

Nathan L. Clark

CURRICULUM VITAE

BIOGRAPHICAL

Website: <http://nclarklab.org> **E-Mail Address:** nclark@utah.edu
Address: 6120 Eccles Institute of Human Genetics **Phone:** 801-587-0990
15 S 2030 E
Salt Lake City, UT 84112

EDUCATION and TRAINING

UNDERGRADUATE:

1994 – 1998 University of Texas at Austin, Austin, TX, USA
Bachelor of Science in Chemistry (1998)

GRADUATE:

2002 – 2007 University of Washington, Seattle, WA, USA
Ph.D. in Genome Sciences (2007) Advisor: Willie J. Swanson

POSTGRADUATE:

2007 – 2011 Cornell University, Ithaca, NY, USA
N.I.H. Postdoctoral Fellow in Genetics Mentor: Charles F. Aquadro

APPOINTMENTS and POSITIONS

ACADEMIC:

2007 – 2011	N.I.H. Postdoctoral Fellow	Cornell University, Ithaca, NY, USA
2012 – 2018	Assistant Professor	Dept. of Computational and Systems Biology University of Pittsburgh School of Medicine
2016 – 2019	Associate Director of PhD program in Computational Biology	Joint Carnegie Mellon University-University of Pittsburgh
2018 – 2019	Associate Professor (now Adjunct)	Dept. of Computational and Systems Biology University of Pittsburgh School of Medicine
2019 – 2023	Associate Professor	Department of Human Genetics University of Utah School of Medicine
2023 – present	Associate Professor	Department of Biological Sciences University of Pittsburgh

MEMBERSHIPS in PROFESSIONAL and SCIENTIFIC SOCIETIES

Society for Molecular Biology and Evolution	2005 – present
Genetics Society of America	2009 – present
International Society for Computational Biology	2015 – present
Society for the Study of Evolution	2016 – present

HONORS

National Merit Scholar

1994

National Merit Scholarship from University of Texas	1994 – 1998
Dean’s Scholars Natural Sciences Honors Program	1994 – 1998
Clara Abbott Foundation Scholarship	1994 – 1998
Columbia HCA Scholarship	1996 – 1998
American Chemical Society Award for Excellence in Organic Chemistry	1998
Parker Award for Best Poster Presentation Genome Sciences, University of Washington	2004
Graduate Student Travel Award (competitive) Society for Molecular Biology and Evolution	2006
N.I.H. Ruth L. Kirschstein Postdoctoral Fellowship	2008 – 2010
Post-doctoral Travel Award (competitive) Society for Molecular Biology and Evolution	2009
Cornell Center for Comparative and Population Genomics Travel Award	2010
Post-doctoral Travel Award (competitive) Society for Molecular Biology and Evolution	2010
Charles E. Kaufman Foundation New Investigator Award	2014
CTSI Biomedical Modeling Pilot Award (U Pittsburgh)	2018
Chancellor’s Distinguished Research Award, Junior Scholar (U Pittsburgh)	2019

PUBLICATIONS

REFEREED ARTICLES:

Bold denotes Clark lab member.

* Indicates co-corresponding authorship.

1. Stewart MK, **Clark NL**, Merrihew G, Galloway EM, Thomas JH. High genetic diversity in the chemoreceptor superfamily of *Caenorhabditis elegans*. *Genetics* 2005; 169(4): 1985-1996. PMC1449585.
2. **Clark NL**, Swanson WJ. Pervasive adaptive evolution in primate seminal proteins. *PLOS Genetics* 2005; 1(3): e35. PMC1201370.
3. Panhuis, TM, **Clark, NL** & Swanson, WJ. Rapid evolution of reproductive proteins in abalone and *Drosophila*. *Philosophical Transactions of the Royal Society B* 2006; 361: 261-268. PMC1569613.
4. **Clark NL**, Findlay GD, Yi X, MacCoss MJ, Swanson WJ. Duplication and selection on abalone sperm lysin in an allopatric population. *Molecular Biology and Evolution*. 2007; 24(9): 2081. PMC17630281.
5. Karn RC, **Clark NL**, Nguyen ED, Swanson WJ. Adaptive evolution in rodent seminal vesicle proteins. *Molecular Biology and Evolution*. 2008; 25(11): 2301. PMC2727389.
6. Dean MD, **Clark NL**, Findlay GD, Karn RC, Yi X, Swanson WJ, MacCoss MJ, Nachman MJ. Proteomics and comparative genomic investigations reveal heterogeneity in evolutionary rate of male reproductive proteins in mice (*Mus domesticus*). *Molecular Biology and Evolution*. 2009; 26(8): 1733. PMC2734151.
7. **Clark NL**, Gasper J, Sekino M, Springer SA, Aquadro CF, Swanson WJ. Coevolution of interacting fertilization proteins. *PLOS Genetics* 2009; 5(7): e1000570. PMC2704960.

8. **Clark NL**, Aquadro CF. A novel method to detect proteins evolving at correlated rates: Identifying new functional relationships between coevolving proteins. *Molecular Biology and Evolution*. 2010; 27(5):1152-61. PMC2877527. **Featured in Faculty of 1000.**
9. Kelleher ES, **Clark NL**, Markow TA. Diversity Enhancing Selection Acts on a Female Reproductive Protease Family in Four Sub-Species of *Drosophila mojavensis*. *Genetics*. 2011; 187(3): 865-76. PMC3063679.
10. **Clark NL**, Alani E, Aquadro CF. Evolutionary rate covariation reveals shared functionality and co-expression of genes. *Genome Research*. 2012; 22(4): 714-720. PMC3317153.
11. **Clark NL**, Alani E, Aquadro CF. Evolutionary rate covariation involving meiotic proteins results from fluctuating evolutionary pressure in yeasts and mammals. *Genetics*. 2013; 193(2): 529-538. PMC3567741. **Selected for Issue Highlight.**
12. Findlay GD, Sitnik JL, Wang W, Aquadro CF, **Clark NL**, Wolfner MF. Evolutionary Rate Covariation Identifies New Members of a Protein Network Required for Drosophila Female Post-Mating Responses. *PLOS Genetics*. 2014; 10(1): e1004108. PMC3894160. **Featured in Faculty of 1000.**
13. **Priedigkeit NM, Wolfe NW, Clark NL**. Evolutionary signatures amongst disease genes permit novel methods for gene prioritization and construction of informative gene networks. *PLOS Genetics*. 2015; 11(2): e1004967. PMC4334549
14. **Meslin C**, Plakke MS, Deutsch AB, **Small BS**, Morehouse NI, **Clark NL**. Digestive Organ in the Female Reproductive Tract Borrows Genes from Multiple Organ Systems to Adopt Critical Functions. *Molecular Biology and Evolution*. 2015. 32(6): 1567-1580. PMC4572785
15. Godin SK, **Meslin C**, Bratton-Palmer DS, Hornack C, Mihalevic MJ, Yoshida K, Kabbinavar F, Sullivan M, **Clark NL***, Bernstein KA*. Evolutionary and functional analysis of the invariant SWIM domain in the conserved Shu2/SWS1 protein family from *Saccharomyces cerevisiae* to *Homo sapiens*. *Genetics*. 2015. 199(4): 1023-1033. PMC4391554 **Selected for Issue Highlight & Featured by Saccharomyces Genome Database Blog.**
16. Hancks DC, Hartley MK, Hagan C, **Clark NL**, Elde NC. Overlapping Patterns of Rapid Evolution in the Nucleic Acid Sensors cGAS and OAS1 Suggest a Common Mechanism of Pathogen Antagonism and Escape. *PLOS Genetics*. 2015. 11(5): e1005203. PMC4420275
17. Plakke MS, Deutsch AB, **Meslin C, Clark NL**, Morehouse NI. Dynamic digestive physiology of a female reproductive organ in a polyandrous butterfly. *Journal of Experimental Biology*. 2015. 218, 1548-1555. PMC4518259 **Featured in "Inside JEB".**
18. Mangels R, Young B, Keeble S, Ardekani R, **Meslin C, Ferreira Z, Clark NL**, Good JM, Dean MD. Genetic and phenotypic influences on copulatory plug survival in mice. *Heredity*. 2015. 115, 496-502. PMC4806896.
19. **Wolfe NW, Clark NL**. ERC Analysis: web-based inference of gene function via Evolutionary Rate Covariation. *Bioinformatics*. 2015. doi:10.1093/bioinformatics/btv454. PMC4751245.
20. Ziegler A, Augustin H, **Clark NL**, Berthelot-Grosjean M, Simonnet M, Steinert J, Geillon F, Maniere G, Featherstone D, and Grosjean Y. The Amino Acid Transporter Jhl-21 Coevolves with Glutamate Receptors, Impacts NMJ Physiology, and Influences Locomotor Activity in *Drosophila* Larvae. *Scientific Reports*. 2016. 6:19692. DOI: 10.1038/srep19692. PMC4726445.
21. Böhm S, Szakal B, Herken BW, Sullivan MR, Mihalevic MJ, Kabbinavar FF, Branzei D, **Clark NL**, Bernstein KA. The budding yeast ubiquitin protease Ubp7 is a novel component involved in S-phase progression. *Journal of Biological Chemistry*. 2016; 291(9): 4442-52. PMC4813472.

22. Chikina M, **Robinson JD**, **Clark NL**. Hundreds of genes experienced convergent shifts in selective pressure in marine mammals. *Molecular Biology and Evolution*. 2016. 33(9): 2182-2192. PMC5854031.
23. Clancy CJ, **Meslin C**, Badrane H, Cheng S, Losada LC, Nierman WC, Vergidis P, **Clark NL**, Nguyen MH. *Candida albicans* transcriptional profiling within biliary fluid from a patient with cholangitis, before and after antifungal treatment and surgical drainage. *Open Forum Infectious Diseases*. 2016; 3(3):ofw120. PMC5047399.
24. **Meslin C**, **Cherwin TS**, Plakke MS, **Small BS**, Goetz BJ, Morehouse NI, **Clark NL**. Structural complexity and molecular heterogeneity of a butterfly ejaculate reflect a complex history of selection. *Proceedings of the National Academy of Sciences, USA*. 2017; 114(27): E5406–E5413. PMC5502654. **Featured in The Atlantic**.
25. **Partha R**, Chauhan BK, **Worman-Ferreria Z**, **Robinson JD**, Lathrop K, Nischal KK, Chikina M*, **Clark NL***. Subterranean mammals show convergent regression in ocular genes and enhancers, along with adaptation to tunneling. *eLife*. 2017; 6: e25884. PMC5643096.
26. Sumitha Nallu, Jason Hill, Kristine Don, Carlos Sahagun, Wei Zhang, **Camille Meslin**, Emilie Snell-Rood, **Nathan L. Clark**, Nathan I. Morehouse, Joy Bergelson, Christopher W. Wheat and Marcus R. Kronforst. The molecular genetic basis of herbivory between butterflies and their host-plants. *Nature: Ecology and Evolution*. 2018; 2: 1418-1427. PMC6149523. [doi:10.1038/s41559-018-0629-9](https://doi.org/10.1038/s41559-018-0629-9)
27. **Wynn K. Meyer**, **Jerrica Jamison**, Rebecca Richter, Stacy E. Woods, **Charles Kronk**, **Raghavendran Partha**, **Amanda Kowalczyk**, Maria Chikina, Robert K. Bonde, Joseph Gaspard, Janet M. Lanyon, Clement E. Furlong, and **Nathan L. Clark**. Ancient convergent losses of *Paraoxonase 1* yield deleterious consequences for modern marine mammals. *Science*. 2018; 361(6402): 591-594. PMC6317340. [doi:10.1126/science.aap7714](https://doi.org/10.1126/science.aap7714) **Featured in the New York Times, The Atlantic, National Geographic and many more.**
28. Hill JA, Neethiraj R, Rastas P, **Clark NL**, Morehouse NI, de la Paz Celorio-Mancera M, Cols JC, Dirksen H, **Meslin C**, Sikkink K, Vives M, Vogel H, Wiklund C, Boggs CL, Nylin, Wheat CW. A butterfly chromonome reveals selection dynamics during extensive and cryptic chromosomal reshuffling. *Science Advances*. 2019; 12:5(6):eaau3648. PMC6561736. [doi: 10.1126/sciadv.aau3648](https://doi.org/10.1126/sciadv.aau3648)
29. Raza Q, Choi JY, Li Y, O'Dowd RM, Watkins SC, Hong Y, **Clark NL**, Kwiatkowski AV. Evolutionary rate covariation identifies the GTPase activating protein Raskol as a signaling component of the cadherin adhesion network in *Drosophila*. *PLOS Genetics*. 2019; 15(2): e1007720. PMC6375579 doi.org/10.1371/journal.pgen.1007720 **Featured in Perspective by Jeffrey Colgren and Scott Nichols. Evolution as a guide for experimental cell biology.**
30. **Partha R**, **Kowalczyk A**, **Clark NL**, Chikina M. Robust methods for detecting convergent shifts in evolutionary rates. *Molecular Biology and Evolution*. 2019; 36(8): 1817-1830. PMC6657723 doi.org/10.1093/molbev/msz107
31. **Kowalczyk A**, **Meyer WK**, **Partha R**, Mao W, **Clark NL**, Chikina M. RERconverge: an R package for associating evolutionary rates with convergent traits. *Bioinformatics*. 2019; 1-3: btz468. PMC6853647 [doi: 10.1093/bioinformatics/btz468](https://doi.org/10.1093/bioinformatics/btz468)
32. **Plakke MS**, **Walker JL**, Lombardo JB, Goetz BJ, Pacella GN, Durrant JD, **Clark NL**, Morehouse NI. Characterization of Female Reproductive Proteases in a Butterfly from Functional and Evolutionary Perspectives. *Physiol Biochem Zool*. 2019; 92(6): 579-590. <https://doi.org/10.1086/705722>

33. Sackton TB and **Clark NL**. Convergent evolution in the genomics era: new insights and directions. *Philosophical Transactions of the Royal Society B*. 2019; 374(1777): Article ID 20190102. PMC6560275. doi.org/10.1098/rstb.2019.0102 **Guest editor of special issue on convergent evolution.**
34. Brunette GJ, Jamalruddin MA, Baldock RA, **Clark NL**, Bernstein KA. Evolution-based screening enables genome-wide prioritization and discovery of DNA repair genes. *Proceedings of the National Academy of Sciences, USA*. 2019; 116(39): 19593-19599. PMC6765268 doi.org/10.1073/pnas.1906559116
35. Cai C, Cooper GF, Lu KN, Ma X, Xu S, Zhao Z, Chen X, Xue Y, Lee AV, **Clark NL**, Chen V, Lu S, Chen L, Yu L, Hochheiser HS, Jiang X, Wang J, Lu X. Systematic discovery of the functional impact of somatic genome alterations in individual tumors through tumor-specific causal inference. *PLoS Computational Biology*. 2019; 15(7): e1007088. PMC6650088. [dx.doi.org/10.1371/journal.pcbi.1007088](https://doi.org/10.1371/journal.pcbi.1007088)
36. **Kowalczyk A, Partha R, Clark NL**, and Chikina M. Pan-mammalian analysis of molecular constraints underlying extended lifespan. *eLife*. 2020; 9: e51089. PMC7012612 <https://doi.org/10.7554/eLife.51089>
37. Talsness DM, Owings KG, Coelho E, Mercenne G, Pleinis JM, Partha R, Hope KA, Zuberi AR, **Clark NL**, Lutz CM, Rodan AR, Chow CY. A *Drosophila* screen identifies NKCC1 as a modifier of NGLY1 deficiency. *eLife*. 2020; 9: e57831. PMC7758059 <https://doi.org/10.7554/eLife.57831>
38. Huang JW, Acharya A, Tagliatalata A, Nambiar TS, Cuella-Martin R, Leuzzi G, Hayward SB, Joseph SA, Brunette GJ, Anand R, Soni RK, **Clark NL**, Bernstein KA, Cejka P, Ciccia A. MCM8IP activates the MCM8-9 helicase to promote DNA synthesis and homologous recombination upon DNA damage. *Nat Commun*. 2020; 11(1): 2948. PMC7290032 <https://doi.org/10.1038/s41467-020-16718-3>
39. **Saputra E, Kowalczyk A, Cusick L, Clark NL**, Chikina M. Phylogenetic Permutations: a statistically rigorous approach to measure confidence in associations between phenotypes and genetic elements in a phylogenetic context. *Molecular Biology and Evolution*. 2021; msab068. PMC8233500 <https://doi.org/10.1093/molbev/msab068>
40. Furman CM, Elbashir R, Pannafino G, **Clark NL**, Alani E. Experimental exchange of paralogous domains in the MLH family provides evidence of sub-functionalization after gene duplication. *G3 Genes|Genomes|Genetics*. 2021. jkab111. PMC8495741 <https://doi.org/10.1093/g3journal/jkab111>
41. Keeble S, Firman RC, Sarver BAJ, **Clark NL**, Simmons LW, Dean MD. Evolutionary, proteomic, and experimental investigations suggest the extracellular matrix of cumulus cells mediates fertilization outcomes. *Biology of Reproduction*. 2021; 105(4): 1043–1055. <https://doi.org/10.1093/biolre/ioab082>
42. **Kowalczyk A**, Gbadamosi O, Kolor K Sosa Jahree, St Croix C, Gibson G, Chikina M, Aizenman E, **Clark NL**, Kiselyov K. Evolutionary rate covariation identifies SLC30A9 (ZnT9) as a mitochondrial zinc transporter. *Biochem J*. 2021; 478 (17): 3205–3220. PMC <https://doi.org/10.1042/BCJ20210342>
43. **Amanda Kowalczyk**, Maria Chikina, **Nathan L Clark**. A cautionary tale on proper use of branch-site models to detect convergent positive selection. bioRxiv 2021.10.26.465984; doi: <https://doi.org/10.1101/2021.10.26.465984>

44. **Amanda Kowalczyk**, Maria Chikina, **Nathan Clark**. Complementary evolution of coding and noncoding sequence underlies mammalian hairlessness. *eLife*. 2022; 11:e76911. <https://doi.org/10.7554/eLife.76911>
45. Wang X-P, Balchak DM, Gentilcore C, **Clark NL**, Kashlan OB. Activation by Cleavage of the Epithelial Na⁺ Channel α and γ Subunits Independently Coevolved with the Vertebrate Terrestrial Migration. *eLife*. 2022; 11: e75796. PMC8791634 <https://doi.org/10.7554/eLife.75796>
46. Catalina Pereira, Gerardo A. Arroyo-Martinez, Matthew Z. Guo, Michael S. Downey, Emma R. Kelly, Kathryn J. Grive, Shantha K. Mahadevaiah, Jennie Sims, Vitor Marcel Faça, Charlton Tsai, Carl J. Schiltz, Niek Wit, Heinz Jacobs, **Nathan L. Clark**, Raimundo Freire, James M. A. Turner, Amy M. Lyndaker, Miguel A. Brieño-Enríquez, Paula E. Cohen, Marcus B. Smolka, Robert S. Weiss. Multiple 9-1-1 complexes promote homolog synapsis, DSB repair, and ATR signaling during mammalian meiosis. *eLife*. 2022. PMC8824475 <https://doi.org/10.1101/2021.04.09.439198>
47. Jana Svobodova, Michaela Frolikova, Lukas Ded, Jiri Cerny, Pavla Postlerova, Veronika Palenikova, Ondrej Simonik, Krystof Basus, Eliska Valaskova, Radek Machan, Allan Pacey, Zuzana Holubcova, Pavel Koubek, Zuzana Ezrova, Zuzana Nahacka, Soojin Park, Ruiwu Liu, **Raghavendran Partha**, **Nathan Clark**, Jiri Neuzil, Masahito Ikawa, Kent Erickson, Kit S. Lam, Harry Moore & Katerina Komrskova. MAIA, Fc receptor-like 3, supersedes JUNO as IZUMO1 receptor during human fertilization. *Science Advances*. 2022; 8: eabn0047.
48. **Sarah A.M. Lucas**, **Allie M Graham**, **Jason S Presnell**, **Nathan L Clark**. Highly Dynamic Gene Family Evolution Suggests Changing Roles for *PON* Genes Within Metazoa. *GBE* 2022.05.17.492316; doi: <https://doi.org/10.1101/2022.05.17.492316>
49. **Allie M Graham**, **Jerrica M Jamison**, **Marisol Bustos**, Clement E Furlong, Rebecca Richter, Judit Marsillach, **Jason S Presnell**, Dan Crocker, Lorrie Rea, **Alexis Michaels**, Ari Fustukjian, **Wynn K Meyer**, and **Nathan L Clark**. Rapid reduction of *Paraoxonase* expression followed by inactivation across semiaquatic mammals suggests adaptive benefit of gene loss. *MBE* 2023.

REVIEWS:

50. **Clark NL**, Aagaard JE, Swanson WJ. Evolution of reproductive proteins from animals and plants. *Reproduction* 2006; 131(1): 11-22. PMC16388004.
51. **Clark NL**. Adaptive evolution of primate sperm proteins. In: *Encyclopedia of Life Sciences (ELS)*. 2008. John Wiley and Sons, Ltd: Chichester.

SELECTED RESEARCH FEATURES / POPULAR PRESS:

- “Co-evolution’s Witness” by Jason Bittel, *Pitt Med Magazine*, Summer 2015.
- “This Common Butterfly Has an Extraordinary Sex Life” by Ed Yong, *The Atlantic*, June 2017.
- “Great Sex: These butterflies have giant sperm packages and vaginal ‘jaws’” by Jessica Wapner, *Newsweek*, June 2017.
- “The birds and bees of butterflies” by Melanie Schefft, *UC Magazine*, June 2017.
- “Most Marine Mammals are Missing One Mysterious Gene” by Nadia Drake, *National Geographic*, August 2018.
- “Marine Mammals Have Lost a Gene That Now They May Desperately Need” by Carl Zimmer, *New York Times*, August 2018.
- “An Ancient Genetic Quirk Could Doom Whales Today” by Ed Yong, *The Atlantic*, August 2018.
- “A missing gene could make marine mammals more vulnerable to common pesticides” by Catalina Jaramillo, *NPR: State Impact Pennsylvania*, August 2018.
- “Meeressäuger: Verhängnisvoller Genverlust?” by Daniela Albat, *Bild der Wissenschaft*, August 2018.

“Les mammifères marins désarmés face à certains pesticides” by Sylvie Burnouf, *Le Monde*, August 2018
 “Mamíferos marinhos perderam gene essencial para a defesa de pesticidas” by Teresa Sofia Serafim, *Público*, August 2018.
 “You don’t know what you’ve got ‘til it’s PON” hosted by Nels Elde and Vincent Racaniello. TWiEVO: This Week in Evolution. August 2018 (podcast).
 +26 additional related press articles on marine mammals across 11 countries, August 2018
 “Humans still have the genes for a full coat of body hair” *Washington Post*. Mark Johnston. 2022
 KSL-TV video feature “Utah professor’s team may have figured out why we lost our fur coat” Peter Rosen. 2022
 +11 other related press articles on genetics of the evolution hairless mammals

PROFESSIONAL ACTIVITIES

MENTORSHIP:

Graduate Faculty Status

Computational Biology PhD program Joint Carnegie Mellon–University of Pittsburgh	2012 – present
Integrative Systems Biology PhD program University of Pittsburgh	2014 – 2019
Medical Scientist Training Program University of Pittsburgh	2012 – 2019
Physician Scientist Training Program University of Pittsburgh School of Medicine	2013 – 2019
Molecular Biology PhD Program University of Utah	2019 – present

Post-doctoral Associates:

Camille Meslin	2012 – 2016
Zelia Ferreira	2013 – 2015
Wynn Meyer	2017 – 2019
Allie Graham (K99 recipient)	2020 – present
Emily Kopania	2022 – present

Ph.D. Students:

Raghav Partha	Joint CMU-Pitt Computational Biology	2014 – 2019
Amanda Kowalczyk	Joint CMU-Pitt Computational Biology	2016 – 2021
Melissa Plakke	Ecology and Evolution, Biol. Sci.	2016 – 2019
Lisa Limeri	Ecology and Evolution, Biol. Sci.	2016 – 2017
Elysia Saputra	Joint CMU-Pitt Computational Biology	2018 – present
Sarah Lucas	Molecular Biology PhD Program	2019 – present
Jordan Little	Molecular Biology PhD Program	2020 – present
Dwon Jordana	Molecular Biology PhD Program	2021 – present

Ph.D. Rotation Students:

Robert Sheehan	Joint CMU-Pitt Computational Biology	2012
Theodore Roman	Joint CMU-Pitt Computational Biology	2012
Rittika Shamsuddin	Joint CMU-Pitt Computational Biology	2012
Nolan Priedigkeit	Medical Scientist Training Program	2013
Timothy Wall	Joint CMU-Pitt Computational Biology	2014
Weiguang Mao	Joint CMU-Pitt Computational Biology	2014

Megan Yates	Medical Scientist Training Program	2017
Feng (Ryan) Shan	Integrative Systems Biology	2017
Carly Houghton	Joint CMU-Pitt Computational Biology	2018
Elysia Saputra	Joint CMU-Pitt Computational Biology	2018
Neha Cheemalavagu	Joint CMU-Pitt Computational Biology	2018
Bianca Argente	Molecular Biology Program	2019
Helena Hopson	Molecular Biology Program	2019
Dinesh Ramadurai	Molecular Biology Program	2019
Sarah LaPotin	Molecular Biology Program	2020
Ping Guo	Molecular Biology Program	2021
Jordan Little	Molecular Biology Program	2021
Michael Lansford	Molecular Biology Program	2021
Dwon Jordan	Molecular Biology Program	2021

Undergraduate Trainees:

Geoff Findlay		2003 – 2005
Sun Woo Kim		2009 – 2011
Jonathan Tyler		2012
Brandon Small		2012 – 2016
Nick Wolfe		2013 – 2015
David Taft		2014 – 2016
Claire Kronk		2014 – 2015
Joseph Robinson		2014
Bella Camacho		2015
Tamara Cherwin		2015 – 2016
Amanda Kowalczyk		2015 – 2016
Jerrica Jamison		2016 – 2019
Brennan Wright		2016 – 2017
Joshua Pirl		2016
Alexis Morrissey		2017
Michelle Patino Calero		2017
Deepika Yerosu		2017 – 2019
Gabrielle Coffing		2018
Luisa Cusick		2018 – 2020
Talia Pietra		2018 – 2019
Kisan Patel		2018 – 2019
Marisol Bustos		2021
Emilia Tugolukova		2021 – 2022
Tacy Christensen		2022

Ph.D./M.S. Committee Member for:

Yuefeng Lin	Bino John lab	2012 – 2014
	Joint Carnegie Mellon-Pitt Graduate program in Computational Biology	
Ranjit Das	Michael Jensen-Seaman lab	2012 – 2014
	Biological Sciences at Duquesne University	
Salim Chowdhury	Russell Schwarz lab	2013 – 2015
	Joint Carnegie Mellon-Pitt Graduate program in Computational Biology	
José Juan Tapia Valenzuela	Jim Faeder lab	2013 – 2016
	Joint Carnegie Mellon-Pitt Graduate program in Computational Biology	
Lujia Chen	Xinghua Lu lab	2014 – 2016
	Biomedical Informatics Graduate Program at the University of Pittsburgh	

Timothy Song	Elodie Ghedin lab	2014 – 2015
Joint Carnegie Mellon-Pitt Graduate program in Computational Biology		
Karina Pena	Kiril Kisolyov lab	2014 – 2015
Molecular, Cellular & Developmental Biology at the University of Pittsburgh		
Jennifer Vill	Michael Jensen-Seaman lab	2015 – 2017
Biological Sciences at Duquesne University		
Travis Mavrich	Graham Hatfull lab	2015 – 2019
Molecular, Cellular & Developmental Biology at the University of Pittsburgh		
Charlotte Darby	Dannie Durand lab	2016
Computational Biology M.S. program at Carnegie-Mellon University		
Lisa Limeri	Nathan Morehouse lab	2016 – 2017
Ecology and Evolution (Biological Sciences) at the University of Pittsburgh		
Aidan Heune	Matthew Nicotra lab	2017 – 2019
Integrative Systems Biology at the University of Pittsburgh		
Katrina Harris	Vaughn Cooper lab	2017 – 2019
Integrative Systems Biology at the University of Pittsburgh		
Eden Odhner	Mark Rebeiz lab	2017 – 2020
Molecular, Cellular & Developmental Biology at the University of Pittsburgh		
She (John) Zhang	Ivet Bahar lab	2017 – 2020
Joint Carnegie Mellon-Pitt Graduate program in Computational Biology		
Michelle (Shelly) Scribner	Vaughn Cooper lab	2018 – 2019
Integrative Systems Biology at the University of Pittsburgh		
David Macar	Allyson O'Donnell lab	2018 – 2019
Molecular, Cellular & Developmental Biology at the University of Pittsburgh		
Brianna Ports	Michael Jensen-Seaman lab	2019 – present
Biological Sciences at Duquesne University		
Michelle Culbertson	Nels Elde lab	2019 – present
Human Genetics at University of Utah		
Dylan Klure	Denise Dearing lab	2019 – present
Biological Sciences at University of Utah		
Helena Hopson	Ellen Leffler lab	2020 – present
Human Genetics at University of Utah		
Holly Thorpe	Clement Chow lab	2020 – present
Human Genetics at University of Utah		
Erin Cafferty	Nels Elde lab	2020 – present
Human Genetics at University of Utah		
Isabelle Cooperstein	Gabor Marth lab	2021 – present
Human Genetics at University of Utah		
Hannah Young	Nels Elde lab	2021 – present
Human Genetics at University of Utah		
Ameris Aponte Pizarro	Sophie Caron lab	2021 – present
Biological Sciences at University of Utah		
Thomas King	Michael Werner lab	2021 – present
Biological Sciences at University of Utah		
Michael Lansford	Marcus Pezzolesi lab	2022 – present
Molecular Biology Program at University of Utah		

Growing diversity and persistence in STEM through mentorship of students

The Clark lab has mentored 24 undergraduate and 8 PhD students, including 7 from underrepresented groups in science (Brandon Small, Claire Kronk, Bella Camacho, Michelle Patino Calero, Marisol Bustos, Tacy Christensen, Dwon Jordana). Brandon Small, an African

American, was in the lab for 4 years; he earned a Summer Undergraduate Research Award, and his contributions have been substantial enough for authorship on 3 publications. Another undergraduate, Claire Kronk, a trans woman, worked with me on multiple computational projects, including 2 that became publications. In fact, Claire performed the initial computational screen that led to our *Science* paper in 2018. Dwon Jordana, a PhD student in the lab, is African-American and a first-generation university student, who overcame substantial obstacles to continue in science. Ten undergraduates in the lab have earned authorship on our publications. In computational biology, women are also underrepresented, and I have mentored 12, each of which is continuing in science after graduation. I was also a participant in POMS at the University of Pittsburgh, the Pre-medical Organization for Minority Students, to provide career guidance and to recruit students for research.

Mentor and Lecturer in undergrad research programs targeting underrepresented students

Training and Experimentation in Computational Biology (TEC-Bio) is an NSF- and DOD-funded REU at the University of Pittsburgh. TEC-Bio recruits heavily from primary undergraduate institutions, especially those far from research universities, and which also prioritizes recruitment of students from underrepresented groups. I have hosted and personally mentored 5 TEC-Bio undergraduates in intensive 10-week research projects, three of which led to the students' authorship on publications. I also hosted question-and-answer sessions and lectures to introduce DNA sequence analysis and evolutionary biology to the TEC-Bio students. **Genomics Summer Research for Minorities (GSRM)**. At the University of Utah, I am working with the GSRM to host and mentor students in research and scientific career paths. We have so far mentored 2 students in this immersive program, guiding them to develop skills in computational and experimental genomics.

Supporting the Drug Discovery, Systems, and Comp Bio Summer Academy (DiSCo Bio)

DiSCo Bio is a program for local Pittsburgh high school students and recruits a large proportion of students from underrepresented and disadvantaged groups. I presented to them about careers in science and a lecture on molecular evolution. My lab hosted 2 DiSCo Bio students for research projects, one of which, Bella Camacho, is from an underrepresented group.

Outreach for Science Careers and Education

My lab participates in multiple annual science events for young students and women in science. We host a genetics and biology careers event for high school girls as part of the "Tour Your Future" program run by the Carnegie Science Center. We also set up a demonstration table on genetic inheritance for SciTech Days, an annual science show for thousands of local high school students at the Carnegie Science Center.

Guest Teacher: Introducing High School Students to Research (2016 – 2019)

In partnership with SciTech Academy, a Pittsburgh public science magnet high school, I presented a yearly module on genetics to Dr. Edwina Kinchington's class "Introduction to Biotechnology". The module spans 2 class periods, presents the evolution of taste receptor genes, and leads the students in a bioinformatics lab activity. SciTech is an urban public school and has a high proportion (>50%) of underrepresented minorities in STEM.

TEACHING:

Teaching while an Undergraduate, PhD student, and Postdoc:

Teaching Assistant (1998) in **Organic Chemistry for Chemical Engineers**, responsible for tutoring and grading. University of Texas at Austin. 3 hours per week.

Full-time High School Science Teacher (1999-2000) at the Technological University of Monterrey, Nuevo Leon, Mexico. Primary Instructor for 9th grade courses covering chemistry, ecology, astronomy, and geology. Lectured 12 hours per week to >90 students. Student evaluations, course planning, and tutoring.

Teaching Assistant (2005) in **Molecular Evolution**, responsible for lecturing, running computer lab section, evaluations, and tutoring. University of Washington. 1 lecture. Responsible for 1 weekly computer lab section of 20 graduate and undergraduate students. 3 hours per week.

Teaching Assistant (2005) in **Introductory Genetics**. University of Washington. Responsible for lecturing in 3 undergraduate laboratory sections per week with 30 students each. Student evaluation and tutoring. 30 lectures. 5 hours per week.

Guest Lecturer (2007) in **Evolution**. Topic: sexual selection. University of Washington. 40 undergraduates. 1 special topics lecture.

Guest Lecturer (2010-2011) in **Population Genetics**. Cornell University. 30 undergraduates. 2 lectures.

At University of Pittsburgh:

Guest Lecturer (2012) at Youngstown State University. Lectured on Adaptive Evolution.

Guest Facilitator (2013) for **Research Basis of Medical Knowledge** session on the “Evolution of cancer and tumor cell populations”. University of Pittsburgh School of Medicine.

Facilitator (2013 – 2015) for **Methods and Logic in Biomedicine (MLB)** – Tsinghua Research Scholars, International Collaborative Program in Medical Sciences. University of Pittsburgh School of Medicine. A discussion-based class that meets every 2 weeks in both Fall and Spring semesters. 8 graduate level students.

Co-course Head (2013 – 2019) for **Molecular Evolution (MSCBIO 2075)**, Created and teach 3-credit course in Computational and Systems Biology. 20 instruction hours per semester for 17 graduate students. University of Pittsburgh School of Medicine. This course is designed to introduce graduate and undergraduate students to the theory of Molecular Evolution and to the current practice of sequence analysis using state-of-the-art computational tools.

Co-course Head (2014 – 2016) for **Seminar in Computational Biology (MSCBIO 2010)**. As co-course head I facilitate the choice of weekly seminar speakers, evaluate student attendance, assign and report grades for ~40 graduate students in the Joint Pitt-CMU Ph.D. Program in Computational Biology.

Lecturer (2015) for Integrative Systems Biology Journal Club, University of Pittsburgh “Molecular Evolution: Adaptive Evolution”

Lecturer (2015 – 2018) in Foundations of Bioinformatics (BIOINF 2051), Department of Biomedical Informatics, University of Pittsburgh. “Phylogenetic theory and methods”

Lecturer (2017 – 2018) in “Comparative Genomics and Convergent Evolution” for Model Organisms course (MSMGDB 2535), taught in Dept. of Developmental Biology, University of Pittsburgh

At University of Utah:

Co-course Head (2022 – present) for **Evolutionary Genetics and Genomics** graduate level course, co-taught with Dr. Ellen Leffler.

RESEARCH:

Current Grant Support:

Grant Number	Grant Title	Role in Project	Years Inclusive	Source
R01 EY030546	Discovery and characterization of ocular regulatory elements through evolutionary analysis	Principal Investigator 25% effort	2020 – 2025	NIH – NEI \$1,588,560

Pending Grant Application:

Grant Number	Grant Title	Role in Project	Years Inclusive	Source
R01 HG009299 renewal	RECOMMENDED FOR FUNDING BY PO Renewal application: Functional Annotation of Genomes via Phenotypic Convergence	Principal Investigator 25% effort	2023 – 2028	NIH – NHGRI

Prior Grant Support:

Grant Number	Grant Title	Role in Project	Years Inclusive	Source
R01 HG009299	Functional Annotation of Genomes via Phenotypic Convergence	Co-Principal Investigator. 25% effort	2017 – 2022	NIH - NHGRI \$861,110
F32 GM084592	Molecular Evolution in the Context of Protein Structure and Stability	Principal Investigator 100% effort	2008 – 2011	NIH NRSA, Ruth Kirschstein Postdoctoral Fellowship \$125,484
SAP# 4100062224	Dissecting the Molecular Mechanisms of Stress- Response Proteins in Cancer	Investigator 34% effort	2013 – 2016	Commonwealth of Pennsylvania Department of Health \$746,765
N/A	Impact of intra-tumor heterogeneity (ITH) on breast cancer prognosis and response to therapy	Investigator 5% effort	2013 – 2015	Breast Cancer Research Foundation \$15,536
KA2014- 73920	Co-Evolutionary Signatures as a Novel Approach to Gene Discovery	Principal Investigator	2014 – 2016	Charles E. Kaufman Foundation \$150,000
P30 DK079307	Identifying Ion Channel Regulators through Evolutionary Signatures	Principal Investigator	2014 – 2016	NIH NIDDK: Pittsburgh Center for Kidney Research Pilot Project \$60,000
U54 HG008540	Center for Causal Modeling and Discovery of Biomedical Knowledge from Big Data	Investigator. 13% effort	2014 – 2018	NIH \$112,852
1553143	CAREER: Regulation of Cargo Selection and Ubiquitination by Protein Trafficking Adaptors	Investigator. No effort permitted.	2016 – 2020	NSF \$50,048
	Biomedical Modeling Pilot Award, Clinical and Translational Science Institute	Principal Investigator	2018 – 2020	University of Pittsburgh \$25,000

2. Seminars and invited lectureships related to research.

Evolution Meeting (SSE, SSB, & ASN). University of Alaska, Fairbanks	2005
Society for Molecular Biology and Evolution. Arizona State University, Tempe	2006
Genomics of the Life Aquatic. University of Washington, Friday Harbor Labs	2006

Society for Molecular Biology and Evolution. Barcelona, Catalonia, Spain	2008
Society for Molecular Biology and Evolution. University of Iowa, Iowa City	2009
Platform Talk at 51 st Drosophila Research Conference. Washington D.C. Genetics Society of America	2010
Center for Vertebrate Genomics, Cornell University, Ithaca, NY	2010
Symposium Speaker at Society for Molecular Biology and Evolution. Lyon, France	2010
Invited Seminar at University of Texas Southwestern Green Center for Reproductive Biology	2010
Invited Seminar at University of Pittsburgh School of Medicine Department of Computational and Systems Biology	2011
Invited Seminar at Pennsylvania State University Biology Department Seminar	2011
Invited Seminar at University of Texas Southwestern McDermott Center for Human Growth and Development	2011
Invited speaker at SCIENCE 2012 "Translation" University of Pittsburgh	2012
Invited Seminar at Youngstown State University Department of Biological Sciences	2012
Invited Seminar at University of Pittsburgh Department of Human Genetics	2012
Invited Seminar at University of Pittsburgh School of Medicine Department of Developmental Biology	2013
Seminar for the Drug Discovery Institute University of Pittsburgh	2013
Invited Seminar at University of Pittsburgh Department of Biological Sciences	2013
Senior Vice Chancellor's Research Seminar University of Pittsburgh School of Medicine	2013
Invited Molecular Medicine Research Seminar Children's Hospital of Pittsburgh	2013
Invited Guest Speaker on "Bioinformatics and Evolutionary Genomics" Spectroscopy Society of Pittsburgh (SSP)	2014
Invited Seminar for the Department of Infectious Diseases and Microbiology Graduate School of Public Health, University of Pittsburgh	2014
Guest Speaker at Chromatin Club Mini-Symposium Hillman Cancer Center	2014
Invited Seminar for the Department of Microbiology and Molecular Genetics University of Pittsburgh School of Medicine	2015
Eye and Ear Institute University of Pittsburgh Medical Center	2015
Renal Research Grand Rounds at the Pittsburgh Center for Kidney Research "Identifying Ion Channel Regulators through Evolutionary Signatures"	2015
Society for Molecular Biology and Evolution. Vienna, Austria "Systems Biology and Evolution"	2015
Invited Seminar at the University of Dijon, France Center for Sciences of Taste and Food	2015
Invited speaker at SCIENCE 2015 "Unleashed" University of Pittsburgh	2015
Invited Seminar "Leveraging co-evolution to Reveal Novel Gene Networks" University of Southern California. Molecular and Computational Biology	2015

Seminar “Co-evolution of reproductive proteins in <i>Drosophila</i> and mammals” College of the Holy Cross – Worcester, Massachusetts	2015
Seminar “Co-evolutionary inference of gene function” Duquesne University. Department of Biology.	2015
Biology Department Invited Seminar Slippery Rock University	2015
Department of Biology Invited Seminar Wooster College, Wooster, Ohio	2016
Oral presentation at “Evolution” conference in Austin, Texas (SSE) “Sexual Cooperation and Conflict in Butterfly Spermatophore Proteins”	2016
Keynote Address at Department of Computational and Systems Biology Retreat Stonewall Resort, Roanoke, West Virginia	2016
Invited Seminar at Department of Human Genetics University of Pittsburgh	2016
Invited seminar in Center for Reproductive Evolution and Biology Department Syracuse University	2016
Invited seminar in the Department of Biology University of Washington – Seattle	2017
Society for Molecular Biology and Evolution. Austin, Texas “On the evolution of complex traits”	2017
Florida Marine Mammal Health Conference VI – Orlando, Florida “Convergent loss of <i>Paraoxonase 1</i> places marine mammals at risk of pesticide toxicity”	2018
Invited seminar at Claremont College “History repeats itself: Convergent genetic evolution and species adaptation”	2018
Lightning talk at Population Evolution and Quantitative Genetics (PEQG) Genetics Society of America, Madison, Wisconsin	2018
Invited seminar at Department of Human Genetics University of Utah	2019
Invited Plenary Address at <i>Biology of Spermatozoa</i> Nynäshamn, Sweden	2019
Invited seminar in School of Biological Sciences University of Utah	2020
Invited seminar in Biological Sciences Oxford Brookes University	2021
Invited seminar for Biosciences Symposium University of Utah	2022
Invited speaker at 8 th International Conference on Paraoxonases Bologna, Italy	2022

3. Other research related activities.

Editorships:

Associate Editor of <i>Evolution</i> (Society for the Study of Evolution)	2022 – present
Guest Editor for special issue of <i>Philosophical Transaction of the Royal Society B</i> “Convergent evolution in the genomics era: new insights and directions”	2019

Manuscript Reviews (121 reviews)

Axios Review

Journal of Insect Science

Biological Reviews

Journal of Molecular Evolution

<i>Biology Letters</i>	<i>Journal of Proteomics</i>
<i>BMC Evolutionary Biology</i>	<i>Molecular Biology and Evolution (MBE)</i>
<i>BMC Genomics</i>	<i>Molecular Ecology</i>
<i>BMC Systems Biology</i>	<i>Nature</i>
<i>Cell</i>	<i>Nature Communications</i>
<i>Cell and Tissue Research</i>	<i>Nature Genetics</i>
<i>Current Biology</i>	<i>Nature Structural and Molecular Biology</i>
<i>eLife</i>	<i>Nucleic Acids Research (NAR)</i>
<i>Evolution</i>	<i>PeerJ</i>
<i>Frontiers in Evolutionary and Pop. Genetics</i>	<i>Physiological Reviews</i>
<i>Frontiers in Plant Science</i>	<i>PLOS Computational Biology</i>
<i>G3</i>	<i>PLOS Genetics</i>
<i>Gene</i>	<i>PLOS ONE</i>
<i>Genetics</i>	<i>PNAS</i>
<i>Genome Biology and Evolution (GBE)</i>	<i>Proc. of the Royal Soc: Biological Sciences</i>
<i>Genome Research</i>	<i>Radiation Research</i>
<i>Heredity</i>	<i>Royal Society Open Science</i>
<i>Insect Biochemistry and Molecular Biology</i>	<i>Scientific Reports</i>
<i>International Jour. of Evolutionary Biology</i>	<i>Trends in Genetics</i>
<i>Journal of Insect Physiology</i>	

Grant Reviewer for:

Human Frontier Science Program (HFSP).	2012
The Leakey Foundation	2013
The Leakey Foundation	2016
United States – Israel Binational Science Foundation (BSF)	2018
National Science Foundation (NSF)	2020 – 22
National Institutes of Health (NIH)	2022

LIST of CURRENT RESEARCH INTERESTS:

Efforts to understand genes and genomes are greatly enhanced by evolutionary analyses. In our group we combine evolutionary inference with direct experiments to determine the relationships between genes and to reveal the genetic changes underlying adaptation between species. Current projects are:

- 1) We study the adaptive evolution of genetic regions in response to extreme environmental pressures. These studies have addressed aquatic mammals and diving, sexual reproduction, and the subterranean habitat. We use our novel computational tools to identify historical cases of adaptive evolution and explore their changing molecular interactions and to determine the driving forces behind their adaptive change in both protein-coding genes and regulatory sequences affecting gene expression.
- 2) Our lab creates and distributes new computational methods for application in comparative and evolutionary genomics. These methods rely on the convergent evolution of traits to identify genes and regulatory regions (non-coding) that responded to the evolution of a specific trait. We distribute these methods in the RERconverge, a software package for the R environment. We have applied RERconverge to traits including lifespan, diving, underground habitat, hair, and dietary specializations.

3) We use zebrafish embryology to identify and characterize regulatory regions responsible for the development and function of the eye. Using results from our genomics screens and experiments we determine when specific regulatory enhancers drive expression and how those patterns have changed between species with different ocular requirements. Specific assays include transgenesis and region/gene knock-outs via CRISP-Cas9.

4) We seek to identify co-evolutionary signatures between genes that function in a common pathway or complex. We then exploit these signatures to infer new genetic interactions and reveal deeper relationships between entire genetic pathways. To date we have performed genome-wide coevolution studies in mammals, yeasts, and *Drosophila* species. With these datasets we have inferred new genes in specific processes for our collaborators and these have resulted in 8 publications.

SERVICE:

1. University and Medical School

Seminar Committee Chair Department of Computational and Systems Biology and Joint CMU-Pitt PhD Program in Computational Biology	2013 – 2016
Graduate Admissions Committee member Joint CMU-Pitt PhD Program in Computational Biology	2013 – 2015
Faculty Search Committee member Department of Computational and Systems Biology	2013 – 2014
Institutional Biosafety Committee member University of Pittsburgh School of Medicine	2014 – 2016
Graduate Admissions Committee member Integrative Systems Biology Program – University of Pittsburgh	2014 – 2017
Associate Director of PhD program in Computational Biology Joint Carnegie Mellon University-University of Pittsburgh	2016 – 2019
Faculty Search Committees – Department of Human Genetics	2020 and 2022
Space Committee – Department of Human Genetics	2021
Head of Faculty Research in Progress – Department of Human Genetics	2022 – present

2. Community Activities

Local

Postdoctoral Advisory Board Member at Cornell University	2011
Yeast Research Group Faculty member Monthly meeting of research groups across Pittsburgh and Morgantown	2012 – 2018
Molecular Evolution Lab Discussion (MELD)	2014 – 2019

I led a group that joins 10 molecular evolution labs in the greater Pittsburgh area. As a group we host popular monthly seminars in which our labs present and discuss our on-going research projects. I oversaw the growth of this group from 4 to 10 labs and formalized the presentation schedule, web presence and email communications. The collegial exchanges in this group have made the University of Pittsburgh and Carnegie Mellon University more attractive to recruit top researchers in molecular evolution and population genetics.

Evolutionary Genetics and Genomics Interest Group (EGG) 2021 – present

I created and lead this interest group that unites groups from 5 departments with interest in evolutionary genetics. As a group we host popular monthly seminars in which our labs present and discuss our on-going research projects. I oversee this group of 15 labs including its presentation schedule, web presence, and email communications.

National

Mentor for Student Biotech Expo, University of Washington 2006

Volunteer for National Geographic Human Genetic History Event 2010

Facilitated DNA sampling of 100 Cornell undergraduates to determine their mitochondrial haplotypes and migratory lineages.

International

Symposium Organizer for Society for Molecular Biology and Evolution, 2014 and 2017

Conceived and Organized symposium topic on “Evolutionary Networks” and “Convergent Evolution” for annual international conference.