interferon genes in breast cancer cells. *BMC Systems Biology* 12: 83.

Role: Co-developed and oversaw all computational aspects of the project

29. Somayaji V, DeNardo D, **Wilson Sayres MA**, Waits K, Fontenele R, Kraberger S, Varsani A. 2018 Genome of single stranded DNA virus identified in Gila monster feces. *Microbiology Resource Announcements* 7: e00925-18.

Role: Collected fecal samples

28. Krishna S, Ulricha P, Wilson E, Parikhe F, Narang P^P, Yang S, Clark A, Kim-Schulze S, Park J, Posner M, **Wilson Sayres MA**, Sikora A, and Anderson KS. 2018. Human papilloma virus specific immunogenicity and dysfunction of CD8+ T cells in head and neck cancer. *Cancer Research* 79(21): 6159-6170.

Role: Conducted HLA-type inference and neoepitope identification

27. Barrett MT, Lenkiewicz E, Malasi S, Basu A, Holmes Yearley J, Annamalai L, McCullough AE, Kosiorek H, Narang P^P, **Wilson Sayres MA**, Chen M, Anderson KS, and BA Pockaj. 2018. The association of genomic lesions and PD-1/PD-L1 expression in resected triple negative breast cancers. *Breast Cancer Research* 20(1): 71.

Role: Conducted breast cancer genomics analyses

26. **Wilson Sayres MA**, Hauser C, Sierk M, Robic S, Rosenwald AG, Smith TM, Triplett, EW, Williams JJ, Dinsdale E, Morgan W, Burnette III JM, Donovan SS, Drew JC, Elgin SCR, Fowlks ER, Galindo-Gonzalez S, Goodman, AL, Grandgenett NF, Goller CC, Jungck J, Newmann JD, Pearson WR, Ryder E, Tosado-Acevedo R, Tappich W, Tobin TC, Toro-Martínez A, Welch LR, Wright R, Ebenbach D, Olney C, McWilliams M, Pauley MA. 2018. Bioinformatics Core Competencies for Undergraduate Life Sciences Education. *PLoS One* 13(6): e0196878.

Role: First author, primary data analysis, writing, and interpretation

25. Damgaard PB... **Wilson Sayres MA**, Taravella AM⁹... and Willerslev E. 2018. 137 ancient human genomes from across the Eurasian steppes. *Nature* 557(7705): 369-374.

Role: Characterizing Y haplotype variation

24. **Wilson Sayres MA**. Genetic diversity on sex chromosomes. 2018. *Genome Biology and Evolution*. 10(4):1064-1078.

Role: Sole author

23. Tollis M, Hutchins E, Stapely J, Eckalbar W, Rupp S^g, Maayan I, Lasku E, Infante C, Dennis S, Robertson J, May C, Crusoe M, Bermingham E, DeNardo D, Hsieh S, Huentelman M, Kulathinal R, McMillan WO, Menke D, Pratt S, Rawls JA, Sanjur O, **Wilson Sayres MA**, Wilson-Rawls J, Fisher R and Kusumi K. 2018. Comparative genomics reveals accelerated evolution in conserved pathways during the diversification of anole lizards. *Genome Biology and Evolution* 10(2):489-506.

Role: Contributor - conducted dN/dS analysis across species

22. Chowell D^g, Napier J, Gupta R, Anderson KS, Maley CC and **Wilson Sayres MA**. 2018. Modeling the subclonal evolution of cancer cells. *Cancer Research* 78(3):830-839.

Role: PI, corresponding author - directed all data analysis and interpretation

2017 (2)

21. Olney K^g, Narang P^P, Taravella A^g, Webster TH^P and **Wilson Sayres MA**. 2017. EvSex16: Evolutionary Genomics of Sex. *Journal of Heredity* 108(7): 707-708. doi: 10.1093/jhered/esx084

Role: PI, corresponding author

20. Rupp S^g, Webster TH^P, Olney K^t, Hutchins E, Kusumi K and **Wilson Sayres MA**. 2017. Evolution of dosage compensation in *Anolis carolinensis*, a reptile with XX/XY chromosomal sex determination. *Genome Biology and Evolution* 9(1): 231-240.

Role: PI, corresponding author - directed all data analysis and interpretation

2016 (6)

19. Taravella A^g and **Wilson Sayres MA**. 2016. Fruitful analysis of sex chromosomes reveals X-treme genetic diversity. *Genome Biology*. 17(1): 244.

Role: PI, corresponding author, equal contributor to writing/interpretation.

18. Narang P^P and **Wilson Sayres MA**. 2016. Variable autosomal and X divergence near and far from genes affects estimates of male mutation bias in great apes. *Genome Biology and Evolution* 8(11): 3393-3405.

Role: PI, corresponding author - directed all data analysis and interpretation

17. Webster T^P and **Wilson Sayres MA**. 2016. Genomic signatures of sex-biased demography: progress and prospects. *Current Opinion in Genetics and Development* 3(41): 62-71. doi:10.1016/j.gde.2016.08.002

Role: PI, corresponding author, co-wrote and interpreted

16. Pagani L... **Wilson Sayres MA**... et al. 2016. Genomic analyses inform on migration events during the peopling of Eurasia. *Nature* 538: 238-242. doi:10.1038/nature19792

Role: Contributor - conducted population genetics analysis, writing, and interpretation

15. Poznik GD, Xue Y, Mendez F, Willems T, Massaia A, **Wilson Sayres MA**, et al. (37 others). 2016. Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. *Nature Genetics* 48: 593-599. doi: 10.1038/ng.3559

Role: Contributor - conducted population genetics simulations, data analysis, writing, and interpretation

14. Cotter DJ^u, Brotman SM^u and **Wilson Sayres MA**. 2016. Genetic diversity on the human X chromosome does not support a strict pseudoautosomal boundary. *Genetics* 203(1): 485-492. doi:10.1534/genetics.114.172692

Role: PI, corresponding author - directed all data analysis and interpretation

2015 (3)

13. 1000 Genomes Consortium ... **Wilson Sayres MA**... . 2015. A global reference for human genetic variation. *Nature* 526: 68-74. doi:10.1038/nature15393

Role: Contributor - conducted computational modeling, discussion, and interpretation

12. Karmin M*, Saag L*, Vicente M*, **Wilson Sayres M***, *et. al (95 others)*. 2015. A recent bottleneck of Y chromosome diversity coincides with a global change in culture. *Genome Research* **25**(4): 459-466. doi:10.1101/gr.186684.114

Role: Co-primary researcher - conducted computational modeling, data analysis, and interpretation

11. Boddy A, Fortunato A, **Wilson Sayres M** and Aktipis A. 2015. Cooperation and conflict beyond the womb: The paradoxical effects of fetal microchimerism on maternal health. *BioEssays* **37**(10): 1106-1118. doi:10.1002/bies.201500059

Role: Co-senior author – Coordinated the project, conducted primary interpretation.

2009-2014 (Prior to starting as faculty: 10)

10. **Wilson Sayres MA**, Lohmueller KE and Nielsen R. 2014. Natural selection reduced diversity on human Y chromosomes. *PLoS Genetics* 10(1): e1004064. doi:10.1371/journal.pgen.1004064

Role: Primary researcher - conducted all experiments, data analysis, and interpretation.

9. Tsai Paulina^u and **Wilson Sayres MA**. 2013. Evolution of the phosphatase gene family across nematode worms and flies. *Berkeley Scientific Journal* 18(1): 87-93.

<http://escholarship.org/uc/item/2sb4992b>

Role: PI, corresponding author - directed all experiments, data analysis, and interpretation.

8. Pandey R*, **Wilson Sayres MA*** and Azad R. 2013. Detecting evolutionary strata on the human X chromosome in the absence of gametologous Y-linked sequences. *Genome Biology and Evolution* **5**(10): 1863-1871. doi:10.1093/gbe/evt139

Role: Co-primary researcher and co-PI - conducted or directed all experiments, data analysis and interpretation

7. Somel M, **Wilson Sayres MA**, Jordan G, Huerta-Sanchez E, Fumagalli M, Ferrer-Admetlla A, and Nielsen R. 2013. A scan for human-specific relaxation of negative selection reveals unexpected polymorphism in the proteasome. *Molecular Biology and Evolution* **30**(8): 1808-1815.

doi:10.1093/molbev/mst098

Role: Collaborator - conducted data analysis, provided advice on analysis and interpretation

6. **Wilson Sayres MA** and Makova KD. 2013. Gene survival and death on the human Y chromosome. *Molecular Biology and Evolution* **30**(3): 781-7. doi:10.1093/molbev/mss267

Role: Primary researcher – conducted all experiments, data analysis and interpretation.

5. **Wilson Sayres MA**, Brooks AJ, Chanock SJ, Cheung V, Goldstein DB, Jin L, and Kwok P-Y. 2012. HGV2011: Personalized genomic medicine meets the incidentalome. *Human Mutation* **33**(3): 582-5. doi:10.1002/humu.22008

Role: Primary researcher – conducted survey and synthesis, coordinated all researchers.

4. **Wilson Sayres MA**, and Makova KD. 2011. Genome analyses substantiate male mutation bias in many species. *BioEssays* **33**(12): 938-45. doi:10.1002/bies.201100091

Role: Primary researcher – conducted survey and synthesis.

3. **Wilson Sayres MA**, Venditti C, Pagel M, and Makova KD. 2011. Do variations in substitution rates and male mutation bias correlate with life-history traits? A study of 32 mammalian genomes. *Evolution* **65**(10): 2800-15. doi:10.1111/j.1558-5646.2011.01337.x

Role: Primary researcher – conducted all experiments, data analysis and interpretation.

2. **Wilson MA**, and Makova, KD. 2009. Genomic analyses of sex chromosome evolution. *Annual Reviews of Human Genetics and Genomics* **10**: 333-54. doi:10.1146/annurev-genom-082908-150105

Role: Primary researcher – conducted survey and synthesis.

1. **Wilson MA**, and Makova, KD. 2009. Evolution and survival on eutherian sex chromosomes. *PLoS Genetics* **5**(7): e1000568. doi:10.1371/journal.pgen.1000568

Role: Primary researcher – conducted all experiments, data analysis and interpretation.

Contributed publications (7 total)

7. Phadke S, Rupp S⁹ and **Wilson MA**. Understanding the evolution of anisogamy in the early diverging fungus, *Allomyces*. BioRxiv: <https://www.biorxiv.org/content/early/2017/12/07/230292>
6. Webster TH^P, Dolby GA, **Wilson Sayres MA** and Kusumi K. 2018. Improved draft of the Mojave Desert tortoise genome *Gopherus agassizii*, version 1.1. PeerJ: <https://peerj.com/preprints/3266/>.
5. Contributor. 2017. Frankenstein: A New Edition for Scientists and Engineers. Editors: Jason Robert, David Guston, and Ed Finn. MIT Press (*ASU's Lincoln Center for Applied Ethics*).
4. **Wilson Sayres MA**. 2016. Pseudoautosomal Linkage, Region, Reference Module in Life Sciences. Brenner's Online Encyclopedia of Genetics.
3. **Wilson Sayres MA**. 2015. "Evolution, Trends in." *Discoveries in Modern Science: Exploration, Invention, Technology*. Ed. James Trefil. Vol. 1. Farmington Hills, MI: Macmillan Reference USA. 330-333.
2. **Wilson Sayres MA***. 2013. Timing of ancient human Y lineage depends on mutation rate: a comment on Mendez et al. *arXiv*. 1304.6098.
1. **Wilson Sayres MA**. 2013. Pseudoautosomal Linkage, Region, In: Brenner's Encyclopedia of Genetics (Second Edition). Elsevier: 514-516.

Software, Patents, and Protocols

5. *EpitopeHunter*, Identifying tumor neoepitopes: <https://github.com/SexChrLab/EpitopePipeline>
4. *Patent*, Activation of tumor suppressor genes in breast cancer cells by a synthetic chromatin effector
3. *XYalign*, Accurate aligning sex chromosomes: <https://github.com/SexChrLab/XYalign>
*Cited in *Nature Reviews Genetics*: The role of sex in the genomics of human complex traits
2. *TumorSim*, Simulating tumor heterogeneity: <https://github.com/WilsonSayresLab/TumorHeterogeneity>
1. *DNA extraction outreach*: <https://www.protocols.io/view/Extracting-DNA-from-bananas-esvbee6>

PLENARY/INVITED TALKS (30 total: 12 Plenary; 17 Conferences; 1 Sponsored)

30. **Invited Conference**, European Society for Evolutionary Biology (ESEB) 2021, Virtual, *Aug 2022*
29. **Plenary**, Human Behavior and Evolution Society (HBES), Santa Fe, New Mexico, *Jun 2021*
28. **Invited Conference**, Bioconductor 2021, Seattle, WA, *Aug 2021*
27. **Invited Conference**, Building Bridges 2020: "Sex, Gender and Precision Medicine", Helsinki, Finland, *Nov 2020*
26. **Invited Conference**, American Society of Human Genetics, Virtual Meeting, *Oct 2020*
25. **Plenary**, TorBUG: Bioinformatics User Group, Toronto, CANADA, *Oct 2020*
24. **Invited Conference**, Biology of Helodermatids (Beaded Lizards and Gila Monster) Mini-Symposium, Chiricahua Desert Museum & Geronimo Event Center, *July 2020 – Cancelled due to COVID19*
23. **Invited Conference**, Lorne GENOME Conference, Lorne Victoria, Australia, *Feb 2020*
22. **Plenary**, 53rd Population Genetics Group meeting (PGG53), University of Leicester, UK, *Jan 2020*
21. **Invited Conference**, 8th annual Mayo Clinic Individualizing Medicine Conference: Precision Cancer Care Through Immunotherapy and Genomics, *Sep 2019*
20. **Invited Conference**, Vertebrate Sex Chromosomes Session, Society for the Study of Evol, *Jun 2019*
19. **Plenary**, NIGMS Director's Early Career Investigator (ECI) Lecturer, *Apr 2019*
18. **Invited Conference**, Genome Informatics, Wellcome Trust, Hinxton, UK, *Sep 2018*
17. **Keynote Plenary**, Annual Integrative & Systems Biol Student Symposium, Laval Univ, Quebec City, *Aug 2018*
16. **Invited Conference**, SMBE Early Career Award Lecture, Yokohama, Japan, *Jul 2018*
15. **Invited Conference**, American Association of Physical Anthropologists, Austin, TX, *Apr 2018*
14. **Invited Symposium**, Women in Sex and Medicine: Why X? SeXY Chromosome Symposium, Stanford University, Palo Alto, CA, *Feb 2018*
13. **Plenary**, International Plant & Animal Genome Conf (PAG) XXVI, San Diego, CA, *Jan 2018*
12. **Invited Conference**, 2017 SW Reg Society for Develop Biol, MD Anderson, Houston, TX, *Oct 2017*
11. **Plenary**, 2017 Data Intensive Biology Summer Institute, Davis, CA, *Jun 2017*

10. **Invited Conference**, Society for the Study of Evol: Education Symposium, Portland, OR, *Jun 2017*
9. **Opening Keynote**, University of Pennsylvania Institute for Biomedical Informatics & Genomics and computational Biology Graduate Group 2017 Annual retreat, Philadelphia, PA, *Jun 2017*
8. **Plenary**, VanBUG: Bioinformatics User Group, Vancouver, CANADA, *May 2017*
7. **Invited Conference**, Experimental Biology, Chicago, IL, *Apr 2017*
6. **Opening Keynote**, Center for Medical Genomics Retreat, State College, PA, *May 2016*
5. **Sponsored Lecture**, Mindlin Sponsored Lecture, University of Washington, Seattle, WA, *Feb 2016*
4. **Invited Conference**, BioConference Live 2015 Genetics and Genomics Conference, *May 2015*
3. **Invited Conference**, The American Society of Human Genetics Meeting, San Diego, CA, *Oct 2015*
2. **Invited Conference**, International Society for Evol, Med, & Public Health, Tempe, AZ, *Mar 2015*
1. **Plenary**, Univ of Nebraska, Lincoln, 8th Annual Regional Math. Conf. Lincoln, NE, *Oct 2006*

INVITED SEMINARS (56 total)

56. **Seminar**, Dept Organismal Biology, Uppsala, Sweden, *May 2021*
55. **Seminar**, Genome Sciences, U of Washington, Seattle, WA, *May 2021*
54. **Seminar**, Dept. of Obstetrics, Gyn & Rep Sci, Yale School of Medicine, New Haven, CT, *Nov 2020*
53. **Seminar**, Dept of Information Science, Univ of Arkansas at Little Rock, Little Rock, AR, *Nov 2020*
52. **Seminar**, Center for Mol Biol & Biotech, Florida Atlantic University, Boca Raton, FL, *Oct 2020*
51. **Seminar**, Vanderbilt University Medical Center, Nashville, TN, *Sep 2020*
50. **Seminar**, Dept of Biochem & Molecular Genet, U of Colorado School of Med, Aurora, CO, *Sept 2019*
49. **Seminar**, Mayo Clinic, Scottsdale, AZ, *Apr 2019*
48. **Seminar**, Dept of Biology, Texas A&M University, College Station, TX, *Mar 2019*
47. **Seminar**, Dept of Biological Sciences, Marquette University, Milwaukee, WI, *Mar 2019*
46. **Seminar**, Dept of Biology, University of Oregon, Eugene, OR, *Dec 2018*
45. **Seminar**, Genetics seminar series, University of Florida, Gainesville, FL, *Jan 2019*
44. **Seminar**, Dept of Biology, Duke University, Durham, NC, *Jan 2019*
43. **Seminar**, Curriculum in Genetics & Molecular Biology, UNC Chapel Hill, Chapel Hill, NC, *Jan 2018*
42. **Seminar**, Institute of Arctic Biology, University of Alaska Fairbanks, Fairbanks, AK, *Nov 2017*
41. **Seminar**, Campus-wide Frontiers in Bioinf & Systems Biol, UCSD, San Diego, CA, *Oct 2017*
40. **Seminar**, Ecology, Evol, Genetics & Genomics, University of Rochester, Rochester, NY, *Sep 2017*
39. **Seminar**, Dept of Genetics, Harvard Medical School, Boston, MA, *Sep 2017*
38. **Seminar**, Biology Dept, University of Nebraska - Lincoln, Lincoln, NE, *Aug 2017*
37. **Seminar**, Dept of Biology, UC Riverside, Riverside, CA, *May 2017*
36. **Seminar**, Dept of Ecology and Evol Biology, University of Toronto, Toronto, CANADA, *Jan 2017*
35. **Seminar**, Human Genetics (Genetics & Genomics) series, UCLA, Los Angeles, CA, *Nov 2016*
34. **Seminar**, Ecology, Evol & Environmental Biol, Columbia University, New York City, NY, *Oct 2016*
33. **Seminar**, Center for the Study of Human Origins colloquium, NYU, New York City, NY, *Oct 2016*
32. **Seminar**, Dept of Human Genetics, Salt Lake City, UT, *Oct 2016*
31. **Seminar**, Evolutionary, Developmental & Population Genetics series, UC-Davis, Davis, CA, *Apr 2016*
30. **Seminar**, Genetics, Genomics & Systems Biology, University of Chicago, Chicago, IL, *Feb 2016*
29. **Seminar**, Dept of Ecology and Evolutionary Biology, University of Arizona, Tuscon, AZ, *Jan 2016*
28. **Seminar**, The School of Plant Sciences, University of Arizona, Tuscon, AZ, *Sept 2015*
27. **Seminar**, Department of Biology and Biochemistry, University of Houston, Houston, TX, *Sept 2015*
26. **Seminar**, Mol & Cellular Biol Graduate Colloquium, Arizona State University, Tempe, AZ, *Oct 2014*
25. **Seminar**, Center for Evolution and Medicine, Arizona State University, Tempe, AZ, *Nov 2014*
24. **Seminar**, Center for Personalized Diagnostics, The Biodesign Institute, ASU, Tempe, AZ, *Oct 2014*
23. **Seminar**, Translational Genomics Research Institute, Phoenix, AZ, *Aug 2014*
22. **Seminar**, Center on Comp, Evol & Human Genomics, Stanford University, Stanford, CA, *Mar 2014*
21. **Seminar**, Department of Biological Sciences, Louisiana State University, Baton Rouge, LA, *Mar 2014*
20. **Seminar**, School of Integrative Biology, The University of Illinois, Campaign-Urbana, IL, *Mar 2014*
19. **Seminar**, Department of Biological Sciences, The University of Alabama, Tuscaloosa, AL, *Feb 2014*
18. **Seminar**, School of Life Sciences, Arizona State University, Tempe, AZ, *Feb 2014*
17. **Seminar**, Biology Department, Clark University, Worcester, MA, *Feb 2014*
16. **Seminar**, Biological Sciences, Auburn University, Auburn, AL, *Feb 2014*
15. **Seminar**, Dept of Biological Statistics & Comp Biology, Cornell University, Ithaca, NY, *Feb 2014*

14. **Seminar**, Dept of Biology and Biotech, Worcester Polytechnic Institute, Worcester, MA, *Feb 2014*
13. **Seminar**, Department of Mathematics, Creighton University, Omaha, NE, *Nov 2013*
12. **Seminar**, Dept of Comp Med & Bioinf, Univ of Michigan Medical School, Ann Arbor, MI, *Nov 2013*
11. **Seminar**, Department of Biology, The University of Texas-Tyler, Tyler, TX, *Nov 2013*
10. **Seminar**, Department of Biology, The University of Kentucky, Lexington, KY, *Nov 2013*
9. **Seminar**, Dept of Ecology & Evolutionary Biology, University of Kansas, Lawrence, KS, *Sep 2013*
8. **Seminar**, Center for Medical Genomics, Pennsylvania State University, State College, PA, *Sep 2013*
7. **Seminar**, Biology Department, University of Nebraska-Lincoln. Lincoln, NE, *Nov 2012*
6. **Seminar**, Mathematics department at the University of North Texas. Denton, TX, *Oct 2012*
5. **Seminar**, Biology Department at Creighton University. Omaha, NE, *Nov 2012*
4. **Seminar**, Ecology & Evol Colloquium at San Francisco State University. San Francisco, CA, *Oct 2011*
3. **Seminar**, Center for Theoretical & Evolutionary Genetics, UC-Berkeley. Berkeley, CA, *Oct 2010*
2. **Seminar**, Ecology and Evolution seminar at The University of Pittsburgh. Pittsburgh, PA, *Sep 2009*
1. **Seminar**, Bioinformatics Research Center at Aarhus University. Aarhus, Denmark, *Sep 2008*

CONTRIBUTED PRESENTATIONS (26 total: 5 by trainees; 21 as primary presenter)

(*presenter; Lab trainees: ^u undergraduate; ^g graduate; ^p postdoctoral; ^t technician/programmer)

27. Wilson MA, Phung T, Emanuel Becquer, . Aberrant epithelial regeneration in idiopathic subglottic stenosis (ISGS). Online, *Sep 2019*
26. Phung T^p, Wilson MA^{*}, Lohmueller K^{*}. Complex patterns of sex-biased demography in canines. *Evolution*, Providence, RI, *Jun 2019*
25. Taravella A^{*g}, **Wilson Sayres M**. The effects of low coverage sequence data on demographic reconstruction. **Contributed talk**. Society for the Study of Evolution. Portland, OR, *Jun 2017*.
24. **Wilson Sayres MA^{*}**, Chowell D^g, Napier J, Gupta R, Faiss L and Maley C. Modeling the subclonal evolution of cancer cell populations. **Platform presentation**. American Society for Human Genetics. Vancouver, BC, CANADA, *Oct 2016*.
23. Narang P^p and **Wilson Sayres MA^{*}**. Variable X/A divergence and male-mutation bias near and far from genes in great apes. **Selected talk**. International Society of Primatologists, Chicago, IL, *Aug 2016*.
22. **Wilson Sayres MA^{*}**. Population history and patterns of sex-biased evolution. **Selected talk**. International Society for Evolutionary Medicine and Public Health, Raleigh-Durham, NC, *June 2016*.
21. Tollis M^{*}, Hutchins E, Stapley J, Eckalbar WL, Rupp SM^g, Maayan I, **Wilson Sayres MA**, Fisher R and Kusumi K. Multiple genomes reveal accelerated evolution in conserved pathways during anolis lizard adaptive radiations. **Selected Talk for Spotlight Session**. Society for the Study of Evolution. Austin, TX, USA, *June 2016*.
20. Olney K^{*t}, Skotte L, Nielsen R and **Wilson Sayres MA**. Accurately inferring imbalanced allele expression using logistic regression models. **Selected Talk**. Southern California Evolutionary Genetics and Genomics Meeting. Los Angeles, CA, USA, *February 2016*.
19. Chowell D^{*g}, Napier J, Maley C and **Wilson Sayres MA**. Dynamics of heterogeneous clonal evolution in cancer cell populations. **Selected talk**. Evolution and Cancer Conference. San Francisco, CA, USA, *December 2015*.
18. **Wilson Sayres MA^{*}**. Diversity varies across recombining and non-recombining regions of the human sex chromosomes. **Selected talk**. American Society of Human Genetics, Baltimore, MD, *October 2015*.
17. Narang P^{*p} and **Wilson Sayres MA**. Variable X/A divergence and male-mutation bias near and far from genes in great apes. **Selected talk**. Society for Molecular Biology and Evolution, Vienna, Austria, *June 2015*.
16. **Wilson Sayres MA^{*}**. Diversity varies across recombining and non-recombining regions of the human sex chromosomes. **Selected talk**. Society for Molecular Biology and Evolution, Vienna, Austria, *June 2015*.
15. Narang P^{*p} and **Wilson Sayres MA**. Variable X/A divergence and male-mutation bias near and far from genes in great apes. **Selected talk** at Southern California Evolution and Genomics meeting, Riverside, CA, *April 2015*.
14. **Wilson Sayres MA^{*}**. Modeling human Y chromosome bottlenecks and historical effective population size. **Selected talk** at Southern California Evolution & Genomics meeting, Riverside, CA, *April 2015*.

13. **Wilson Sayres MA***, Lohmueller K, and Nielsen R. Abundant natural selection reduced diversity on human Y chromosomes. **Selected talk**. ASHG. San Francisco, CA, *November 2012*.
12. **Wilson Sayres MA***, Venditti C, Chairmonte F, Pagel M, and Makova KD. Life history traits affect the magnitude of male mutation bias across 32 eutherian mammals. **Selected talk**. Society for Molecular Biology and Evolution 2010. Lyon, France, *July 2010*.
11. **Wilson Sayres MA***, Venditti C, Chairmonte F, Pagel M, and Makova KD. Life history traits affect the magnitude of male mutation bias across 32 eutherian mammals. **Talk**. Evolution 2010. Portland State University, Portland, OR, *June 2010*.
10. **Wilson Sayres MA***, Venditti C, Chairmonte F, Pagel M, and Makova KD. Life history traits affect the magnitude of male mutation bias across 32 eutherian mammals. **Seminar**. The Institute for Molecular Evolutionary Genetics at The Pennsylvania State University. State College, PA, *April 2010*.
9. **Wilson MA***, Chiaromonte F and Makova KD. Male mutation bias observed across 34 mammalian genomes. **Selected talk**. Sex and Recombination: In Theory & In Practice. Iowa City, IA, *June 2009*.
8. **Wilson MA*** and Makova KD. Evolution and survival on eutherian sex chromosomes. **Talk**. Munich EES Summer School on "The Evolution of Sex Chromosomes". Germany, *September 2008*.
7. **Wilson MA*** and Makova KD. Evolution and survival on eutherian sex chromosomes. **Talk**. Evolution 2008. Minneapolis, MN, *June 2008*.
6. **Wilson MA*** and Makova KD. Evolution and survival on eutherian sex chromosomes. **Seminar**. Institute for Mol Evol Genetics at The Pennsylvania State University, State College, PA, *March 2008*.
5. **Wilson MA*** and Zelnio K. A natural history of unintelligent design: In celebration of Darwin day. **Talk**. The Biology Department Graduate Student Association. State College, PA, *February 2008*.
4. **Wilson MA*** and Makova KD. A unique type of duplication: how do genes survive on sex chromosomes? **Selected talk**. SMBE 2007. Nova Scotia, Canada, *June 2007*.
3. **Wilson MA*** and Malkmus D. Assessing the status of undergraduate women students at Penn State University. **Talk** to Dr. Graham Spanier, President Penn State, University Park, PA, *March 2007*.
2. **Wilson MA** and Makova KD. Evolution of sex linked genes versus their autosomal counterparts: A comparison between human, mouse & opossum. **Talk**. Evolution 2006. Stony Brook, NY, *July 2006*.
1. **Wilson MA***, Ufimtsev V and Deng B. A Stoichiometric model for tumor formation. **Talk**. the Joint Am Mathematics Assoc/Mathematics Assoc of America National meeting. Atlanta, GA, *January 2005*.

POSTER PRESENTATIONS (85 total: 67 by lab trainees; 8 as primary presenter)

(*presenter; Lab trainees: ^u undergraduate; ^g graduate; ^p postdoctoral; ^t technician/programmer)

85. Taravella Oill AM^g, Carla Handley, Emma K. Howell, Anne C. Stone, Sarah Mathew, **Wilson MA**. Genomic analysis reveal geography rather than culture as the predominant factor shaping genetic variation in northern Kenyan human populations. The American Society of Human Genetics 2020, Virtual, *Oct 2020*.
84. Olney KC^g, Phung TN^p, **Wilson MA**. Comparison of sex differences in human placentas to adult tissues differences. ASHG, Virtual, *Oct 2020*
83. Olney KC^g, Phung TN^p, **Wilson MA**. Comparison of sex differences in human placentas to adult tissues differences. Abstract 2378. Presented at the 70th Virtual Meeting of The American Society of Human Genetics conference, Virtual Meeting, *Oct 2020*
82. Taravella Oill AM^g, Carla Handley, Emma K. Howell^u, Anne C. Stone, Sarah Mathew, **Wilson MA**. Genomic analysis reveal geography rather than culture as the predominant factor shaping genetic variation in northern Kenyan human populations. Genome Informatics 2020, Virtual, *Sep 2020*.
81. Olney KC^g, Phung TN^p, **Wilson MA**. An approach for quantifying allele-specific expression estimates on the X chromosome. Abstract 87. Genome Informatics, Virtual Meeting, *Sep 2020*
80. Peters M^g, Chiou K, Natri H^p, Buetow K, Snyder-Mackler N, **Wilson MA**. Investigating Sex Biased Gene Expression in the Brain to Explain Alzheimer's Disease Mechanisms: Genome Informatics 2020, virtual, *Sep 2020*
79. Peters M^g, Chiou K, Natri H^p, Buetow K, Snyder-Mackler N, **Wilson MA**. Investigating Sex Biased Gene Expression in the Brain to Explain Alzheimer's Disease Mechanisms: American Society for Human Genetics 2020, virtual, *Aug 2020*

78. Peters M⁹, Evanovich A^u, Buetow K, **Wilson MA**. Investigating Sex Biased Gene Expression in the Brain to Explain Alzheimer's Disease Mechanisms: ASU-BNI Neuroscience Research Symposium 2020, Phoenix, AZ, *Jan 2020*
77. Phung TN^p, Olney KC^g, **Wilson MA**. Patchy, incomplete, and heterogeneous X-inactivation in the human placenta. ASHG, Houston, TX *Oct 2019*
76. Olney KC^g, Phung TN^p, **Wilson MA**. Sex differences found in human placentas. ASHG, Houston, TX *Oct 2019*
75. Dolby GA^p, Webster TH^p, DeNardo D, **Wilson MA**, Kusumi K. Population genomic analysis of speciation among threatened desert tortoises. Poster presentation. Evolution, Providence, RI, *Jun 2019*
74. Peters M⁹, Natri H^p, Evanovich A^p, **Wilson MA**. Investigating sex differences in healthy brains to explain Alzheimer's Disease mechanisms. Arizona Alzheimer's Consortium. Tempe, AZ, *May 2019*.
73. Dolby GA, Webster TH^p, DeNardo D, **Wilson MA**, Kusumi K (2019) Genomic insights into speciation of southwestern desert tortoises. Oral presentation. Desert Tortoise Council Annual Symposium, Tucson, AZ, *Feb 2019*
72. Chen M, Yuvaraj P, Sharma AA, Narang P^p, **Wilson Sayres MA**, Anderson KA. Targeting neo-epitopes from PIK3CA and p53 mutations for immunotherapy of breast cancer. San Antonio Breast Cancer Symposium. San Antonio, TX, *Dec 2018*.
71. Olney K^g, **Wilson Sayres M**. Sex differences in human placenta. ISEMPH. Park City, UT, *Aug 2018*.
70. Andrews J^u, Olney K^g, Brotman S^u, Valverde-Vesling V^u, **Wilson Sayres MA**. Sex chromosome informed RNAseq mapping increases X chromosome expression in female (46, XX) and male (46, XY) samples. ISEMPH. Park City, UT, *Aug 2018*.
69. Taravella AM^g, Deshpande AJ^u, **Wilson Sayres MA**. PopInf: A method for visualizing population ancestry using genomic data. IPS. Nairobi, Kenya, *Aug 2018*
68. Olney K^g, Brotman S^u, Andrews J^u, Valverde-Vesling V^u, **Wilson Sayres M**. Sex chromosome informed RNAseq mapping increases X chromosome expression in female (46, XX) and male (46, XY) samples. SMBE. Yokohama, Japan, *Jul 2018*.
67. Ozga A, Webster T^p, Nieves-Colon M, Fowler K, Siford R, **Wilson Sayres M**, Nockerts R, Wilson ML, Gilby IC, Pusey A, Li Y, Hahn B, and Stone A. Mitochondrial and exome diversity in *Pan troglodytes schweinfurthii* at Gombe National Park. SMBE. Yokohama, Japan, *Jul 2018*.
66. Natri H^p, **Wilson Sayres MA**, Buetow K. Sex-specific genomic architecture and regulatory mechanisms underlying hepatocellular carcinoma (HCC). AACR. Chicago, IL, *Apr 2018*
65. Dolby GA, Webster TH^p, DeNardo D, Wilson Sayres MA, Kusumi K. Geologic history and genomic divergence between *Gopherus agassizii* and *G. morafkai*. Oral presentation. Annual Meeting and Symposium of the Desert Tortoise Council, Las Vegas, NV, *Feb 2018*
64. Dolby GA, Webster TH^p, DeNardo D, **Wilson Sayres MA**, Kusumi K. Extrinsic forcing of genomic evolution during speciation: a geo-genomic study of *Gopherus* desert tortoises. Plant and Animal Genome XXVI. San Diego, CA, *Jan 2018*
63. Narang P^p, Chen M, Sharma AA, Anderson KS, **Wilson Sayres MA**. The neo-epitope landscape of breast cancer: implications for immunotherapy. SABC Symposium. San Antonio, TX, USA, *Dec 2017*.
62. **Wilson Sayres MA**, Dinsdale E, Hauser C, Morgan W, Rosenwald AG, Sierk M, Triplett E, Pauley MA. Bioinformatics core competencies for undergraduate life scientists. American Society for Cell Biology. Philadelphia, PA, *Dec 2017*.
61. Natri H^p, **Wilson Sayres M**, and Buetow K. Characterization of global molecular architecture and regulatory mechanisms underlying hepatocellular carcinoma. ASHG. Orlando, FL, USA, *Oct 2017*.
60. Nyer DB, Henning A, Olney KC^{*g}, **Wilson Sayres M**, and Haynes K. A synthetic, chromatin-targeted effector activates tumor suppressor genes in breast cancer cells. Engineering Biology Research Consortium Retreat. Atlanta, GA, USA, *Sep 2017*.
59. **Wilson Sayres M**, Dinsdale E, Hauser C, Morgan W, Rosenwald AG, Sierk M, Triplett E, Paule MA. Bioinformatics Core Competencies for Undergraduate Life Sciences. Gordon Research Conference: Undergraduate Biology Education Research. Easton, MA, USA, *Jul 2017*.
58. Ozga A^p, Nieves-Colon M, Webster T^p, **Wilson Sayres M**, Nockerts R, Wilson M, Gilby I, Pusey A, and Stone A. Short term reduction in *Pan troglodytes schweinfurthii* genetic diversity at Gombe National Park. SMBE. Austin, TX, USA, *Jul 2017*.
57. Phung T^g, Marsden C, Wayne R, Lohmueller K, **Wilson Sayres M**. Domestication of dogs has impacted genetic diversity on the X chromosome. Austin, TX, USA, *July 2017*.

56. Olney K^g, Brotman S^u, **Wilson Sayres M**. Standard mapping protocols misestimate sex-linked gene expression. SMBE. Austin, TX, USA, *Jul 2017*.
55. Olney KC^g, Nyer DB, **Wilson Sayres M**, and Haynes K. Synthetic chromatin protein to regulate gene expression in breast cancer cells. Mol, Cell & Tissue Bioengineer Symp. Tempe, AZ, USA, *Apr 2017*.
54. Valverde-Vesling V^{*u}, Olney K^g, **Wilson Sayres M**. Sex-biased gene expression in the human placenta. SOLUR Symposium. Tempe, AZ, USA, *Apr 2017*.
53. Brotman S^u, Olney K^g, **Wilson Sayres M**. Standard mapping protocols misestimate sex-linked gene expression. SOLUR Symposium. Tempe, AZ, USA, *Apr 2017*.
52. Daly S^u, Narang P^p, Amidan A^u and **Wilson Sayres MA**. Measuring mal mutation bias in Drosophila. ASU SOLUR Poster Symposium. Tempe, AZ, USA, *Apr 2017*.
51. Barrett M, Lenkiewicz E, Malasi S, Webster T^p, **Wilson Sayres MA**, McCullough AE, Anderson KS and Pockaj BA. Clonal heterogeneity in breast cancer and its impacts on clinical biomarkers. San Antonio Breast Cancers Symposium. San Antonio, TX, USA, *Dec 2016*.
50. Olney K^{*g}, Skotte L, Nielsen R and **Wilson Sayres MA**. Accurately inferring imbalanced allele expression using logistic regression models. EvSex16, Tempe, AZ, *Nov 2016*.
49. Cotter D^{*u}, Webster T^p, and **Wilson Sayres MA**. Diversity across the pseudoautosomal boundary varies across human populations. EvSex16, Tempe, AZ, *Nov 2016*.
48. Brotman S^{*u}, and **Wilson Sayres MA**. Genes that are routinely subject to inactivation and genes that routinely escape inactivation are highly expressed, and are candidates in Turner syndrome phenotype. EvSex16, Tempe, AZ, *Nov 2016*.
47. Narang P^{*p}, Walters JR, Challis RJ, Kumar S, and Wilson Sayres MA. Estimating male mutation bias in Lepidoptera. EvSex16, Tempe, AZ, *Nov 2016*.
46. Daly S^{*u}, Amidan A^u and **Wilson Sayres MA**. Male mutation bias in Drosophila. EvSex16, Tempe, AZ, *Nov 2016*.
45. Valverde-Vesling V^{*u}, Olney K^g, **Wilson Sayres M**. Sex-biased gene expression in the human placenta. EvSex16, Tempe, AZ, *Nov 2016*.
44. Webster TH^{*p}, Phung T, Grande B, Karlins E, Richmond P, Couse M, Whitford W, and **Wilson Sayres MA**. XYalign: Inferring and correcting for sex chromosome ploidy in next-generation sequencing data. EvSex16, Tempe, AZ, *Nov 2016*.
43. Brotman S^{*u}, and **Wilson Sayres MA**. Genes that are routinely subject to inactivation and genes that routinely escape inactivation are highly expressed, and are candidates in Turner syndrome phenotype. American Society for Human Genetics. Vancouver, BC, CANADA, *Oct 2016*.
42. Cotter D^{*u}, Webster T^p, and **Wilson Sayres MA**. Diversity across the pseudoautosomal boundary varies across human populations. ASHG. Vancouver, BC, CANADA, *Oct 2016*.
41. Valverde-Vesling V^{*u}, Webster T^p, and **Wilson Sayres MA**. Modeling effects of time since human bottleneck on genetic diversity. SACNAS. Long Beach, CA, USA, *Oct 2016*.
40. Narang P^{*p}, Anderson KS, Barrett MT, Pockaj BA and **Wilson Sayres MA**. Identifying the neoepitope landscape of triple negative breast cancer. Advances in Genome Biology and Technology Precision Health Meeting. Scottsdale, AZ, USA, *Sep 2016*.
39. Rupp S^{*g} and **Wilson Sayres MA**. Characterizing sex-biased gene expression in the green anole. Arizona Bioindustry Association Expo, Phoenix, AZ, USA, *April 2015*.
38. Stone AC^{*}, Ozga, AT, Nieves-Colon MA, Nockerts R, Webster T^p, **Wilson Sayres MA**, Wilson M, Gilby I, Pusey A and Marean C. The preservation of DNA from bone, dentin, and calculus from Gombe National Park and Pinnacle Point in Africa. International Symposium on Biomolecular Archaeology. Oxford, UK, *Sep 2016*.
37. Grizante MB^{*p}, DeNardo DF, Kohlsdorf T, **Wilson Sayres MA**, Fisher RE and Kusumi K. Evolution of the maintenance and loss of regeneration in lizards: comparative analysis of functional anatomy and genetic mechanisms. Society for Developmental Biology. Boston, MA, USA, *Aug 2016*.
36. Boddy A^{*p}, Fortunata A, **Wilson Sayres MA** and Aktipis A. Fetal microchimerism and maternal health: A review and evolutionary analysis of cooperation and conflict beyond the womb. Human Behavior and Evolution Society. Vancouver, BC, CANADA, *July 2016*.
35. Rupp S^{*g}, Webster T^p, Olney K^t, Hutchins E, Kusumi K and **Wilson Sayres MA**. Characterizing sex-biased gene expression in the green anole. Society for Molecular Biology and Evolution. Gold Coast, Queensland, CANADA, *July 2016*.
34. Berger S^{*u}, Clark T^u, **Wilson Sayres MA** and Mead L. A primer for population genomics. International Society for Evolutionary Medicine and Public Health. Durham, NC, USA, *June 2016*.

33. Boddy A^{*p}, Fortunata A, **Wilson Sayres MA** and Aktipis A. Fetal microchimerism and maternal health: A review and evolutionary analysis of cooperation and conflict beyond the womb. International Society for Evolutionary Medicine and Public Health. Durham, NC, USA, *June 2016*.
32. Olney K^{*t}, Skotte L, Nielsen R and **Wilson Sayres MA**. Accurately inferring imbalanced allele expression using logistic regression models. International Society for Evolutionary Medicine and Public Health. Durham, NC, USA, *June 2016*.
31. Clark T^{*u}, Berger S^u, **Wilson Sayres MA** and Mead L. A primer for population genomics. Society for the Study of Evolution. Austin, TX, USA, *June 2016*.
30. Chowell D^{*g}, Napier J, Gupta R, Faiss L, and **Wilson Sayres MA**. The extent of intratumor subclonal variation: a computational modeling analysis. Systems Approaches to Cancer Biology. Woods Hole, MA, USA, *April 2016*.
29. DeLuca V^{*u}, Taili M, Zismann V, Yi H, Sereduk C, Poorman K, **Wilson Sayres MA**, Maley C, Sekulic A, Trent J, and Hendricks W. Impact of vemurafenib concentration on adaptation rate in a BRAF^{V600E} melanoma cell line: A proof-of-principle experiment to monitor a cancer's rate of adaptation to targeted therapy. SOLUR Symposium. Tempe, AZ, USA, *April 2016*.
28. Daly S^{*u}, Amidan A^{*u} and **Wilson Sayres MA**. Male mutation bias in Drosophila. ASU School of Life Sciences Undergraduate Research Poster Symposium. Tempe, AZ, USA, *April 2016*.
27. Valverde-Vesling V^{*u}, Webster T^p and **Wilson Sayres MA**. Modeling effects of time since human bottleneck on genetic diversity. SOLUR Symposium. Tempe, AZ, USA, *April 2016*.
26. Brotman S^{*u}, Cotter D^{*u} and **Wilson Sayres MA**. Genetic diversity on the human X chromosome does not support a strict pseudoautosomal boundary. ASU School of Life Sciences Undergraduate Research Poster Symposium. Tempe, AZ, USA, *April 2016*.
25. Rupp S^{*g}, Webster T^p, Olney K^t, Hutchins E, Kusumi K and **Wilson Sayres MA**. Characterizing sex-biased gene expression in the green anole. SCALE. Los Angeles, CA, USA, *February 2016*.
24. Brotman S^{*u}, Cotter D^{*u} and **Wilson Sayres MA**. Using diversity to measure boundaries of the pseudoautosomal regions in human sex chromosomes. SCALE. Los Angeles, CA, USA, *Feb 2016*.
23. Olney K^{*t}, Skotte L, Nielsen R and **Wilson Sayres MA**. Accurately inferring imbalanced allele expression using logistic regression models. ASHG. Baltimore, MD, USA, *October 2015*.
22. Wang J^{*u}, Styers M^u and **Wilson Sayres MA**. Parent-of-origin effects in people with Turner syndrome. AZ BioIndustry Association (AZBio). Phoenix, AZ, USA, *October 2015*.
21. Olney K^{*t}, Skotte L, Nielsen R and **Wilson Sayres MA**. Accurately inferring imbalanced allele expression using logistic regression models. AZBioindustry. Phoenix, AZ, USA, *October 2015*.
20. Boddy A^{*p}, Fortunata A, **Wilson Sayres MA** and Aktipis A. Fetal microchimerism and maternal health: A review and evolutionary analysis of cooperation and conflict beyond the womb. Personalized Medicine Conference. Tuscon, AZ, USA, *September 2015*.
19. Wang J^{*u}, Styers M^u and **Wilson Sayres MA**. Parent-of-origin effects in people with Turner syndrome. SOLUR Symposium. Tempe, AZ, USA, *April 2015*.
18. Brotman S^{*u}, Cotter D^{*u} and **Wilson Sayres MA**. Using diversity to measure boundaries of the pseudoautosomal regions in human sex chromosomes. SOLUR Symp. Tempe, AZ, USA, *April 2015*.
17. Vu B^{*u} and **Wilson Sayres MA**. Patterns of evolution across vertebrate sex determining genes. ASU School of Life Sciences Undergraduate Research Poster Symposium. Tempe, AZ, USA, *April 2015*.
16. Rupp S^{*u}, Olney K^t, Hutchins E, Kusumi K and **Wilson Sayres MA**. Characterizing sex-biased gene expression in the green anole. SOLUR Symposium. Tempe, AZ, USA, *April 2015*.
15. Rupp S^{*u}, Olney K^t, Hutchins E, Kusumi K and **Wilson Sayres MA**. Characterizing sex-biased gene expression in the green anole. Arizona Bioindustry Association Expo, Phoenix, AZ, USA, *April 2015*.
14. Wang J^{*u}, Styers M^u and **Wilson Sayres MA**. Parent-of-origin effects in people with Turner syndrome. International Society for Evolution, Medicine, & Public Health. Tempe, AZ, USA, *March 2015*.
13. Jenner M^{*u}, Amidan A^{*u} and **Wilson Sayres MA**. Modeling the contrasting Neolithic lineage expansions in Europe and Africa. ISEMPH. Tempe, AZ, USA, *March 2015*.
12. Rupp S^{*u}, Olney K^t, Hutchins E, Kusumi K and **Wilson Sayres MA**. Characterizing sex-biased gene expression in the green anole. ISEMPH. Tempe, AZ, USA, *March 2015*.
11. Vu B^{*u} and **Wilson Sayres MA**. Patterns of evolution across vertebrate sex determining genes. International Society for Evolution, Medicine, & Public Health. Tempe, AZ, USA, *March 2015*.
10. Schaffer K^{*u} and **Wilson Sayres MA**. Evolutionary perspective suggests candidate genes for variation in Turner Syndrome phenotype. ISEMPH. Tempe, AZ, USA, *March 2015*.

9. Brotman S^u, Cotter D^u and **Wilson Sayres MA**. Using diversity to measure boundaries of the pseudoautosomal regions in human sex chromosomes. International Society for Evolution, Medicine, & Public Health. Tempe, AZ, USA, *March 2015*.
8. **Wilson Sayres MA*** and Luo K^u. Dating evolutionary strata on the human sex chromosomes reveals complex history of X-Y recombination suppression. SMBE 2014. San Juan, Puerto Rico, *June 2014*.
7. **Wilson Sayres MA***, Shankey Pander R^g, and Azad R. Detecting evolutionary strata on the human X chromosome: Markov segmentation & clustering analysis. ASHG 2013. Boston, MA, USA, *Oct 2013*.
6. **Wilson Sayres MA***, Lohmueller K, and Nielsen R. Natural selection reduced diversity on human Y chromosomes. Society for Molecular Biology and Evolution 2014. Chicago, IL, USA, *July 2013*.
5. **Wilson Sayres MA*** and Makova KD. Learning from genetic fossils on the human Y chromosome. Society for Molecular Biology and Evolution 2012. Dublin, Ireland, *June 2012*.
4. **Wilson Sayres MA*** and Makova KD. Can features of X-linked genes predict the demise of their Y-linked homologs? Human Genome Variation 2011. Berkeley, CA, USA *September 2011*.
3. **Wilson Sayres MA***, Venditti C, Chairmonte F, Pagel M, and Makova KD. Life history traits affect the magnitude of male mutation bias across 32 eutherian mammals. The Biology of Genomes. Cold Spring Harbor, NY, USA *May 2010*.
2. **Wilson Sayres MA***, Venditti C, Chairmonte F, Pagel M, and Makova KD. Life history traits affect the magnitude of male mutation bias across 32 eutherian mammals. Grad Exhibition State College, PA, USA *March 2010*.
1. **Wilson MA***, Chairmonte F and Makova KD. Male mutation bias observed across 34 mammalian genomes. Society for Molecular Biology and Evolution 2009. Iowa City, IA, USA *June 2009*.

RESEARCH SUPPORT

Active (7: \$1,900,000):	Duration	Total	Status
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Individual (1: \$1,650,000):

1. NIH MIRA	Sept 2017 – Aug 2022	\$1.65M	active
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"Population dynamics and medical consequences of sex chromosome evolution."

PI: **Wilson**

Collaborative (1: \$300,000):

1. NSF- IUSE (2044096)	Mar 2021 – Feb 2024	\$300K	active
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"Developing a Bioinformatics Course-based Undergraduate Research Experience for Online Students."

PI: **Wilson**; co-I: Brownell; co-I: Cooper

Completed (18: \$1,904,294):	Duration	Total	Status
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Individual (9: \$390,000):

9. Foundation for Women's Wellness	Dec 2018 – Dec 2019	\$25K	completed
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"The role of X chromosome inactivation in breast cancer."

PI: **Wilson Sayres (100%)**

8. MF17-UMR02 (Mindlin Foundation)	Jan 2017 – Dec 2017	\$5000	completed
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"Mathematical modeling of nevi to understand melanoma"

PI: **Wilson Sayres (100%)**

7. Experiment.com	Apr 2016-Apr 2017	\$10K	completed
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"Gila monster genomics: conservation, venom, and treatments for Type-II diabetes"

PI: **Wilson Sayres (100%)**

6. Center for Evolution and Medicine	Oct 2016	\$15K	completed
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Internal Event Award

"Molecular Evolution of Sex"

PI: **Wilson Sayres (100%)**

5. American Genetic Association	Oct 2016	\$15K	completed
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Special Event Award

“Molecular Evolution of Sex”

PI: **Wilson Sayres (100%)**

4. MF15-UMR02 (Mindlin Foundation) Jan 2015 – Dec 2015 \$2500 *completed*
“Characterizing sex-biased gene expression in the green anole”
PI: **Wilson Sayres (100%)**

3. MF15-UMR03 (Mindlin Foundation) Jan 2015 – Dec 2015 \$2500 *completed*
“Patterns of evolution across vertebrate sex determining genes”
PI: **Wilson Sayres (100%)**

2. Miller Institute for Basic Research in Science Postdoctoral Fellowship July 2011 – June 2014 \$225K *completed*
PI: **Wilson Sayres (100%)**

1. NSF Graduate Research Fellowship July 2006 – June 2009 \$90K *completed*
PI: **Wilson Sayres (100%)**

Collaborative (17: \$2,064,294):

18. Breast Cancer Research Foundation Oct 2020 – Sep 2021 \$250K *completed*
“Targeting breast cancer tumor antigens for immunotherapy.”
PI: Anderson; Co-I: **Wilson (5%; \$12,500)**

17. AZ Alzheimer’s Disease Consortium July 2019 – June 2020 \$300K *completed*
Co-I: **Wilson Sayres (10%; \$30,000)**

16. Breast Cancer Research Foundation Oct 2019 – Sep 2020 \$250K *completed*
“Targeting breast cancer tumor antigens for immunotherapy.”
PI: Anderson; Co-I: **Wilson Sayres (5%; \$12,500)**; Co-I: Borges

15. Marley Foundation Jan 2019 – Dec 2019 \$75K *completed*
Mutational and neo-epitope landscape of colorectal cancers in Lynch syndrome patients
Mayo PI: Barrett (70%); ASU PI: **Wilson Sayres (30%; \$26,922)**

14. Breast Cancer Research Foundation Oct 2018 – Sep 2019 \$250K *completed*
“Targeting breast cancer tumor antigens for immunotherapy.”
PI: Anderson; Co-I: **Wilson Sayres (5%; \$12,500)**; Co-I: Borges

13. AZ Alzheimer’s Disease Consortium July 2018 – June 2019 \$300K *completed*
Co-I: **Wilson Sayres (10%; \$30,000)**

12. Leakey Foundation Jul 2018 – Jun 2019 \$25K *completed*
“Understanding the evolutionary genetic origins of hominin sexual dimorphism.”
PI: **Wilson Sayres (100%)**; Co-I: Webster; Co-I: Higham

11. AZ Game and Fish: Heritage Jul 2017 – Jun 2019 \$33K *completed*
“Characterizing Gopherus hybrids and speciation through genomics analyses.”
PI: **Wilson Sayres (100%)**; Co-I: Webster; Co-I: Dolby

10. Lincoln Center for Applied Ethics May 2017 – May 2018 \$5500 *completed*
“Race and Ethnicity: Incorporating History, Society, and Genetics to Improve Human Health.”
PI: **Wilson Sayres (100%)**; Co-I: Delmont; Co-I: Wernimont

9. Breast Cancer Research Foundation Oct 2017 – Sep 2018 \$250K *completed*
“Targeting breast cancer tumor antigens for immunotherapy.”
PI: Anderson; Co-I: **Wilson Sayres (10%; \$25,906)**; Co-I: Borges

8. Cancer Genomics Cloud	Feb 2017 – Dec 2017	\$10K	<i>completed</i>
<i>“Resources for Collaborative Projects on Seven Bridges CGC.”</i>			
PI-I: Wilson Sayres (100%) ; co-I: Pooja Narang;			
7. ASU-Mayo Seed Grant	Jan 2017 – Dec 2017	\$50K	<i>completed</i>
<i>“Evolution of X-inactivation in breast cancers.”</i>			
ASU Co-I: Wilson Sayres (30%; \$15,025) ; Mayo Co-I: Barrett (70%)			
6 Breast Cancer Research Foundation	Oct 2016 – Sept 2017	\$250K	<i>completed</i>
<i>“Targeting breast cancer tumor antigens for immunotherapy.”</i>			
PI: Anderson; Co-I: Wilson Sayres (10%; \$24,283) , Borges			
5. SOLS Internal RTI	June 2016 – Dec 2016	\$7500	<i>completed</i>
<i>“Deciphering ecological drivers of speciation & local adaptation in the desert tortoise complex”</i>			
Co-I: Wilson Sayres (internal funding) ; Co-I: Kusumi; Trainees: Webster and Dolby			
4. Flinn Foundation	Jan 2016 – June 2016	\$100K	<i>completed</i>
<i>“Melanoma Transformative Medical Alliance: The role of sex in melanoma drug resistance.”</i>			
PI: Sekulic; Co-I: Hendricks; Co-I: Wilson Sayres (33%; \$33,333) ; Co-I: Maley			
3. ASU IHO	Aug 2015 – June 2016	\$100K	<i>completed</i>
<i>“DNA and human origins at ASU”</i>			
PI: Stone; Co-I: Gilby; Co-I: Rosenberg; Co-I: Wilson Sayres (0%) ; Co-I: Cartwright			
2. NSF DBI 1446483 (BEACON)	Aug 2015 – June 2016	\$48,294	<i>completed</i>
<i>“Assessing human-specific evolutionary pressures on genes involved in early puberty”</i>			
The goals of the project are to develop trainee skills in programming skills including Unix, R, perl and python, and to investigate molecular relics of early puberty development in the human genome.			
PI: Mead; Co-PI: Wilson Sayres (0%; all to support trainees)			
1. Outreach Thematic Initiative Fund	July 2009 – June 2010	\$10K	<i>completed</i>
<i>“Public Service Announcements Promoting Careers in Science and Mathematics.”</i>			
PI: Nathaniel Brown, co-PI: Melissa Wilson (0%; all funds to production) , Barbara Houtz, Babs L Bengtson, Elizabeth Hutton, rural Multi-District Academic Space Alliance			
<u><i>Trainee (3: \$44,069):</i></u>			
4. NIH NICHD 1 F31 HD101252-01	Jan 2020 – Dec 2021	\$36,569	<i>active</i>
<i>Characterization of sex differences in human placentas, graduate fellowship</i>			
PI: Wilson ; Trainee: Kimberly Olney			
3. Prevent Cancer Foundation	Jan 2018 – Dec 2020	\$150,000	<i>completed</i>
<i>Postdoctoral Fellowship</i>			
PI: Wilson ; Trainee: Heini Natri			
2. NIH IMSD	Sept 2016 – May 2017	\$2500	<i>completed</i>
<i>Initiative for Maximizing Student Development, undergraduate fellowship</i>			
PI: Wilson Sayres (all to support trainee) ; Trainee: Samantha Daly			
1. NIH IMSD	Jan 2016 – May 2017	\$5000	<i>completed</i>
<i>Initiative for Maximizing Student Development, undergraduate fellowship</i>			
PI: Wilson Sayres (all to support trainee) ; Trainee: Valeria Valverde-Vesling			
<u>Arizona State University trainee research funding (11):</u>			
Fall 2019 – Spring 2020	SOLUR mentored award, Karina Morris		
Jan 2019 – May 2019	Bidstrup Foundation Undergraduate Fellowship, Karina Morris		

Fall 2017 – Spring 2020	SOLUR mentored award, Emma Howell
Fall 2017 – Spring 2018	SOLUR mentored award, Avery Underwood
Summer 2016	SOLUR Summer Research Experience Award, Ephrance Kalungi
Summer 2016	CLAS Undergraduate Summer Enrichment, Samantha Daly
Summer 2015 – Spring 2016	SOLUR mentored award, Samantha Daly
Summer 2015 – Fall 2016	SOLUR mentored award, Sarah Brotman
Spring 2015 – Fall 2016	SOLUR mentored award, Shawn Rupp
Summer 2015	CLAS Undergraduate Summer Enrichment, Sarah Brotman
Dec 2014 – May 2015	Bidstrup Foundation Undergraduate Fellowship, Kara Schaffer

MENTORED TRAINEE HONORS & AWARDS

- 2020 Mario Apata^g, Harry Lowell Swift Advancing Health Scholarship
Kimberly Olney^g, Achieving Research Scholars Award
Kimberly Olney^g, Harry Lowell Swift Advancing Health Scholarship
Angela Taravella Oill^g, Achieving Research Scholars Award
Angela Taravella Oill^g, Harry Lowell Swift Advancing Health Scholarship
- 2019 Kimberly Olney^g, Achieving Research Scholars Award
Kimberly Olney^g, CLAS Graduate Excellence Fellowship
Angela Taravella^g, CLAS Graduate Excellence Fellowship
Mollie Peters^g, CLAS Graduate Excellence Fellowship
- 2018 Heini Natri^p, Prevent Cancer Foundation Postdoctoral Fellowship
Kimberly Olney^g, Achieving Research Scholars Award
Kimberly Olney^g, Distinguished Graduate Student, Faculty Women's Association, ASU
Kimberly Olney^g, Research Excellence Award, Graduate & Professional Student Assoc.
Angela Taravella^g, CLAS Graduate Excellence Fellowship
Daniel Cotter^u, Outstanding Graduating Senior; Genetics
Daniel Cotter^u, NSF Graduate Research Fellowship
- 2017 Heini Natri^p, Center for Evolution and Medicine Postdoctoral Fellowship
Kimberly Olney^g, Harry Lowell Swift Advancing Health Scholarship
Imani Sharpe^g, Harry Lowell Swift Advancing Health Scholarship
Angela Taravella^g, CLAS Graduate Excellence Fellowship
Sarah Brotman^u, Outstanding Graduating Senior; Student of the Year-Biological Sciences
Daniel Cotter^u, Origins Project Undergraduate Research Award
Daniel Cotter^u, Ralph A. Fisher, Jr. Scholarship
- 2016 Shawn Rupp^g, SMBE Travel Award
Samantha Daly^u, Dean's Research Scholarship
Shawn Rupp^u, Origins Project Norm Perrill Scholarship
Sarah Brotman^u, Undergraduate Outstanding Service award
Danny Cotter^u, Ralph A. Fisher, Jr. Scholarship
Lidia Peon^u, Jerome Aronson Plant Biology Scholarship
- 2015 Shawn Rupp^u, Selected to attend "Bioinformatics & Biodiversity"
Pooja Narang^p, Society for Molecular Biol & Evolution Young Investigator Travel Award

PROFESSIONAL SERVICE

National/International Conference Organizing, Reviewing, and Moderating

- 2017-2020 Organizing Committee Member, Genome Informatics Annual Conference
2017 Session organizer, "Mechanisms of phenotypic evolution", SMBE, Austin, TX, USA, July
2016 Conference organizer, "Evolutionary genomics of sex", Tempe, AZ, USA, October
* *Funded by the American Genetic Association & Center for Evolution and Medicine*

Edited Special Issue, Journal of Heredity: Evolutionary Genomics of Sex
<https://academic.oup.com/jhered/issue/108/7>

- 2016 Session moderator, “Inferring the action of natural selection”, at ASHG 2016 meeting, in Vancouver, CANADA, October
- 2016 Symposium co-organizer and moderator, “Primate evolutionary history and comparative genomics”, at the joint meeting of the International Primatological Society and the American Society of Primatologists in Chicago, IL, USA, August
- 2016 Program committee, Bioinformatics Open Source Conf, BOSC, Orlando, FL, July
- 2016 Session moderator, “Selection, stress, and homeostasis”, International Society for Evolutionary Medicine and Public Health, Durham, NC, USA, June
- 2015 Symposium co-organizer and moderator, “Genomics of sex bias: Addressing questions with or without genomes”, at SMBE 2015 in Vienna, Austria, July
- 2014 Symposium co-organizer, moderator, “The X-factor of Complex Disease: From Evolution to Association Studies of the X chromosomes”, at ASHG 2014 in San Diego, CA, October
- 2014 Symposium co-organizer, “Mutation: The ultimate source of molecular variation”, at SMBE 2014 in San Juan, Puerto Rico, June
- 2013 Session moderator, “Which comes first: The Sequence or the Biology”, at ASHG 2013 meeting, in Boston, MA, USA, June
- 2013 Organizer, Bay Area Population Genomics (BAPG) IX Conference, Berkeley, CA, USA
- 2012-2013 2013 Miller Symposium Planning Committee member, Tomales Bay, CA, USA, July
- 2012 Moderator, “Population Genetics Genome-Wide”, ASHG, San Francisco, CA, USA Nov
- 2012 Symposium Co-organizer, “Sex chromosome evolution illuminated by next-generation sequencing technology”, at SMBE 2012 in Dublin, Ireland, June
- 2011-2012 2012 Miller Symposium Planning Committee member
- 2006 Session moderator at Evolution 2006

Peer Reviewer, See record: <https://publons.com/author/303792/melissa-wilson-sayres>

American J. of Human Genetics	Genetics	PLoS Genetics
Annals of Human Genetics	Genome Biology	PLoS ONE
Biology Letters	Genome Biology and Evolution	PNAS
Biology Direct	Genome Research	Science
BMC Genomics	Heredity	Systematic Biology
Computational Biology & Chemistry	Journal of Genetics and Genomics	Theoretical Biology and Mathematical Modeling
Dovepress	Journal of Molecular Evolution	Mathematical Modeling
Frontiers	Molecular Biology and Evolution	Trends in Genetics
G3: Genes, Genomes, Genetics	Nature	
	Nature Communications	

Society Service

- 2017-present Associate Editor, Molecular Biology and Evolution
- 2017-present Associate Editor, Journal of Heredity
- 2017-2020 Associate Editor, Evolution
- 2017 Guest Associate Editor, PLoS Genetics
- 2017-2019 Council Member, American Genetic Association
- 2016-2017 Editorial Board Member, Chimerism

National and International Grants and Fellowships Reviewer

- 2021 NIH reviewer, Genetic Variation and Evolution (GVE) study section
- 2021 NIH F08 reviewer, Fellowship: Genes, Genomes, and Genetics
- 2016-present Board member, Science Ambassador Scholarship, Cards Against Humanity
- 2015-present Leakey Foundation
- 2017-2020 2019 Chair, American Genetic Association Grad/Postdoc awards committee
- 2017 *ad hoc* NSF Division of Molecular and Cellular Biosciences
- 2016 *ad hoc* NSF Division of Environmental Biology
- 2016 Biotechnology and Biological Sciences Research Council (BBSRC)
- 2015 Agency for Science, Technology & Research (A*STAR) in Singapore

2014-2015 NSF Graduate Research Fellowship
2011-2012 National Graduate Women in Science (GWIS) Fellowships

Computational Biology and Bioinformatics Education/Training

2019-present Co-developing M.S. in Computational Life Sciences
2017-present Co-Director, Established undergraduate ([website](#)) and graduate certificates in Computational Life Sciences
**Completed and submitted all paperwork, attended University Senate meetings, and adjusted certificate per feedback. The program is housed in the School of Life Sciences, but includes electives from all relevant units including other departments and Colleges.*

2016-present Organizer, ASU Computational Life Sciences group. Example workshops:
Intro to HPC/Research computing, 2-hour workshop (28 participants)
R: Reproducible molecular evolution, 2-hour workshop (23 participants)
De novo genome assembly workshop, 2-hour workshop (45 participants)
CoGe (comparative genomics server), Full-day workshop, sponsored by Biodiversity Knowledge Integration Center (35 participants)
Intro to the awk, 1-hour workshop (34 trainees)
Intro to command line, 1-hour workshop (15 trainees)
[Galaxy \(bio-computing\)](#), Full-day workshop, sponsored by BioKIC (48 trainees)
Intensive Python Bootcamp, Full-day workshop (15 trainees)

2014-2020 Invited Member, (NSF-funded) *Network for Integrating Bioinformatics into Life Sciences Education (NIBLSE) Research Coordination Network (RCN)* [Award 1346559](#)
2019-2020: Genomics Education Alliance Member. To identify and curate resources to ensure the sustainability of undergraduate education in bioinformatics and genomics.
2018-2020: Core Competencies Implementation Member. To implement change to integrate bioinformatics into the classroom.
2015-2018: Core Competencies Working Group Member. To develop a standardized set of training goals for undergrad education in bioinformatics.
April 2015: Workshop participant. To advance and develop a standardized set of training goals for undergraduate education in bioinformatics.

2017, 2018 Invited lecturer, Cold Spring Harbor Lab Course: Foundations of Comp Genomics
2016 Team leader, HackSeq (<http://www.hackseq.com>), October

Arizona State University: College of Liberal Arts and Sciences

2018-2020 Member, Graduate College Completion Fellowships Award Committee
2017-2019 Member, Ask A Biologist Advisory Board
2017-2019 SOLS representative, Data science undergraduate major development
Developed Biosciences track

2017-2018 Organizer, Developing Educational Scholars Initiative
Institute for the Science of Teaching and Learning

2016-2017 Training committee chair, Faculty Research Computing Working Group
2016 ASU participant, Hortonworks Genomics Initiative
2015-2016 Member, Faculty Research Computing Working Group
2015 Panelist, Funding success skills series: Professors and Proposals @ 1, 5 and 10 years
2014-2015 Member, Biocomputing Advisory Committee

Arizona State University: School of Life Sciences (SOLS) and Center affiliations

2021-2022 Member, SOLS Education Working group: Career Readiness Experiential Opportunities
2021 Chair, SOLS Search Committee
2020-2021 Member, Evolutionary Biology Graduate Program Steering Committee
2020-2021 Member, SOLS/Center for Evolution and Medicine Instructor Search Committee
2019-2020 Member, SOLS/Center for Evolution and Medicine Faculty Search Committee
2016-2020 Chair, Evolutionary Biology Graduate Program
**Oversee ~30 PhD students, including annual evaluations, recruitment, run core courses*

2016-present Member, Developing BIO 345: Evolution, curriculum committee

2015-present Guest lecturer, BioBridge (Head start program for Biology majors)
 2018-2019 Member, SOLS/Center for Mechanisms of Evolution search committee
 2017-2019 Member, Life Sciences Ethics Board (Hosted Bioethics Breakfast on Race & Genetics)
 2017-2018 Member, SOLS/Center for Mechanisms of Evolution search committee (2 positions)
 2016-2018 Member, CEM Research Committee
 2016-2017 Member, SOLS/Center for Evolution and Medicine search committee (2 positions)
 2015-2016 Organizer, SOLS Seminar Series
 2016 Fellow applicant reviewer, School of Life Sciences Undergraduate Research program
 2015-2016 Member, Evolutionary Biology Graduate Program Steering Committee
 2015 Faculty participant, Barrett Honors Event for SOLS student
 2015 Moderator, SOLS Spark program (welcome to incoming SOLS majors)
 2015 Participant, SOLS New Student Orientation Lunch: May 29, June 11, June 15, July 1
 2014 Faculty participant, Barrett Honors Event for SOLS student
 2014-2015 Member, Curriculum Reform Committee

MENTORING

Postdoctoral Research Scientist Mentor, Arizona State University (1 current, 4 total)

2019-2021 **Tanya Phung, Ph.D.**
 Sex chromosome evolution in dogs, cancer, and neoepitopes.
 2017-2020 **Heini Natri, Ph.D., Center for Evolution and Medicine Fellow**
 Evolution of resistance and the role of sex chromosomes in cancer.
**Awarded Prevent Cancer postdoctoral fellowship*
 2015-2018 **Tim Webster, Ph.D.**
 Sex-biased population history, genetic diversity, and breast cancer exome variation.
**Obtained tenure-track faculty position at University of Utah, Department of Anthropology*
 2015-2017 **Pooja Narang, Ph.D.**
 Sex chromosome evolution and the role of sex-linked genes in cancer etiology.
**Awarded travel fellowship to present results at SMBE in Austria*

Ph.D Student Primary Advisor, Arizona State University (4 current)

2020-present **Ph.D. Thesis Advisor, Mario Apata**
 Adaptation in the Andes
 2018-present **Ph.D. Thesis Advisor, Mollie Peters**
 Sex differences in the brain and Alzheimer's disease
 2016-present **Ph.D. Thesis Advisor, Kimberly Olney**
 Allele-specific expression in the human placenta
 2016-present **Ph.D. Thesis Advisor, Angela Taravella**
 Human genetic variation in Northern Kenya

M.S. Student Primary Advisor, Arizona State University (1 current; 4 total)

2020-present **M.S. Thesis Advisor, Yan Yap,**
 Neoantigen landscape in HBV and HCV mediated liver cancer.
 2018-2019 **M.S. Thesis Advisor, Karen Funderburk, graduated May 2019**
 Sex differences in cancer over time and across populations
**Accepted to Computational Biology PhD program at Brown University*
 2017-2019 **M.S. Thesis Advisor, Avery Underwood, graduated May 2019**
 Biased allele-expression in Nasonia jewel wasps
**Obtained Research Scientist Position at Arizona State University*
 2016-2018 **M.S. Thesis Advisor, Lidia Peon, graduated May 2018**
 Effect of genetic glossary on experience of genetic counseling
 2014-2016 **M.S. Thesis Advisor, Shawn Rupp, graduated December 2016**
 Squamate sex chromosome evolution and dosage compensation
**Obtained Bioinformatics Research Scientist Position at Arizona State University*

ASU Graduate Student Committee Member (13 current; 19 total)

- 2020-present **Ph.D. Thesis Committee Member, Gaurav Bilolikar, SOLS, ASU**
Predicting patterns of epistasis in the *S. cerevisiae* HSP90 regulatory network.
- 2020-present **M.S. Thesis Committee Member, Erik Olson, SOLS, ASU**
Liver cancer sex differences.
- 2020-present **M.S. Thesis Committee Member, Thomas Rheling, SOLS, ASU**
Pathway analysis in cancer.
- 2020-present **Ph.D. Thesis Committee Member, Jacob Klemm, SOLS, ASU**
Regeneration in *Drosophila*.
- 2019-present **Ph.D. Thesis Committee Member, Mary Pardhe, SOLS, ASU**
Vaccine development.
- 2019-present **Ph.D. Thesis Committee Member, Adele Crane, SOLS, ASU**
Tuberculosis genomics.
- 2019-present **Ph.D. Thesis Committee Member, Evan Mee, SOLS, ASU**
Protist genomics.
- 2018-present **Ph.D. Thesis Committee Member, Sareh Seyedi, SOLS, ASU**
Multi-drug adaptive therapies for breast cancer.
- 2018-present **Ph.D. Thesis Committee Member, Kelly Blevins, SHESC, ASU**
Disease ecology, Aztec site, urbanization and colonization using TB & oral microbiome.
- 2018-present **Ph.D. Thesis Committee Member, Rafaela Salgado Fontenele, SOLS, ASU**
Viral discovery in cacti.
- 2017-present **Ph.D. Thesis Committee Member, Stevie Winingear, SHESC, ASU**
Ancient human DNA in Tierra del Fuego.
- 2017-present **Ph.D. Thesis Committee Member, Adam Orr, SOLS, ASU**
Modeling NGS error, and studying error correction.
- 2016-present **Ph.D. Thesis Committee Member, Kevin Klicki, SOLS, ASU**
Microbiology research.
- 2018-2019 **Ph.D. Thesis Committee Member, Stephan Baehr, SOLS, ASU**
Mutation accumulation.
- 2018-2019 **M.S. Thesis Committee Member, Yuri Bonilla, BMI, ASU**
Breast cancer network analysis.
- 2016-2019 **Ph.D. Thesis Committee Member, Adrienne H. Smith, SOLS, ASU**
Transcriptome variation across the human brain.
- 2015-2016 **Ph.D. Thesis Committee Member, Diego Chowell, Applied Math, ASU July 2016**
Mathematical model of tumor heterogeneity.
- 2015-2016 **Ph.D. Thesis Committee Member, Tara Furstenau, SOLS, ASU, May 2016**
Population genetics modeling, self-incompatibility, and isolation-by-distance.

Outside Universities, Graduate Student Committee Member (1 current; 2 total)

- 2018-present **Ph.D. Thesis Committee Member, Shannon Keating, Biol Sci, Marquette University**
Sex chromosome evolution in geckos.
- 2016-2018 **Ph.D. Thesis Committee Member, Tanya Phung, EEB, UCLA, defended Nov 2018**
Dog sex chromosome population genetics.

Barrett Honors Undergraduate Thesis director, Arizona State University (3 current; 14 total)

- Current **Thesis Director, Brittney Jimenez**, Biological Sciences major
Health inequities in Latino communities in Alzheimer's Disease
- Current **Thesis Director, Vasiliki Laloudakis**, Biological Sciences major
Maladjustment in patients with Mayer-Rokitansky-Kuster-Hausner Syndrome
- Current **Thesis Director, Karina Morris**, Biological Sciences major
X chromosome inactivation
- 2020 **Thesis Director, Emma Howell**, Biological Sciences major
African population genetics
- 2019 **Thesis Director, Anagha Deshpande**, Biological Sciences major
Isoform variation across breast cancers
- 2019 **Thesis Director, Austin Evanovich**, Biological Sciences major
Gene expression variation in the human brain

- 2019 **Thesis Director, Lovender Phiri**, Biological Sciences major
Gene expression evolution
- 2019 **Thesis Director, Tristan Neal**, Biological Sciences major
Cancer evolution
- 2018 **Thesis Director, Ariel Baber**, Biological Sciences major
Expanding career options for Life Sciences Majors
- 2017 **Thesis Director, Darius Gallegos**, Biological Sciences major
Career options in the Life Sciences
- 2017 **Thesis Director, Sarah Brotman**, Biological Sciences major
X-inactivation across the human brain
- 2017 **Thesis Director, Val Deluca**, Biological Sciences major
Monitoring cancer's rate of adaptation
- 2016 **Thesis Director, Daniel Cotter**, Biological Sciences major
Genetic diversity across the pseudoautosomal boundary varies across humans
- 2015 **Thesis Director, Kara Schaffer**, Biochemistry major
Evolutionary perspective suggests candidate genes for Turner Syndrome phenotype

Barrett Honors Undergrad Thesis committee member, Arizona State University (8 total)

- 2019 **Second reader, Alexis Boschi**, Biological Sciences major
Delta like three signaling
- 2018 **Second reader, Aika Schneider-Utaka**, Biological Sciences major
Cancer suppression in placental mammals
- 2017 **Second reader, Abigail Howell**, Biological Sciences major
An analysis of the benchmark test lzbench for open-source compressors
- 2016 **Second reader, Diana Arroyo**, Biological Sciences major
Mammalian genome variation
- 2016 **Second reader, Ardesher Aghili**, Molecular Biology and Biotechnology major
A network analysis of SNP association in the antigen presentation pathway of hepatocellular carcinoma
- 2015 **Second reader, Brendan Fries**, Biological Sciences major
Analyzing the spread of the Chikungunya virus in the Caribbean 2013-2015
- 2015 **Second reader, Ben Roos**, Computer Science major
Genie: A population genetics simulation built with JavaScript
- 2015 **Third reader, Elise Kulik**, Biological Sciences major, Mathematics minor
The Sonoran Desert Tortoise and Conservation Biology

Undergraduate Research Mentor (6 current; 59 former, shown is the last year the student was in lab)

Current (0): 1. Brittney Jimenez 2. Youssef Aboelnaga 3. Nisha Kalmadi 4. Brittney Jimenez 5. Vasiliki Laloudakis 6. Karina Morris

Former, in academic year they graduated the lab:

2019-2020 (5): 1. Karina Morris (Bidstrup Fellow) 2. Ryan Maner 3. Arisha Khan 4. Emma Howell 5. Haley Harelson

2018-2019 (10) ASU: 1. Leilani Pfeifer (Leap Scholar) 2. Selena Cortez 3. Anagha Deshpande 4. Grant Dembrock 5. Jocelyn Andrews (presented poster at ISEMPH) 6. David Levy 7. Ndey Bassin Jobe 8. Austin Evanovich (presented poster at ISEMPH) 9. Lovender Phiri 10. Suhail Ghafoor

2017-2018 (12) ASU: 1. Sarah Bearman (internship at AZ game and fish) 2. Afeefah Rashid 3. Michelle Weinstein 4. Ephrance Peninah Kalungi (SOLUR SRE funded) 5. Ka'anani Amanonce 6. Alyssa Harris (Mindlin funded) 7. Nilofar Ghulam Hazrat 8. Amanda Wolf 9. Brock Williams (internship at AZ game and fish) 10. Ariel Baber 11. Daniel Cotter (Presented poster of research findings (x2); authored manuscript) 12. Avery Underwood (Joined MS program)

2016-2017 (6) ASU: 1. Sarah Brotman, (Presented poster of research findings (x2) SOLUR funded; CLAS Summer REU student, authored manuscript) 2. Sam Daly (SOLUR funded; CLAS USE; IMSD funded, Presented poster of research findings) 3. Valeria Valverde-Vesling (IMSD funded) 4. Noah Stone; 5. Mostafa Adina 6. Christopher Sleiman

- 2015-2016 (11)** ASU: **1.** Carlos Meza-Torres **2.** Kirk Flamm **3.** Victoria Reid **4.** Kellie Kodoma **5.** Parker Shea **6.** Lidia Peon (Joined MS program) **7.** Jacinda Garcia **8.** Margaret Walters **9.** Ashley Amidan (Presented poster of research findings) **10.** Reena Marie Ygot **11.** Ethan Bate
- 2014-2015 (12)** ASU: **1.** Jada Wang (Presented poster of research findings); **2.** Kara Schaffer (Supported by Bidstrup Fellowship) **3.** Marshall Styers (Presented poster of research findings) **4.** Melinda Jenner (Presented poster of research findings) **5.** David Barclay **6.** Joy Cruz **7.** Caroline Erickson **8.** Brittany Hammis **9.** William Martelly **10.** Alexandra Marinello **11.** Christopher Negrich **12.** Jaclyn Williams
- 2013-2014 (3)** UC Berkeley: **1.** Michelle Senar (Student accepted full time position as Associate Software Engineer at BrightSpace, 2015) **2.** Logan Curtis-Whitchurch (Student accepted to University of Louisville Medical School, 2015) **3.** Kellie Ottoboni (Student accepted for PhD program at UC Berkeley, 2015)
- 2012-2013 (2)** UC Berkeley: **1.** Kevin Luo (Preliminary data for grant generated. Student accepted to computer science graduate program at Stanford, 2015); **2.** Paulina Tsai (Manuscript accepted at Berkeley Scientific Journal.)

Other Formal Mentoring

- 2014-present *ASHG Trainee Networking Mentor.* Meet with graduate students and postdoctoral researchers to discuss research, networking and future career options.
- 2015-2016 **Pia Whai-Singh**, High school student, BASIS Ahwatukee High School
- 2006-2010 **Integrative Biosciences, Graduate student mentor (9 students).** Met routinely with graduate students to acclimate to graduate life & assist with the program.
- 2010 **2010 SMBE Undergraduate and Diversity Mentoring Program Mentor (1 student).** Attend sessions with and serve as contact point for the student.
- 2009-2010 **Lydia Krasilnikova.** High school student, Student accepted into MIT Mathematics major

TEACHING AT ARIZONA STATE UNIVERSITY

Courses Developed/Primary Instructor

Computing for Research (BIO/EVO 439/539): (3 credit; elective for undergrad and grad students)

Hands-on introduction to computing for analysis of life sciences data. Developed into formal course, including training in command line, genomics tools, and high performance computing.

Spring 2019 (13 undergraduates, 10 graduates enrolled; 2 audit): *in progress*

Fall 2018 (13 undergraduates, 10 graduates enrolled; 2 audit): 1.7 out of 5 (1 high)

Spring 2018 (10 undergraduates, 16 graduates enrolled; 5 audit): 1.2 out of 5 (1 high)

Fall 2016 (BIO/EVO/MCB 598 only; 7 enrolled; routinely 20-30 present): 1.7 out of 5 (1 high)

Practical Applications in Computational Life Sciences (BIO/EVO 498/598): (3 credit; elective for undergrad and grad students). Hands-on workshop for trouble-shooting computational analysis of life sciences data, topics range from cancer to plant biology, epigenetics, transcriptomics, and phylogenetics.

Spring 2019 (3 enrolled; routinely 5-10 in attendance)

Fall 2018 (1 enrolled; routinely 5-10 in attendance)

Current Topics in Evolutionary Biology (EVO 591): (1 credit; elective for grad students)

Seminar on Evolutionary Biology current papers. Each session also open to the ASU community.

Spring 2018 (8 enrolled; routinely 20 in attendance)

Fall 2018 (9 enrolled; routinely 25 in attendance): 1.9 out of 5 (1 high)

Research Computing Brown Bag (BIO/EVO/MCB 591): (1 credit; elective for grad students)

Seminar on computing across disciplines at Arizona State University. Each session also open to the ASU community, in collaboration with Research Computing.

Fall 2016 (3 enrolled; routinely 12-15 in attendance): 1.3 out of 5 (1 high)

Evolution (BIO 345) & Honors: (3 credits; required for undergraduate majors)

This course is designed to introduce students to the concepts of evolutionary theory including phylogenetic analysis, adaptive and non-adaptive evolution, population genetics, and modern human

evolution. There are two lectures per week, and a series of recitations where students are broken into smaller groups to work on problem solving and critical thinking. For Honors students, I meet separately in an extra recitation session, to read/discuss a book, including a written component.

Spring 2017 (384 students): 2.2 out of 5 for course, 1.5 for instructor (1 high)

Spring 2016 (340 students): 1.7 out of 5 for course, 1.4 for instructor (1 high)

Spring 2015 (322 students): 1.9 out of 5 for course, 1.7 for instructor (1 high; Dept-wide average is 1.9)

Topic: Evolution and Medicine Visiting Speaker Recitation (BIO/ASM 394): (1 credit; elective)

Meeting with Evolution and Medicine seminar speakers and discussing research.

Fall 2018 (4 students): 1 out of 5 (1 high)

Research Areas of Evolution (EVO 610): (1 credit; required for Evolutionary Biology grad students)

Overview of research areas in Evolution.

Spring 2019 (9 students): *in progress*

Fall 2018 (9 students): 1.6 out of 5 (1 high)

Spring 2018 (6 students): 1.6 out of 5 (1 high)

Fall 2017 (9 students): 1.6 out of 5 (1 high)

Spring 2017 (10 students): 1.5 out of 5 (1 high)

Fall 2016 (5 students): 1.7 out of 5 (1 high)

Decoding Sex (BIO 494/BIO 598): (3 credits; undergraduate/graduate elective)

This course covers the evolution of sex determination mechanisms across plants and animals. We will ask how separate sexes evolved, study the range of sex determination mechanisms, investigate why some species have only two sexes (and why some have more!), learn about the effects of sexual selection, and delve into the unique features of genetic sex determination. We will cover modern sequencing technology and its uses for studying sex chromosome divergence and diversity, including introduction to command line programming. Finally, we will discuss common misunderstandings about biological sex, gender identity, and sexual orientation. The course is discussion-based, evaluations throughout the semester include presentations and extensions of course material, and essays, all of which are evaluated by the instructor, and by peers.

Fall 2015 (17 students): 1.6 out of 5 (1 high; Dept-wide average is 1.9)

Life Sciences Career Paths Recitation (BIO 189): (5 lectures; required for undergraduate majors)

Topic: Sex, evolution, and relevance for human health

Freshmen School of Life Sciences students participate in an overview of the opportunities for and complexities of biological research including comparative genomics, evolution, and sex-biased health.

Fall 2015 (19 students): No instructor evaluations

Undergraduate Research (MIC/MBB/BIO 495) (1-3 credits; undergraduate elective)

Supervised research in biology/microbiology/molecular biosciences and biotechnology.

Fall 2014-present: No instructor evaluations

Guest Lectures

Guest lecturing is an important way to support I routinely contribute to courses taught by other faculty across ASU. When possible, I contribute to other courses taught across the University.

April 2018 **NSF GRF Writing Course (BIO 598):** Guest Lecture (1) – “Evaluating NSF graduate fellowships”

Apr 2018 **Advanced Molecular and Cellular Biology II (MCB 556):** Guest Lecture (1) – “Plant and animal sex chromosome evolution.”

Feb 2018 **Science Communication (BIO 591):** Guest Lecture (1) – “Social Media communication.”

Apr 2017 **Advanced Molecular and Cellular Biology II (MCB 556):** Guest Lecture (1) – “Plant and animal sex chromosome evolution.”

Sep 2016 **Principles of Evolution (EVO 601):** Guest Lecture (1) – “Absence of recombination”

Sep 2016 **Human Genetics (ASM/BIO 546):** Guest Lectures (2) – “Human population genetics” & “Tests of selection”

Apr 2016 **Advanced Molecular and Cellular Biology II (MCB 556):** Guest Lecture (1) – “Plant and animal sex chromosome evolution.”

- Feb 2016 **Research Topics in Evolution (EVO 610):** Guest Lecture (1) – “Evolution of sex determination mechanisms.”
- Oct 2015 **Life Sciences Career Paths (BIO 189):** Guest Lectures (2) – “Disciplines in the life sciences, career paths, courses and research opportunities: learn to code.”
- Sep 2015 **NSF GRF Writing Course (BIO 598):** Guest Lecture (1) – “Evaluating NSF graduate fellowships”
- Oct 2014 **Principles of Evolution (EVO 601):** Guest Lecture (1) – “Genomics of sex determination”
- Oct 2014 **Organic Evolution (BIO 345):** Guest Lecture (1) – “Hominid evolution, continuing evolution in modern humans, and medical relevance”
- Nov 2014 **Human Genetics (ASM/BIO 546):** Guest Lecture (1) – “Adaptive Evolution”

TEACHING EXPERIENCE PRIOR TO ARIZONA STATE UNIVERSITY

University of California-Berkeley

- Fall 2013 Integrative Biology Honors Research Project, Primary Research Mentor
- Fall 2013 Comparative Literature R1B: Misplaced Identities, Guest Lecture, “Scientific Writing”
- Fall 2013 Bioengineering Undergraduate Design Research, Primary Research Mentor
- Spring 2013 Statistical Genomics, Guest Lecture, “Bioinformatics Methods & Accessing Data”

Berkeley High School, Guest Lectures

- Spring ‘12, ‘13 Introduction to phylogenetic interpretation and analysis.

The Pennsylvania State University

- Jun 2010 Guest Lecturer, Introduction to Health and Human Sexuality, “Comparative Sexuality”
- Apr 2010 Guest Lecturer, Molecular Evolution, “Male Mutation Bias”
- Fall 2006 Teaching Assistant, Calculus and Biology I, Weekly recitations, proctor/grade exams
- 2006-2007 Introductory Physiology, Exam Proctor

State College High School, Graduate Students as Teachers in Biotechnology

- 2006-2010 Taught hands on biotechnology, molecular biology and evolution annually to high school students in a week-long and day-long courses, 2010 program organizer

Creighton University

- Spring 2005 Teaching Assistant, Multi-variable Calculus
- 2001-2005 Tutor, Mathematics department, Geometry through Multivariable Calculus

TEACHING TRAINING COURSES

- Sept 2014 “Peer-learning in the classroom”
- Sept 2014 “Demofest at ASU: Innovating Teaching Practices”
- Sept 2014 “Digital Portfolios at ASU”
- Sept 2014 “Web-Conferencing: Engaging Your Students in Real Time!”
- March 2012 “Preparing Future Faculty: How to Teach a Large Course”
- March 2012 “Assessment of Teaching and Learning”
- Feb 2012 “Strategies for Grading Efficiently and Effectively”
- April 2010 “Hybrid Class Designs as a Way to Maximize Student Learning”
- April 2010 “Graduate Instructor 102: Beyond the Basics of Course Design”
- April 2010 “Making General Education Courses Relevant”

ORGANIZATIONS & AFFILIATIONS

- 2016-present American Genetic Association
- 2015-present International Society for Evolutionary Medicine and Public Health
- 2012-present American Society of Human Genetics
- 2007-present Society for Molecular Biology and Evolution
- 2006-present Society for the Study of Evolution
- 2015-2016 International Primatological Society

inducted 2002 Pi Mu Epsilon: Honorary National Mathematics Society

PROFESSIONAL DEVELOPMENT

Mar 2016 "CV preparation for Tenure and Promotion" by CLAS, ASU
Apr 2015 "Preparing for the Tenure Review" by CLAS, ASU
Apr 2015 "Lunch with the Dean" by CLAS, ASU
Apr 2015 "Developing a Three-Year Plan" by CLAS, ASU
Feb 2015 "Jumping into the Mix: How to Tackle Grant or Fellowship Proposals" by CLAS, ASU
Nov 2014 "Article Driven Research" by CLAS, ASU
Nov 2014 "Lunch with the Dean" by CLAS, ASU
Nov 2014 "What I Wish I Knew Then: Advice from Seasoned Colleagues" by CLAS, ASU
Oct 2014 "Writing & Designing NSF Proposals" by Grant Training Center
Sep 2014 "OKED New Faculty Workshop" by Knowledge Enterprise Development, ASU
Sep 2014 "Prepping for Class at ASU" by CLAS, ASU
Sep 2014 "Understanding ASU and the Culture of your Department" by CLAS, ASU
Sep 2014 "Writing & Designing NIH Proposals" by Grant Training Center

SCIENCE OUTREACH AND ENGAGEMENT

Ongoing **Science communication**, Regular contributor at [Ask a Biologist](http://askabiologist.asu.edu), for K-12 students.
Podcast interview: <https://askabiologist.asu.edu/explore/monster-dna>.
DNA extraction (65,011 views): <https://askabiologist.asu.edu/activities/banana-dna>
Breaking proteins (861 views): <https://askabiologist.asu.edu/activities/breaking-proteins>

Ongoing **Science communication**, Regular science and academic posts, and follow-up discussion, at mathbionerd.blogspot.com.

Ongoing **March Mammals Madness**, Biology & ecology, mammal, and natural history education
Mar 2020, Wilson and Stone assembled and shared genetics facts.
Mar 2019, Wilson and Stone assembled and shared genetics facts.
Used as a teaching tool in to reach over 250,000 students this year.
Mar 2018, Wilson Sayres and Stone assembled and shared genetics facts.
Mar 2017, Wilson Sayres and Stone shared genetics facts; narrated a battle.
Mar 2016, Wilson Sayres and Stone Lab compiled and shared genetics information

Ongoing **SACNAS: Advancing Chicano/Hispanic and Native Americans in Science**
Feb 2017, Graduate School Panelist
Jan 2016, Introduction To Command Line Lesson
Nov 2015, Inspiring Science Career Paths Panelist

Ongoing **ASU School of Life Sciences Homecoming Booth**,
Nov 2018, Extracting Banana DNA; More than 1000 visitors
Oct 2017, Extracting Banana DNA; More than 1000 visitors
Oct 2016, Extracting Banana DNA; More than 1000 visitors
Sep 2015, Vaccine awareness. 800-1000 visitors.

Ongoing **Open Door organizer/participant, Arizona State University, 15,000 people yearly**
Feb 2017, Ran two hours of narrated mammal battles for March Mammals Madness.
Feb 2016, Developed & implemented hands-on DNA extraction.
Feb 2015, Developed & implemented hands-on dog genetics and phylogenetic activities.

Ongoing **Science Panelists, Phoenix ComiCon/FanFusion, Phoenix AZ (>6400 attendees).**
May 2019
No it Isn't that Simple: Science of Gender
Viruses as Treatments: Learning from the Best
Who's your Daddy? The Science of Forensics
May 2018
NASA Twins Study: A Twist in DNA (115 people)
Captain Kirk: Planting Seeds Across the Galaxy (27 people)
May 2017
No Controversy to Teach: Climate, Vaccines, & Evolution (59 people)
Building the Future: How to become a STEM professional (43 people)

- It's Alive: The Science of Frankenstein (74 people)
Jun 2016
 X-men, mutations, and you (113 people)
 Dragon Balls: The Science of Reproduction (42 people)
 Letter to the Gene Editor: Science of DNA Seq (54 people)
May 2015
 Safe Alien Sex (220 people)
 It's Not a Debate: Evolution, Vaccines, and GMOs (80 people)
- Mar 2017 **CompuGirls camp mentors**, Wilson Sayres lab trainees served as mentors for 13-17 year old girls to recruit to computing careers (Taravella, Valverde-Vesling)
- Jun 2016 **Mathematical and Theoretical Biology Institute (MTBI) presenter**, Program to increase the number of underrepresented minorities in math and sciences.
- May 2016 **I'm A Scientist USA participant and winner**, Online public science engagement, Skype with students across the USA: <http://heliuma16.imascientist.us/profile/melissasayres/>.
- Apr 2016 **Go Bananas for DNA: National DNA Day activity**, Extracting DNA at the library.
- Apr 2016 **GirlTalk.org, presentation and discussion**. Scientific career opportunities discussion with Nepalese orphan girls (www.nepalorphanshome.org).
- Feb 2016 **Middle School Science Fair Judge, Self Development Academy, Mesa, AZ**, 9 lab members.
- Aug 2015 **Are women superior to men? A panel discussion on evolution and sex differences**, Invited panelist for public lecture and discussion, Center for Evolution and Medicine.
- Mar 2015 **Communicating the relevance of human evolution**, Invited participant in NESCent working group.
- Apr 2014 **@RealScientists curator**:
<http://mathbionerd.blogspot.com/2014/04/my-time-as-real-scientist-realscientists.html>
- 2011-2014 **Berkeley High School Outreach Organizer**, Taught lesson on phylogenetics to high school students; volunteered for the rest of a series of six evolution & forensics lessons.
- March 2013 **Reporting Across the Culture Wars: Engaging Media on Evolution**, Invited participant in NESCent catalysis group.
- 2007-2011 **Girl Scout Workshop Chair**, Initiated, organized and developed infrastructure for a bi-annual science outreach workshop, serving 50 7th-12th grade Girl Scouts each workshop. Chaired for 3 years, then served as training co-chair for 1 year.
- 2010 **USA Science and Engineering Festival, National GWIS Coordinator**, Develop and implement an interactive scientific activity for approximately 10,000 participants.
- 2007, '08, '10 **Pennsylvania Junior Academy of Science Research Presentation Judge**
- 2010 **The Pennsylvania State University Undergraduate Exhibition Poster Judge**
- 2009-2011 **Women in the Sciences and Engineering Internal Advisory Board member**
- 2009 **WISE Week Day Camp Workshop Volunteer**, "Engineering: Designing Possibilities"
- 2008-2009 **Bioinformatics and Genomics Research Club Coordinator**, Initiated and organized monthly graduate student research presentations.
- 2008 **Pennsylvania Junior Science & Humanities Symposium (PA-JSHS) Poster Judge**
- 2008 **Tyrone Science Day Organizer**, Designed/ran "Dragon Genetics" workshop for 175 first grade students in Tyrone school district, Pennsylvania.
- 2008 **WISE Week Day Camp Workshop Coordinator**, "Dragon Genetics" for 12th grade
- 2008-2010 **Inside the Scientist's Studio coordinator**, GWIS, Penn State University
- 2007-2010 **Graduate Women in Science Voices conference committee member**, 2009-10 **chair**
- 2007 **WISE Week Day Camp Program Assistant**, Women in the Sciences and Engineering
- 2007-2009 **Graduate Women in Science, Nu chapter president**
- 2007-2009 **Commission for Women, Marketing committee chair**, co-chair, Penn State University
- 2006-2007 **Graduate Women in Science, Nu chapter vice president**

PUBLIC LECTURES (14 Total)

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14. **Public lecture**, Arizona Bioethics Network, webinar, *Aug 2019*
13. **Public lecture**, AZ Celebrates The 19th Amendment, ASU West, Glendale, AZ, *Aug 2018*
12. **Public lecture**, Salon of the Senses, Paradise Valley, AZ, *May 2018*

11. **Public lecture**, Rio Verde-ASU lecture series, Rio Verde, AZ, *Jan 2018*
10. **Public lecture**, ASU Emeritus College lecture series, Tempe, AZ, *Nov 2017*
9. **Public lecture**, Wiseguise, Scottsdale, AZ, *Apr 2017*
8. **Public lecture**, Secular Day at the Capitol, Arizona State Capitol, Phoenix, AZ, *Mar 2017*
7. **Public lecture**, Salon of the Senses, Paradise Valley, AZ, *Mar 2017*
6. **Public lecture**, Arizona State Legislature, Arizona State Capitol, Phoenix, AZ, *Mar 2017*
5. **Public lecture**, Data Science Phoenix, Tempe, AZ, *Jul 2016*
4. **Public lecture**, hosted by Salon of the Senses & Biodesign Institute, Tempe, AZ, *July 2015*
3. **Public lecture**, hosted by the Bay Area Skeptics, Berkeley, CA, *Aug 2013*
2. **Public lecture**, hosted by Graduate Women in Science - Omicron Chapter, Bethesda, MD, *Jun 2013*
1. **Public lecture**, hosted at Creighton University. Omaha, NE *Oct 2007*

SCIENCE IN THE MEDIA

- 2019** The Atlantic: [A breakthrough in the mystery of why women get so many autoimmune diseases](#)
 NIH Reporter front page: [Sex chromosomes can trade DNA in two places](#)
 Information (Danish newspaper): [Intelligence and Race](#)
 ASU Now DNA Day: [The future of DNA is unfolding now](#)
 Scholastic Pathways Magazine Profile: [The Gene Detective](#)
 Gizmodo, [What's the Least Useful Body Part?](#)
 Arizona PBS Catalyst series (Video): [Gila monster genomes](#)
- 2018** 105 Experts, Motherboard, "[105 Experts: What Scares and Inspires You?](#)"
 Smithsonian Magazine interview, "[Earliest mammals kept their cool with descended testicles](#)"
 New York Times expert about evolution of the Y chromosome in "[Secrets of the Y chromosome](#)"
- 2017** Family and DNA with ASU Now: "[Tips for surviving family table talk this Thanksgiving](#)"
 Expert geneticist, Univision, Daniela Zavala: "Pruebas genéticas permiten determinar la vulnerabilidad a enfermedades hereditarias" (Television: [Video](#))
 Quoted in "[Did we come from pigs](#)" by Steph Yin about human genetics for The Outline.
 Radio interview on "The Science Show" with Robyn Williams on ABC: [Gila monster may reveal evolution of sex chromosomes.](#)
 Featured nominee for "[BadAss women of ASU](#)"
 Interviewed about [sex and gender](#) for Idea Spermatheca by Caitlin E McDonough.
 Featured guest discussing genetics and sex on Reality Trip with Ben Fama Jr. ([Video Podcast](#)).
- 2016** Discussing [accuracy of personalized genomics](#) on ABC 15 news television.
[Arizona's Adorable Monster](#) by Ed Yong in The Atlantic.
 Expert reference for article about giraffe speciation for [Scholastic Math](#).
 Research on male mutation bias featured in [ASUNow](#).
 Research on anole speciation featured in [Anole Annals](#).
 News stories about Gila monster research project: Cronkite News Arizona PBS ([video](#)).
[Career path for Dr. Wilson Sayres](#) for Ask a Biologist.
[Monster DNA](#) for Ask a Biologist.
 News stories about publication on X-Y chromosome swapping: ASU news ([news article](#)); Picked up by [17 news outlets](#).
 Featured in NatureJobs, [The Faculty series: Applying for grants](#), by Viviane Callier.
- 2015** Research coverage about our research on microchimerism and maternal health by journalists at [The New York Times](#), [National Geographic](#), [The Smithsonian Magazine](#).
 Our research: "[Human Sex Chromosomes are Sloppy DNA Swappers](#)", by Viviane Callier.
 Interviewed by Ed Yong from National Geographic as an expert about [temperature-dependent and genetic sex determination](#) in bearded dragons.
 Interviewed about my research, graduate experience, training, and academic life for the [Rock Your Research](#) podcast series.

- Interviewed our published research, "[A recent bottleneck of Y chromosome diversity coincides with a global change in culture](#)", interviewed by, Danielle Paquette, Washington Post; Mark Brodie, KJZZ NPR; Francie Diep, Pacific Stand; and featured on: Slate, IFLS, and reddit.
- 2014** Interviewed about co-organized session, "The X-factor of Complex Disease," at ASHG Science featured in [Meeting report in Genome Biology](#).
- Interviewed about [bioinformatics research](#) as part of a series with notable bioinformaticians.
- Interviewed about [genomic testing](#) as new resources for Phoenix Children's Hospital.
- Interviewed about [open access publishing](#) for Open Access Week by ASU Library.
- Profiled for early career scientists on "[Breaking the \(bio\)code](#)."
- Profiled for 9th grade science class: Provided a summary of life as a scientist, and answered high school questions about scientific research, training, and education.
- Breaking Bio Episode #65: "[Sex chromosomes & Math for Biologists, Dr. Melissa Wilson Sayres](#)."
- Conference on World Affairs panelist, "[56 different points on the gender spectrum](#)."
- Interviewed by Maria Armoudian on The Scholar's Circle along with Jeremy Nathans, [about the X and Y chromosomes](#).
- Interviewed about Y chromosomes by Jonathan Green of ABC (Australian Broadcasting Company) Radio National – "[Y chromosome not superfluous: new research](#)."
- Interviewed about work studying variation on the human Y chromosome by journalists at [The Guardian](#), [Huffington Post](#), and [Zeit Online](#) (German).
- 2013** Interviewed by Ed Yong from National Geographic about [inherited human sex reversal](#) due to variations in the SRY gene.
- Requested to comment on [TMRCA of Y and mtDNA](#), and [timing of Y common ancestor](#)
- Interviewed separately by: Tia Gohsh, Live Science; Erin Wayman, Science News
- Commented on [identification of an ancient Y lineage](#), Interviewed by: Alan Boyle, NBC Science
- 2012** Regarding my research, "[Natural selection reduced diversity on human Y chromosomes](#)", Interviewed by: Tia Gohsh, Live Science
- Commented on [the Rhesus Y chromosome](#), Interviewed by Dinsa Sachan, Down to Earth magazine
- 2009** Regarding, "[Evolution and survival on eutherian sex chromosomes](#)", Interviewed by ABC Health News, ScienceNOW, Science podcast, Los Angeles Times, Popular Science, L'Espresso, and The Discovery Channel