

Biographical Information

FULL NAME: Edward Louis Braun

CURRENT POSITION: Professor of Biology

WORK ADDRESS: Department of Biology
University of Florida
P.O. Box 118525
Gainesville, FL 32611-8525

DATE OF BIRTH: 12 July 1968

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My research focus is the intersection of biodiversity and genomics. Most of my work has been in the areas of molecular evolution, phylogenetics, and computational biology. I am interested in models of genomic change and the use of those models to make functional inferences at a variety of scales (ranging from molecules to whole organisms and populations).

Appointments

- **Professor**, Department of Biology, University of Florida, 2016-present.
 - Currently UF Term Professor
- **Associate Professor**, Department of Biology, University of Florida, 2009-2016
- **Assistant Professor**, Department of Zoology, University of Florida, 2001-2009.
 - Additional appointments:
 - Graduate Faculty in Genetics and Genomics, University of Florida Genetics Institute
 - Affiliate Associate Curator in Invertebrate Zoology, Department of Natural History, Florida Museum of Natural History

Professional Preparation

- 1998-2001 **Postdoctoral Scientist**,
Department of Plant Biology and Plant Biotechnology Center
The Ohio State University, Columbus, OH
 - Postdoctoral Mentor: Erich Grotewold
- 1997-1998 **Postdoctoral Scientist**,
Position split between: National Center for Genome Resources (NCGR),
Santa Fe, NM & University of New Mexico (UNM), Albuquerque, NM
 - Postdoctoral Mentors: Donald O. Natvig (UNM) & Peter A. Schad (NCGR)
- 1991-1997 **Ph.D. in Biology**, University of New Mexico, Albuquerque, NM
 - Advisor: Margaret Werner-Washburne
 - Dissertation: Protein synthesis in stationary phase yeast: global patterns and characterization of Snz1p, a novel stationary-phase protein
 - Research and teaching experience as a Ph.D. student:
 - Research assistant for Margaret Werner-Washburne
 - Research assistant at the High-Performance Computing, Education, and Research Center at the University of New Mexico

- Teaching assistant for Microbiology
- 1986-1991 **B.S. in Biology**, University of New Mexico, Albuquerque, NM
- Additional Education:
 - 1995 Woods Hole Workshop on Molecular Evolution
 - 2011 Summer Institute on Undergraduate Science and Math Education West Virginia University.

Publications

Total citations: 10,729

h-index: 47

*i*10-index: 78

Based on Google Scholar: <http://scholar.google.com/citations?user=31XPDbYAAAAJ>

ORCID page: <http://orcid.org/0000-0003-1643-5212>

I have published a total of 92 peer-reviewed papers and three peer-reviewed book chapters. All of these publications are listed in this section (reverse chronological order, alphabetical within years). Additional scholarly works that were not peer-reviewed are listed at the end of this CV, along with manuscripts in progress.

Co-authors that I mentored (as advisor, committee member, or informally) are indicated with superscripts (U for undergraduates, G for graduate students, and P for post-doctoral scientists). Altmetric scores are listed alongside papers published after 2013 when they are in the top 5% of outputs of the same age.

1. **Braun, EL**, J Cracraft & P Houde. *In press*. Resolving the avian tree of life from top to bottom: The promise and potential boundaries of the phylogenomic era. (invited chapter for *Avian Genomics in Ecology and Evolution - From the lab into the wild*, book to be published by Springer, edited by RHS Kraus, Max Planck Institute for Ornithology).
2. Oliveros, CH, DJ Field, DT Ksepka, FK Barker, A Aleixo, MJ Andersen, P. Alström, BW Benz, **EL Braun**, MJ Braun, GA Bravo, RT Brumfield, RT Chesser, S Claramunt, J Cracraft, AM Cuervo, EP Derryberry, TC Glenn, MG Harvey, PA Hosner, L Joseph, RT Kimball, AL Mack, CM Miskelly, AT Peterson, MB Robbins, FH Sheldon, LF Silveira, BT Smith, ND White, RG Moyle, BC Faircloth. 2019. Earth history and the passerine superradiation. *Proceedings of the National Academy of Sciences*, **116**: 7916-7925. (Altmetric 288; top 5%)
 - Featured as cover illustration
 - Attracted substantial attention from the press, the UF contribution was highlighted in <https://www.futurity.org/perching-birds-genomes-australia-2023592>
3. Tamashiro, RA^U, ND White, MJ Braun, BC Faircloth, **EL Braun**, RT Kimball. 2019. What are the roles of taxon sampling and model fit in tests of cyto-nuclear discordance using avian mitogenomic data? *Molecular Phylogenetics and Evolution*, **130**: 132-142.
4. **Braun, EL**. 2018. An evolutionary model motivated by physicochemical properties of amino acids reveals variation among proteins. *Bioinformatics*, **34**: i350-i356.
5. Chen, D^P, **EL Braun**, M Forthman, RT Kimball, Z Zhang. 2018. A simple strategy for recovering ultraconserved elements, exons, and introns from low coverage shotgun sequencing of museum specimens: placement of the partridge genus *Tropicoperdix* within the Galliformes. *Molecular Phylogenetics and Evolution*, **129**: 304-314.
6. Eimanifar, A^P, RT Kimball, **EL Braun** & JD Ellis. 2018. Mitochondrial genome diversity and population structure of two western honey bee subspecies in the Republic of South Africa. *Scientific Reports*, **8**: 1333.
7. Liang, B, N Wang, N Li, RT Kimball & **EL Braun**. 2018. Comparative genomics reveals a

- burst of homoplasmy-free *numt* insertions, *Molecular Biology and Evolution*, 35: 2060-2064.
8. Tiley, GP^G, RT Kimball, **EL Braun** & JG Burleigh. 2018. Comparison of the Chinese bamboo partridge and red junglefowl genome sequences highlights the importance of demography in genome evolution. *BMC Genomics*, 19: 336.
 9. Ascunce, MS^P, JC Huguete-Tapia^P, A Ortiz-Urquiza, NO Keyhani, **EL Braun** & EM Goss. 2017. Phylogenomic analysis supports multiple instances of polyphyly in the oomycete peronosporalean lineage. *Molecular Phylogenetics and Evolution*, 114: 199-211.
 - Corresponding authors: Braun and Goss
 10. Hosner, PA^P, JA Tobias, **EL Braun** & RT Kimball. 2017. How do seemingly non-vagile clades accomplish trans-marine dispersal? Trait and dispersal evolution in the landfowl. *Proceedings of the Royal Society B: Biological Sciences*, 284: 20170210.
 11. Feng, G^G, JG Burleigh, **EL Braun**, W Mei & WB Barbazuk. 2017. Evolution of the 3R-MYB gene family in plants. *Genome Biology and Evolution*, 9: 1013-1029.
 12. Reddy, S, RT Kimball, A Pandey^G, PA Hosner^P, MJ Braun, SJ Hackett, K-L Han, J Harshman, CJ Huddleston, S Kingston, BD Marks, KJ Miglia, WS Moore, FH Sheldon, CC Witt, T Yuri & **EL Braun**. 2017. Why do phylogenomic data sets yield conflicting trees? Data type influences the avian tree of life more than taxon sampling. *Systematic Biology*, 66: 857-879. (Altmetric 43; top 5%)
 13. Wang, N, RT Kimball, **EL Braun**, B Liang & Z Zhang. 2017. Ancestral range reconstruction of Galliformes: the effects of topology and taxon sampling. *Journal of Biogeography*, 44: 122-135.
 14. Wang, N, PA Hosner^P, B Liang, **EL Braun** & RT Kimball. 2017. Historical relationships of three enigmatic phasianid genera (Aves: Galliformes) inferred using phylogenomic and mitogenomic data. *Molecular Phylogenetics and Evolution*, 109: 217-225.
 15. Corrochano, LM, A Kuo, M Marcet-Houben, S Polaino, A Salamov, JM Villalobos, MI Álvarez, J Avalos, EP Benito, I Benoit, G Burger, LP Camino, D Cánovas, E Cerdá-Olmedo, J-F Cheng, A Domínguez, M Eliáš, AP Eslava, F Glaser, J Grimwood, G Gutiérrez, J Heitman, B Henrissat, EA Iturriaga, BF Lang, JL Lavín, SC Lee, We Li, E Lindquist, S López-García, EM Luque, AT Marcos, J Martin, K McCluskey, HR Medina, A Miralles-Durán, A Miyazaki, E Muñoz-Torres, JA Oguiza, R Ohm, M Olmedo, M Orejas, L Ortiz-Castellanos, AG Pisabarro, J Rodríguez-Romero, J Ruiz-Herrera, R Ruiz-Vázquez, C Sanz, W Schackwitz, J Schmutz, M Shahriari, E Shelest, F Silva-Franco, D Soanes, K Syed, VG Tagua, NJ Talbot, M Thon, RP de Vries, A Wiebenga, JS Yadav, **EL Braun**, S Baker, V Garre, B Horwitz, S Torres-Martínez, A Idnurm, A Herrera-Estrella, T Gabaldón & IV Grigoriev. Expansion of signal transduction pathways in fungi by whole-genome duplication. *Current Biology*, 26: 1577-1584. (Altmetric 46; top 5%)
 16. Hosner, PA^P, **EL Braun** & RT Kimball. 2016. Rapid and recent diversification of curassows, guans, and chachalacas (Galliformes: Cracidae) out of Mesoamerica: Phylogeny inferred from mitochondrial, intron, and ultraconserved element sequences. *Molecular Phylogenetics and Evolution*, 102: 320-330.
 17. Hosner, PA^P, BC Faircloth, TC Glenn, **EL Braun** & RT Kimball. 2016. Avoiding missing data biases in phylogenomic inference: an empirical study in the landfowl (Aves: Galliformes). *Molecular Biology and Evolution*, 33: 1110-1125.
 18. Meiklejohn, KA^P, BC Faircloth, TC Glenn, RT Kimball & **EL Braun**. 2016. Analysis of a rapid evolutionary radiation using ultraconserved elements (UCEs): Evidence for a bias in some multi-species coalescent methods. *Systematic Biology*, 65: 612-627.

19. Persons, NW^U, PA Hosner^P, KA Meiklejohn^P, **EL Braun** & RT Kimball. 2016. Sorting out relationships among the grouse and ptarmigan using intron, mitochondrial, and ultra-conserved element sequences. *Molecular Phylogenetics and Evolution*, **98**: 123-132.
20. Burleigh, JG, RT Kimball & **EL Braun**. 2015. Building the avian tree of life using a large-scale, sparse supermatrix. *Molecular Phylogenetics and Evolution*, **84**: 53-63.
 - Third most highly downloaded paper in *MPE* in the 90 days preceding May 2015
21. Cracraft, J, P Houde, SYW Ho, DP Mindell, J Fjeldså, B Lindow, SV Edwards, C Rahbek, S Mirarab, T Warnow, MTP Gilbert, G Zhang, **EL Braun** & ED Jarvis. 2015. Response to comment on “Whole-genome analyses resolve early branches in the Tree of Life of modern birds” *Science*, **349**: 1460. (Altmetric 28; top 5%)
 - Corresponding authors: Cracraft, Braun, and Jarvis
22. Hosner, PA^P, **EL Braun** & RT Kimball. 2015. Tertiary land bridges and global cooling shaped the colonization history and diversification of New World quail (Aves: Galliformes: Odontophoridae). *Journal of Biogeography*, **42**: 1883-1895.
23. Jarvis, ED, S Mirarab, AJ Aberer, Bo Li, P Houde, C Li, SYW Ho, BC Faircloth, B Nabholz, JT Howard, A Suh, CC Weber, RR da Fonseca, A Alfaro-Núñez, N Narula, L Liu, D Burt, H Ellegren, SV Edwards, A Stamatakis, DP Mindell, J Cracraft, **EL Braun**, T Warnow, Wang J, MTP Gilbert, G Zhang & The Avian Phylogenomics Consortium. 2015. Phylogenomic analyses data of the Avian Phylogenomics Project. *GigaScience*, **4**: 4.
24. Pope, WH, CA Bowman, DA Russell, D Jacobs-Sera, DJ Asai, SG Cresawn, WR Jacobs, RW Hendrix, JG Lawrence, GF Hatfull, **Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science**, Phage Hunters Integrating Research and Education & Mycobacterial Genetics Course. 2015. Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. *Elife*, **4**: e06416. (Altmetric 539; top 5%)
 - Braun contributed to this paper as an instructor in the UF SEA “phage hunters” course.
25. Suh, A, G Churakov, MP Ramakodi, RN Platt II, J Jurka, KK Kojima, J Caballero, A Smit, FG Hoffmann, J Brosius, **EL Braun**, RE Green, H Ellegren, DA Ray & J Schmitz. 2015. Multiple lineages of ancient CR1 retroposons shaped the early genome evolution of amniotes. *Genome Biology and Evolution*, **7**: 205-217.
26. Green, RE, **EL Braun**, J Armstrong, D Earl, N Nguyen, MW Vandewege, JA St John, S Capella-Gutiérrez, TA Castoe, C Kern, MK Fujita, JC Opazo, J Jurka, KK Kojima, J Caballero, RM Hubley, AAF Smit, RN Platt II, CA Lavoie, M Ramakodi, JW Finger, A Suh, SR Isberg, L Miles, AY Chong, W Jaratlerdsiri, J Gongora, C Moran, A Iriarte, BC Faircloth, J McCormack, SC Burgess, SV Edwards, E Lyons, C Williams, M Breen, CR Gresham, DG Peterson, J Schmitz, DD Pollock, D Haussler, EW Triplett, G Zhang, N Irie, ED Jarvis, CA Brochu, C Schmidt, F McCarthy, FG Hoffmann, TC Glenn, T Gabaldón, B Paten & DA Ray. 2014. Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. *Science*, **346**: 1254449. (Altmetric 291; top 5%)
 - Part of a special issue of *Science* (along with Jarvis et al. 2014 and Zhang et al. 2014)
27. Jarvis, ED, S Mirarab, AJ Aberer, B Li, P Houde, C Li, SYW Ho, BC Faircloth, B Nabholz, JT Howard, A Suh, CC Weber, RR da Fonseca, J Li, F Zhang, H Li, L Zhou, N Narula, L Liu, G Ganapathy, B Boussau, Md S Bayzid, V Zavidovych, S Subramanian, T Gabaldón, S Capella-Gutiérrez, J Huerta-Cepas, B Rekepalli, K Munch, M Schierup, B Lindow, WC Warren, D Ray, RE Green, M Bruford, X Zhan, A Dixon, S Li, N Li, Y Huang, EP Derryberry, MF Bertelsen, F Sheldon, RT Brumfield, C Mello, PV Lovell, M Wirthlin, JA Samaniego, AMV Velazquez, A Alfaro-Núñez, PF Campos, T Sicheritz-Ponten, A Pas, T Bailey, P

- Scofield, M Bunce, D Lambert, Q Zhou, P Perelman, AC Driskell, G Ruby, B Shapiro, Z Xiong, Y Zeng, S Liu, Z Li, B Liu, K Wu, J Xiao, X Yinqi, Q Zheng, Y Zhang, H Yang, J Wang, L Smeds, FE Rheindt, M Braun, J Fjeldså, L Orlando, K Barker, KA Jönsson, W Johnson, K-P Koepfli, S O'Brien, D Haussler, OA Ryder, C Rahbek, E Willerslev, GR Graves, TC Glenn, J McCormack, D Burt, H Ellegren, P Alström, SV Edwards, A Stamatakis, DP Mindell, J Cracraft, **EL Braun**, T Warnow, Wang J, MTP Gilbert & G Zhang. 2014. Whole genome analyses resolve the early branches in the Tree of Life of modern birds. *Science*, **346**: 1320-1331. (Altmetric 630; top 5%)
- Part of a special issue of *Science* (along with Green et al. 2014 and Zhang et al. 2014)
 - Received extensive media coverage; examples of interviews include:
 - National Public Radio (Geoff Brumfiel interview featuring me and ED Jarvis); permanently available at <http://www.npr.org/blogs/health/2014/12/11/370087804/birds-of-a-feather-arent-necessarily-related>.
 - Xinhua news (interview featuring me and G Zhang); permanently available at http://news.xinhuanet.com/english/china/2014-12/12/c_133849238.htm
28. Kimball, RT & **EL Braun**. 2014. Does more sequence data improve estimates of galliform phylogeny? Analyses of a rapid radiation using a complete data matrix. *PeerJ*, **2**: e361.
29. Meiklejohn, KA^P, MJ Danielson, BC Faircloth, TC Glenn, **EL Braun** & RT Kimball. 2014. Incongruence among different mitochondrial regions: A case study using complete mitogenomes. *Molecular Phylogenetics and Evolution*, **78**:314-323.
30. Suh, A, CC Weber, C Kehlmaier, **EL Braun**, RE Green, U Fritz, DA Ray & H Ellegren. 2014. Early Mesozoic coexistence of amniotes and Hepadnaviridae. *PLoS Genetics*, **10**: e1004559. (Altmetric 24; top 5%)
31. Sun, K, KA Meiklejohn^P, BC Faircloth, TC Glenn, **EL Braun** & RT Kimball. 2014. The evolution of peafowl and other taxa with ocelli (eyespot): a phylogenomic approach. *Proceedings of the Royal Society B: Biological Sciences*, **281**:20140823. (Altmetric 38; top 5%)
- Faculty of 1000 recommendation (<http://f1000.com/718511958>)
32. Zhang G, C Li, Q Li, B Li, DM Larkin, C Lee, JF Storz, A Antunes, RW Meredith, A Ödeen, J Cui, Q Zhou, L Xu, H Pan, Z Wang, L Jin, P Zhang, H Hu, W Yang, J Hu, J Xiao, Z Yang, Y Liu, Q Xie, J Lian, P Wen, F Zhang, H Li, Y Zeng, Z Xiong, S Liu, L Zhou, Z Huang, N An, J Wang, Q Zheng, Y Xiong, G Wang, B Wang, J Wang, Y Fang, R da Fonseca, A Alfaro-Núñez, M Schubert, L Orlando, T Mourier, J Howard, G Ganapathy, J Smith, M Farré, J Narayan, G Slavov, MN Romanov, R Borges, JP Machado, I Khan, MS Springer, J Gatesy, FG Hoffmann, JC Opazo, O Håstad, MJ Greenwold, RH Sawyer, H Kim, K-W Kim, N Li, Y Huang, MW Bruford, X Zhan, A Dixon, M Bertelsen, E Derryberry, W Warren, S Li, DA Ray, RE Green, SJ O'Brien, D Griffin, WE Johnson, D Haussler, OA Ryder, E Willerslev, G Graves, P Alström, J Fjeldså, D Mindell, SV Edwards, **EL Braun**, C Rahbek, DW Burt, P Houde, Y Zhang, H Yang, J Wang, Avian Genome Consortium, ED Jarvis, MTP Gilbert & Wang J. 2014. Comparative genomics across modern bird species reveal insights into pan-avian genome evolution and trait biodiversity. *Science*, **346**: 1311-1320. (Altmetric 242; top 5%)
- Part of a special issue of *Science* (along with Green et al. 2014 and Jarvis et al. 2014)
33. Kimball, RT, N Wang^G, V Heimer-McGinn^U, C Ferguson^U, **EL Braun**. 2013. Identifying localized biases in large datasets: A case study using the Avian Tree of Life. *Molecular Phylogenetics and Evolution*, **69**: 1021-1032.
34. Patel, S^G, RT Kimball & **EL Braun**. 2013. Error in phylogenetic estimation for bushes in the Tree of Life. *Journal of Phylogenetics & Evolutionary Biology*, **1**: 110.

35. Shaffer, HB, P Minx, DE Warren, AM Shedlock, RC Thomson, N Valenzuela, J Abramyan, CT Amemiya, D Badenhorst, KK Biggar, GM Borchert, CW Botka, RM Bowden, **EL Braun**, AM Bronikowski, BG Bruneau, LT Buck, B Capel, TA Castoe, M Czerwinski, KD Delehaunty, SV Edwards, CC Fronick, MK Fujita, L Fulton, TA Graves, RE Green, W Haerty, R Hariharan, O Hernandez, LW Hillier, AK Holloway, D Janes, FJ Janzen, C Kandoth, L Kong, APJ de Koning, Y Li, R Literman, SE McGaugh, L Mork, M O’Laughlin, RT Paitz, DD Pollock, CP Ponting, S Radhakrishnan, BJ Raney, JM Richman, J St. John, T Schwartz, A Sethuraman, PQ Spinks, KB Storey, N Thane, T Vinar, LM Zimmerman, WC Warren, ER Mardis & RK Wilson. 2013. The Western Painted Turtle genome: the evolution of extreme physiological adaptations in a slowly evolving lineage. **Genome Biology**, **14**: R28. (Altmetric 150; top 5%)
- Editors pick, highly accessed, and featured on BioMed Central blog
36. Smith, JV^{U,G}, **EL Braun** & RT Kimball. 2013. Ratite non-monophyly: Independent evidence from 40 novel loci. **Systematic Biology**, **62**: 35-49.
37. Wang, N^G, RT Kimball, **EL Braun**, B Liang & Z Zhang. 2013. Assessing phylogenetic relationships among Galliformes: A multigene phylogeny with expanded taxon sampling in Phasianidae. **PLoS ONE**, **8**:e64312.
38. Yuri, T^P, RT Kimball, J Harshman, RCK Bowie, MJ Braun, JL Chojnowski^G, SJ Hackett, K-L Han^G, SJ Hackett, CJ Huddleston, WS Moore, S Reddy, FH Sheldon, DW Steadman, CC Witt & **EL Braun**. 2013. Parsimony and model-based analyses of indels in avian nuclear genes reveal congruent and incongruent phylogenetic signals. **Biology**, **2**: 419-444.
39. Chojnowski, JL^G & **EL Braun**. 2012. An unbiased approach to identify genes involved in development in a turtle with temperature-dependent sex determination. **BMC Genomics**, **13**: 308.
- Editors pick, highly accessed, and on “Gulliver Turtle’s Blog” (highlights research published in BMC journals)
40. Ponciano, JM, JG Burleigh, **EL Braun** & ML Taper. 2012. Assessing parameter identifiability in phylogenetic models using Data Cloning. **Systematic Biology**, **61**: 955-972.
41. St John, JA, **EL Braun**, SR Isberg, LB Miles, AY Chong, J Gongora, P Dalzell, C Moran, B Bed’hom, A Abzhanov, SC Burgess, AM Cooksey, TA Castoe, NG Crawford, LD Densmore, JC Drew, SV Edwards, BC Faircloth, MK Fujita, MJ Greenwald, FG Hoffmann, JM Howard, T Iguchi, DE Janes, SY Khan, S Kohno, APJ de Koning, SL Lance, FM McCarthy, JE McCormack, ME Merchant, DG Peterson, DD Pollock, N Pourmand, BJ Raney, KA Roessler, JR Sanford, RH Sawyer, CJ Schmidt, EW Triplett, TD Tuberville, M Venegas-Anaya, JT Howard, ED Jarvis, LJ Guillelte Jr, TC Glenn, RE Green & DA Ray. 2012. Sequencing three crocodylian genomes to illuminate the evolution of archosaurs and amniotes. **Genome Biology**, **13**: 415.
- Editors pick and highly accessed
42. Wang, N^G, **EL Braun** & RT Kimball. 2012. Testing hypotheses about the sister group of the Passeriformes using an independent 30 locus dataset. **Molecular Biology and Evolution**, **29**: 737-750.
43. **Braun, EL**, RT Kimball, K-L Han^G, N Iuhasz-Velez^{U,G}, AJ Bonilla^U, JL Chojnowski^G, JV Smith^{U,G}, RCK Bowie, MJ Braun, SJ Hackett, J Harshman, CJ Huddleston, BD Marks, KJ Miglia, WS Moore, S Reddy, FH Sheldon, CC Witt & T Yuri^P. 2011. Homoplastic microinversions and the avian tree of life. **BMC Evolutionary Biology**, **11**: 141.
- Highly accessed
44. Feller, A, K Machemer, **EL Braun** & E Grotewold. 2011. Evolutionary and comparative

- analysis of MYB and bHLH plant transcription factors. *The Plant Journal*, **66**: 94-116.
- Invited manuscript
45. Han, K-L^G, **EL Braun**, RT Kimball, S Reddy, RCK Bowie, MJ Braun, JL Chojnowski[†], SJ Hackett, J Harshman, CJ Huddleston, BD Marks, KJ Miglia, WS Moore, FH Sheldon, DW Steadman, CC Witt & T Yuri^P. 2011. Are transposable element insertions homoplasy free? An examination using the avian tree of life. *Systematic Biology*, **60**: 375-386.
46. Kimball, RT, CM St Mary & **EL Braun**. 2011. A macroevolutionary perspective on multiple sexual traits in the Phasianidae (Galliformes). *International Journal of Evolutionary Biology*, Article ID 423938. (doi:10.4061/2011/423938)
- Invited manuscript
47. Lim, CH, T Hamazaki, **EL Braun**, J Wade & N Terada. 2011. Evolutionary genomics indicates a specific function of *Slc25a31* in mammalian and anole lizard germ cells. *PLoS ONE*, **6**: e23122.
48. Bonilla, AJ^U, **EL Braun** & RT Kimball. 2010. Comparative molecular evolution and phylogenetic utility of 3'-UTRs and introns in Galliformes. *Molecular Phylogenetics and Evolution*, **56**: 536-542.
49. Zhu, J^G, **EL Braun**, S Kohno, M Antenos, EY Xu, RW Cook, SJ Lin, BC Moore, LJ Guillette Jr, TS Jardetzky & TK Woodruff. 2010. Phylogenomic analyses reveal the evolutionary origin of the inhibin α -subunit, a unique TGF β superfamily antagonist. *PLoS ONE*, **5**: e9457.
50. Katsu, Y^P, **EL Braun**, LJ Guillette Jr & T Iguchi. 2009. From reptilian phylogenomics to reptilian genomes: Analyses of *c-Jun* and *DJ-1* proto-oncogenes. *Cytogenetic and Genome Research*, **127**: 79-93.
- Invited manuscript
 - Katsu and Braun contributed equally, Braun corresponding author
51. Kimball, RT, **EL Braun**, FK Barker, RCK Bowie, MJ Braun, JL Chojnowski^G, SJ Hackett, K-L Han^G, J Harshman, V Heimer-Torres^U, W Holznagel, CJ Huddleston, BD Marks, KJ Miglia, WS Moore, S Reddy, FH Sheldon, JV Smith^{U,G}, CC Witt & T Yuri^P. 2009. A well-tested set of primers to amplify regions spread across the avian genome. *Molecular Phylogenetics and Evolution*, **50**: 654-660.
52. **Braun, EL** & N Phillips. 2008. Phylogenomics and secondary plastids: A look back and a look ahead. *Journal of Phycology*, **44**: 2-6.
- Invited manuscript, featured as cover illustration (cover designed by EL Braun and S Gould)
 - Contribution to the "Borrowed Chloroplasts: Secondary Endosymbiosis and the Chromalveolates" symposium (organized by N Phillips, EL Braun and D Bhattacharya)
53. Chojnowski, JL^G & **EL Braun**. 2008. Turtle isochore structure is intermediate between amphibians and other amniotes. *Integrative and Comparative Biology*, **48**: 454-462.
54. Chojnowski, JL^G, RT Kimball & **EL Braun**. 2008. Introns outperform exons in analyses of basal avian phylogeny using clathrin heavy chain genes. *Gene*, **410**: 89-96.
55. Georgelis, N^G, **EL Braun** & LC Hannah. 2008. Duplication and functional divergence of ADP-glucose pyrophosphorylase genes in plants. *BMC Evolutionary Biology*, **8**: 232.
56. Hackett, SJ, RT Kimball, S Reddy, RCK Bowie, **EL Braun**, MJ Braun, JL Chojnowski^G, WA Cox^U, K-L Han^G, J Harshman, CJ Huddleston, BD Marks, KJ Miglia, WS Moore, FH Sheldon, DW Steadman, CC Witt & T Yuri^P. 2008. A phylogenomic study of birds reveals their evolutionary history. *Science* **320**: 1763-1768.
- Recommended by Faculty of 1000 <http://f1000.com/1115666>

57. Harshman, J, **EL Braun**, MJ Braun, CJ Huddleston, RCK Bowie, JL Chojnowski^G, SJ Hackett, K-L Han^G, RT Kimball, BD Marks, KJ Miglia, WS Moore, S Reddy, FH Sheldon, DW Steadman, SJ Steppan, CC Witt & T Yuri^P. 2008. Phylogenomic evidence for multiple losses of flight in ratite birds. *Proceedings of the National Academy of Sciences USA*, **105**: 13462-13467.
- Harshman, EL Braun, and MJ Braun contributed equally, EL Braun corresponding author
58. Kimball, RT & **EL Braun**. 2008. A multigene phylogeny of Galliformes supports a single origin of erectile ability in non-feathered facial traits. *Journal of Avian Biology*, **39**: 438-445.
59. Phillips, N, S Calhoun, A Moustafa, D Bhattacharya & **EL Braun**. 2008. Genomic insights into evolutionary relationships among heterokont lineages emphasizing the Phaeophyceae. *Journal of Phycology*, **44**: 15-18.
- Contribution to the "Borrowed Chloroplasts: Secondary Endosymbiosis and the Chromalveolates" symposium (organized by N Phillips, EL Braun & D Bhattacharya); see notes for Braun & Phillips (2008).
60. Yuri, T[†], RT Kimball, **EL Braun** & MJ Braun. 2008. Duplication and accelerated evolution of growth hormone gene in passerine birds. *Molecular Biology and Evolution*, **25**: 352-361.
61. Chojnowski, JL^G, J Franklin^U, Y Katsu, T Iguchi, LJ Guillette Jr, RT Kimball & **EL Braun**. 2007. Patterns of vertebrate isochore evolution revealed by comparison of expressed mammalian, avian and crocodylian genes. *Journal of Molecular Evolution*, **65**: 259-266.
62. Cox, WA^U, RT Kimball & **EL Braun**. 2007. Phylogenetic position of the New World Quail (Odontophoridae): Eight nuclear loci and three mitochondrial regions contradict morphology and the Sibley-Ahlquist Tapestry. *The Auk*, **124**: 74-84.
63. Georgelis, N[†], **EL Braun**, JR Shaw & LC Hannah. 2007. The two AGPase subunits evolve at different rates in angiosperms, yet they are equally sensitive to activity-altering amino acid changes when expressed in bacteria. *Plant Cell*, **19**: 1458-1472.
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- Invited book chapter
69. Katsu, Y, DS Bermudez, **EL Braun**, C Helbing, S Miyagawa, MP Gunderson, S Kohno, TA Bryan, LJ Guillette Jr & T Iguchi. 2004. Molecular cloning of the estrogen and progesterone receptors of the American Alligator. *General and Comparative Endocrinology*, **136**: 122-133.

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- Invited manuscript
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- Dias and Braun contributed equally
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- Recommended by Faculty of 1000 (<http://f1000.com/1012265>)
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- Invited book chapter
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187-198.

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 - Rabinowicz and Braun contributed equally
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90. Nelson, MA, S Kang, **EL Braun**, ME Crawford, PL Dolan, PM Leonard, J Mitchell^U, AM Armijo^U, L Bean^U, E Blueeyes^U, T Cushing^U, A Errett^U, M Fleharty^U, M Gorman^U, K Judson^U, R Miller, J Ortega^U, I Pavlova^U, J Perea^U, S Todisco^U, R Trujillo^U, J Valentine^U, A Wells^U, M Werner-Washburne, S Yazzie^U & DO Natvig. 1997. Expressed sequences from conidial, mycelial and sexual stages of *Neurospora crassa*. ***Fungal Genetics and Biology***, 21: 348-363.
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92. Werner-Washburne, M, **EL Braun**, ME Crawford & VM Peck. 1996. Stationary phase in *Saccharomyces cerevisiae*. ***Molecular Microbiology***, 19: 1159-1166.
93. Fuge, EK, **EL Braun** & M Werner-Washburne. 1994. Protein synthesis in long-term stationary phase cultures of *Saccharomyces cerevisiae*. ***Journal of Bacteriology***, 176: 5802-5813.
 - Fuge and Braun contributed equally

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95. Werner-Washburne, M, D Brown & **E Braun**. 1991. Bcy1, the regulatory subunit of cAMP-dependent protein kinase in yeast, is differentially modified in response to the physiological status of the cell. *Journal of Biological Chemistry*, **266**: 19704-19709.

White Papers

1. Baker, S, J Magnuson, L Lasure, **E Braun**, R Roberson, K McCluskey & D Natvig. Submitted to the DoE Microbial Genome Program for the 1 July 2004 deadline. Nomination to sequence the genome of *Allomyces macrogynus*, a chytrid fungus. (not chosen for sequencing in the summer 2004 round)
2. Baker, SE, M Morrison, J Hackstein, C McSweeney, **E Braun**, J Boore & J Magnuson. Submitted to the DoE Community Sequencing Program for the 15 Feb 2005 deadline. A genome sequence project for the anaerobic chytrid fungus, *Piromyces* sp. E2 (CHOSEN for sequencing in the summer 2005 round)
3. **Braun, EL**, SE Baker, G Burger, BF Lang, J Boore & J Magnuson. Submitted to the DoE Community Sequencing Program for the 15 Feb 2005 deadline. Connecting the animals and fungi using genomic survey sequences and ESTs from the mesomycetozoean (DRIP) *Amoebidium parasiticum*. (not chosen for sequencing in the summer 2005 round)
4. Corrochano, LM, SE Baker & **E Braun**. Submitted to the DoE Community Sequencing Program for the 15 Feb 2005 deadline. Genome sequence of the zygomycete fungus *Phycomyces blakesleeanus*. (CHOSEN for sequencing in the summer 2005 round)
5. Losos, J, **E Braun**, D Brown, S Clifton, S Edwards, J Gibson-Brown, T Glenn, L Guillette, D Main, P Minx, W Modi, M Pfreder, D Pollock, D Ray, A Shedlock & W Warren. Submitted to the National Institutes of Health for the 10 July 2005 deadline. Proposal to sequence the first reptilian genome: The green anole lizard, *Anolis carolinensis*. (CHOSEN for sequencing in the summer 2005 round)

Funded Grant Proposals

(a) Major funded grant proposals (more than \$80,000)

- 2017 **National Science Foundation**: All Birds: A time-scaled avian tree from integrated phylogenomic and fossil data. 4 years, **\$1,421,651** (with co-principle investigators BT Smith, FK Barker, RT Brumfield, RT Chesser, BC Faircloth, RT Kimball & D Ksepka, UF portion **\$258,323**)
- 2012 **University of Florida Opportunity Fund**: Evolution and epidemiology of the plant and animal pathogen *Pythium insidiosum*. 2 years, **\$88,161**. (with co-principal investigators EM Goss, N Keyhani & JA Hernandez).
- 2011 **National Science Foundation**: A taxon-rich phylogeny of Galliformes: Using multiple loci to resolve conflicts among previous studies. Award Number DEB-1118823; Program: Systematics. 3 years, **\$394,229**. (with co-principal investigator RT Kimball).
- 2009 **National Science Foundation**: Sequencing gators: Building a genome science Curriculum for the University of Florida and beyond. Award Number DUE-0920151; Program: CCLI (TUES). 4 years, **\$499,888**. (with co-principal investigators E Triplett, V de Crecy, T Kahveci & G Casella).
- 2003 **University of Florida Opportunity Fund**: The *Alligator* expressed genome project. 1 year, **\$99,998**. (with co-principal investigators LJ Guillette Jr & ND Denslow)

2002 **National Science Foundation:** Early Bird: A collaborative project to resolve the deep nodes of avian phylogeny. Award Number DEB-0228682; Program: Assembling the Tree of Life. 4 years (funding began 2003), **\$2,057,626**. (with co-principal investigators SJ Hackett, RT Kimball, WS Moore, FH Sheldon & DW Steadman, UF portion **\$454,697**).

1999 **United States Department of Agriculture:** The function and evolution of plant Myb proteins. Award Number 1999-01582; Program: Plant Genetic Mechanisms. 2 years, **\$90,000**.

(b) Selected additional grants (as principal investigator or other senior personnel)

- **Donor support for iGEM activities:** A private donor (Wesley Belden) has provided funds for student activities associated with the International Genetically Engineered Machine (iGEM) synthetic biology competition (**\$250 quarterly donations**, ongoing)
- **National Science Foundation:** Participant in manakin genomics research coordination network "RCN: Enabling comparative studies of the process and products of sexual selection in a genomic context" Award Number DEB-1457541 Principal investigator: B Loiselle, co-PIs: M Braun, E DuVal, WA Boyle & C Balakrishnan (**\$499,901**)
- **University of Florida Biodiversity Institute:** BridgeTree: A toolbox to mobilize big biodiversity data to understand and communicate pattern and process. With co-PIs: RP Guralnick, RT Kimball, JAB Fortes, RJ Figueirido, J Krieger, HA Owens & J Allen. (**\$45,000**, currently active).
- **Howard Hughes Medical Institute:** Science Education Alliance PHAGES program (HHMI is supporting a freshman bacteriophage genomics course; with D. Julian, BM Dunn, M Atherton & AE Donnelly).
- **National Science Foundation:** Major Research Instrumentation grant "Acquisition of CASTOR: A High-Performance Communication and Storage Backbone for Data-Intensive Scientific and Engineering Computing," Award Number CNS-0421200. 3 years. Principal investigators: S Ranka, co-PIs: P Avery, A George, P Sheng & S Trickey; participated as one of the senior personnel, which also included: A Banerjee, S-s Chen, R Figueiredo, J Fortes, V Frouhar, C Griffin, J Hammer, C Jermaine, D Pokorney, S Sahni, S Sinnott & Y Xia (**\$600,000**)
- **National Science Foundation:** Major Research Instrumentation grant "Acquisition of GatorCloud: Enabling High-Impact Scientific Research and Collaboration via Software Defined Networks and Cloud Services," Award Number ACI-1229576. 4 years. Principal investigator: X Li, co-PIs: A George, E Deumens, P Avery & S Ranka; participated as one of the senior personnel, which also included: S Balachandar, E Ford, C Griffin, P Khargonekar, D Pokorney, S Sahni, B Sanders, D Wu & Y Xia (**\$1,172,354**)
- **Singer Biology Fund:** "Evolution of avian olfactory systems: Assessing genetic and genomic changes associated with shifts in behavior" with RT Kimball & JG Burleigh (**\$10,000**)
- **Singer Biology Fund:** "Understanding gene flow in sessile, coral-associated invertebrates" with CW Osenberg (**\$3,000**)
- **Smithsonian Scholarly Studies Program:** "Adapting Next Generation sequencing technologies for efficient large-scale phylogenetics" with MJ Braun and P Houde (**\$70,000**; funds controlled by MJ Braun, National Museum of Natural History, Smithsonian Institution and used to support a collaborative project)
- **Smithsonian Institution Next Generation Sequencing small grant proposal:** "Phylogenetic utility of ultra-conserved elements for the avian tree of life" with MJ Braun,

N White, T Glenn, B Faircloth, R Brumfield, J McCormack, and N Crawford (**\$100,000 plus \$10,000 supplement**; funds controlled by MJ Braun, National Museum of Natural History, Smithsonian Institution and used to support a collaborative project)

Awards and Honors

- 2016 UF Term Professor (3-year award, active)
- 2000 Invited to Arthur Neish Young Investigators' Symposium at the meeting of the Phytochemical Society of North America (PSNA) in Beltsville, MD.
- This symposium talk was featured in the November 2000 issue of PSNA News.

Awards and honors received as a student:

- Elected to Golden Key (1989) and Phi Beta Kappa (1990) National Honor Societies
- Outstanding Graduating Senior Award, New Mexico Biological Society (1991)
- Outstanding oral presentation awards, Univ New Mexico research day (1992 & 1994)
- Scholarship from the Marine Biological Laboratory, Woods Hole, MA. (1995).

Service, Synergistic Activities, and Society Memberships

(a) Service to Institution

- University service: chair of *ICBR bioinformatics core advisory committee*, member of the *Biology major executive committee*.
- College (*Liberal Arts and Sciences*) service: *Sabbatical committee* (as chair), *Chair search committee for the Department of Biology*, and *Mathematical Sciences committee*.
- Departmental service: *Curriculum committee* (as chair), *Computer/IT Committee* (as chair for *IT committee*), *Interdisciplinary Center for Biotechnology Research [ICBR] advisory committee*, *Executive committee*, *Graduate admissions committee*, *Space committee*, and multiple *search committees* (some as chair)
- Undergraduate Coordinator for Botany, Zoology, and a Liberal Arts and Sciences Marine Science majors (2011-2014) with a marine biology focus and Liberal Arts and Sciences Biology majors (2011-2012). Duties included:
 - a. Evaluate and approve petitions; make student advisor comments regarding students
 - b. Contribute to governance of those degrees
 - c. Review and edit catalog copy
 - d. Provide other information to majors and prospective students
 - e. Approve applications for undergraduate research (and encourage student research)
 - f. Approve end of semester research reports and undergraduate honors theses.

(b) Editorial Service

- Associate Editor, *Molecular Phylogenetics and Evolution*
- Associate Editor, *PeerJ*
- Editorial Board, *Biology*

(c) Grant Proposal Review

- National Science Foundation (also served on the NSF ARI-R² grant panel in 2009)
- United States Department of Agriculture
- United States Army Corps of Engineers Engineer Research and Development Center
- Chilean Superior Council of the National Fund for Scientific & Technological Development (FONDECYT)
- Canadian Natural Sciences and Engineering Research Council (NSERC)
- Deutsche Forschungsgemeinschaft (German Research Foundation)
- Icelandic Research Fund

- Marsden Fund (New Zealand Research Foundation)
- (d) Manuscript Review for the following journals:
- The Auk, Biology (also editorial board member), BMC Evolutionary Biology, BMC Genomics, BMC Plant Biology, Critical Reviews in Biochemistry & Molecular Biology, Frontiers in Genetics, Fungal Genetics and Biology, Genome Biology and Evolution, Genomics, Integrative Zoology, Journal of Molecular Evolution, Molecular Biology and Evolution, Molecular Phylogenetics and Evolution, Nature Communications, Plant Molecular Biology, Plant Science, PLoS ONE, Proceedings of the National Academy of Sciences USA, Proceedings of the Royal Society of London, series B, Royal Society Open Science, RNA, Scientific Reports (Nature publishing group), Systematic Biology, Zoological Journal of the Linnean Society
- (e) Miscellaneous Community Service
- External consultant on the strategic plan for next-generation sequencing at the Smithsonian Institution (drafted 2011).
 - Advisory committee member (2010) and judge (multiple years) for the WD Hamilton award (given by the Society for Study of Evolution for outstanding student talks at the Evolution meeting).
 - Co-organizer (with N Phillips & D Bhattacharya) of the “Borrowed Chloroplasts: Secondary Endosymbiosis and the Chromalveolates” symposium at the Botany and Plant Biology 2007 Joint Congress (funded in part by the *NSF* and the *Botanical Society of America*).
- (f) Society Memberships
- American Association for the Advancement of Sciences, Genetics Society of America, Sigma Xi, Society of Systematic Biologists, Society for the Study of Evolution.

Mentoring Activities

I have supervised or co-supervised students in the mathematics and zoology programs and post-doctoral scientists. I have served as a committee member for graduate students in botany, computer engineering, genetics and genomics, the UF biomedical sciences interdisciplinary program (IDP), plant molecular and cellular biology, plant pathology, and zoology. My mentees since joining the UF faculty are listed on the next page.

- (a) Graduate Students and Post-doctoral Scientists Supervised:
- Deena Bermudez (M.S.T. Zoology; co-supervised with RT Kimball)
 - Jena L Chojnowski (Ph.D. Zoology)
Now Assistant Professor, University of South Carolina, Beaufort
 - Sarah Haas (M.S. Zoology, co-supervised with RT Kimball)
Now post-doctoral scientist, University of Colorado, Boulder
 - Peter A Hosner (post-doctoral scientist; supported by DEB-1118823)
Now Assistant Professor, University of Copenhagen
 - Naomi R Iuhasz-Velez (M.S. Mathematics; co-supervised with SS Pilyugin)
 - Kelly A Meiklejohn (post-doctoral scientist; supported by DEB-1118823)
Now permanent employee FBI, forensics research
 - Akanksha Pandey (currently Ph.D. student, Zoology)
 - Jessica L Sabo (M.S. Zoology)
 - Jordan V Smith (M.S. Zoology)
Now Molecular Diagnostics Supervisor at Miraca Life Sciences
 - Tamaki Yuri (post-doctoral scientist; supported by DEB-0228682)
Now collections manager, University of Oklahoma and Sam Noble Museum

(b) Served as Committee Member (Ph.D. students listed, co-authors indicated in bold):

- Nathaniel Evans Andrea L Eveland, **Guanqiao Feng**, Ronald D French, **Kin-Lan Han**, Wei Hou, Haiyan Jia, Hye Won Lee, **Chae Ho Lim**, **Brandon Moore**, Zach Randall, Matthew P Salomon, **Slim O Sassi**, Anne M Vitoreli, HF (Scooter) Willis IV

(c) Undergraduates (only Univ Florida undergraduates listed):

- Research experiences: Vipa Bernhardt, Miguel Bonilla, Michelle Burch, Tara Conway, W Andrew Cox, Jessica E Cunio, Melany Danielson, J Brooke Dayton, Rebecca Drucker, Syki Q Duong, Elon Fernandez, Robert Fields, Carly Ferguson, Timothy Foster, Janessa Graham, Victoria Heimer-McGinn (née Heimer-Torres), Glenn Hannah, Amanda Hudson, Naomi Iuhasz-Velez, Dieula John, Kevin Johnson, Karen Kung, Andrea V Padron, Laura Patterson, Sarah A Ring, Katherine Rozofski, Frantzie Saint Juste, Rachel Seibert, Jordan V Smith, Doug Storch, Padmaksi Tester, and Rebecca Theobald
- Students who received support from the UF University Scholars program: Michelle Burch, Jessica E Cunio, and Syki Q Duong
- Students supported by HHMI Science for Life program: Melany Danielson
- Students supported by NSF REU supplements:
 - To DEB-0228682: Elon Fernandez & Victoria Heimer-Torres
 - To DEB-1118823: Melany Danielson, Andrea V Padron, Frantzie Saint Juste & Sarah A Ring
- Teaching Interns: Tejan Elmariah (née Ottallah), Ariane Maico, and Jennifer Westcott

Courses Taught

Introductory Genetics	4 credit hours (PCB3063)
<i>This course has been my primary teaching activity at the University of Florida</i>	
Introductory Biology (Genetics section)	3 credit hours (BSC2010)
<i>The genetics section of this course was originally part of BSC2011.</i>	
Genetics and Genomics	3 credit undergraduate course
Models and Molecular Evolution	3 credit hour graduate course
<i>I have also offered a 2 credit hour version of this course.</i>	
Phage Genomics	Have offered several versions
4 credit hour course (Fall 2011)/2 credit hour course (Spring 2012)	
4 credit hour immersion course (5 weeks of daily meetings, offered Spring 2018)	
<i>Offered both majors and non-majors sections in 2011/2012.</i>	
<i>Supported in part by the Howard Hughes Medical Institute (see grants).</i>	
Synthetic Biology	3 credit hours
<i>I have mentored with the UF iGEM team (see above, additional grants)</i>	
Graduate Seminars:	1 or 2 credit hour graduate courses
<i>Seminar topics include Phylogenomics, Rare Genomic Changes, Computational Methods, and Phylogenetic Comparative Methods (the last was co-taught with RT Kimball).</i>	

Presentations since receiving PhD (asterisk indicates I was the presenter)

2019:

- 1) *Workshop Talk**, "Coalescent analyses of genome-scale indel (insertion-deletion) data provide a unique source of information about avian species tree and ancestral population sizes," co-authored with P Houde, N Narula & S Mirarab. Plant and Animal Genome XXVII Conference (PAG), San Diego, California.

2018:

- 2) *Seminar**, “What can we learn from models of protein evolution?” Northeast Normal University, Changchun, China.
- 3) *Proceedings Talk**, “An evolutionary model motivated by physicochemical properties of amino acids reveals variation among proteins,” sole author. 26th Annual Conference on Intelligent Systems for Molecular Biology, Chicago, Illinois (ISMB 2018 proceedings are peer-reviewed; acceptance rate of 19.6%).
- 4) *Poster**, “Unlocking the phylogenomic (super)tree of birds (and other organisms),” co-authored with RT Kimball, CH Oliveros, N Wang, FK Barker, DJ Field, DT Ksepka, RT Chesser, RG Moyle, RT Brumfield, BC Faircloth & BT Smith. Genome 10K Annual Conference, Rockefeller University, New York, New York.
- 5) *Talk*, “Manakin phylogeny based on ultraconserved element sequence capture,” progress report based on work conducted in collaboration with RT Kimball, RN Leite, EP Derryberry, PA Hosner, GE Derryberry, M Anciães, J McKay D Meyer, A Aleixo, CC Ribas, RT Brumfield & J Cracraft presented at the Manakin Genomics RCN meeting in Gamboa, Panama.
- 6) *Poster*, “Why do phylogenomics analyses of early animal evolution continue to disagree? Sites in different structural environment yield different answers,” co-authored with A Pandey. 26th Annual Conference on Intelligent Systems for Molecular Biology, Chicago, Illinois.
- 7) *Poster*, “OpenWings: Collaborative construction of a fossil calibrated species-level bird phylogeny,” co-authored with CH Oliveros, RT Brumfield, BC Faircloth, BT Smith, RT Kimball & FK Barker. 2018 American Ornithological Society meeting, Tucson, Arizona.

2017:

- 8) *Talk**, “Can we effectively estimate ancestral effective population sizes? A case study in Galliformes,” co-authored with RT Kimball. American Ornithology 2017, East Lansing Michigan.
- 9) *Talk*, “Slow markers and fast birds: A subspecific phylogeny of the New World quail using thousands of UCE loci,” co-authored with JG Salter, PA Hosner, RT Kimball & BC Faircloth. American Ornithology 2017, East Lansing Michigan.
- 10) *Talk*, “Testing the limits of phylogenomics for resolving the bird tree of life. co-authored with S Reddy & R. Kimball. Evolution 2017, Portland, Oregon.
- 11) *Talk*, Analyses of New World vulture olfactory receptor repertoires reveals dynamic patterns of evolution. co-authored with JE Wright, RT Kimball & JG Burleigh. Evolution 2017, Portland, Oregon.
- 12) *Talk*, “Phylogenomics using target capture of ultraconserved elements and exons reveals deep relationships within the Neotropical manakins (Aves: Pipridae),” co-authored with RN Leite, RT Kimball, EP Derryberry, PA Hosner, GE Derryberry, M Anciães, J McKay D Meyer, A Aleixo, CC Ribas, RT Brumfield & J Cracraft. Evolution 2017, Portland, Oregon.
- 13) *Talk*, “Implications of protein-structure based partitioning on phylogenetics inference,” co-authored with A Pandey. Society of Systematic Biologists Standalone Meeting, Baton Rouge, LA
- 14) *Lightning talk*, “How super are supermatrices?” co-authored with PA Hosner & RT Kimball. American Ornithology 2017, East Lansing Michigan.

2016:

- 15) *Seminar**, “Facing up to differences among data types in phylogenomics,” Department of Biology, New Mexico State University, Las Cruces, NM.
- 16) *Plenary**, “Insights into the evolution of pheasants from whole genome sequencing,” talk based on collaborative work involving G Tiley, P Hosner, JG Burleigh & R Kimball. 2016 International Symposium on Galliformes, Beijing, China.
- 17) *Talk**, “The genome of *Bambusicola thoracicus* and insights on molecular evolution in Phasianidae,” co-authored with G Tiley, P Hosner, JG Burleigh & R Kimball. North American Ornithological Conference, Washington, DC.

- 18) *Talk**, “The impact of taxon sampling and data type on difficult problems in phylogenomics: Birds in a bush revisited?” co-authored with S Reddy, R Kimball, A Pandey, P Hosner, M Braun, K-L Han, J Harshman, S Hackett, C Huddleston, S Kingston, B Marks, K Miglia, W Moore, F Sheldon, C Witt & T Yuri. North American Ornithological Conference, Washington, DC.
- 19) *Talk*, “Phylogenomics and mitogenomics place enigmatic phasianids (Aves: Galliformes),” co-authored with N Wang, P Hosner & Rebecca Kimball. North American Ornithological Conference, Washington, DC.
- 20) *Talk*, Evolution of vagility and convergent island gigantism in quail (Aves: *Coturnix*). co-authored with P Hosner, J Tobias & R Kimball. North American Ornithological Conference, Washington, DC.
- 21) *Poster*, “Complex adaptation to high altitude: A case study using complete mitogenomes,” co-authored with B Liang, N Wang, R Kimball & W Liang. North American Ornithological Conference, Washington, DC.
- 22) *Talk*, “Evolution of vagility and convergent island gigantism in quail (Aves: *Coturnix*),” co-authored with P Hosner, J Tobias & R Kimball. Evolution 2016, Austin, TX.
- 23) *Poster*, “Progress in resolving the avian tree of life,” co-authored with N White, M Braun & B Faircloth. Evolution 2016, Austin, TX.
- 24) *Poster*, “The genome of *Bambusicola thoracicus* and insights on molecular evolution in Phasianidae,” co-authored with G Tiley, R Kimball, P Hosner & JG Burleigh. Evolution 2016, Austin, TX.

2015:

- 25) *Poster**, “Whole genome phylogeny places the emerging mammalian pathogen *Pythium insidiosum* in the oomycete tree of life,” co-authored with MS Ascunce, JC Huguet-Tapia, A Ortiz-Urquiza, NO Keyhani & E Goss. 10th Annual International Conference on Bioinformatics (meeting focus: the genomics and evolution of pathogens and hosts), Atlanta, GA.
- 26) *Talk*, “Resolving the avian Tree of Life using ultraconserved elements,” co-authored with N White, B Faircloth, J McCormack, R Brumfield, T Glenn & M Braun. Evolution 2015, Guarujá, Brazil.
- 27) *Talk*, “Sorting out phylogenetic relationships among the grouse and ptarmigan,” co-authored with RT Kimball, N Persons & PA Hosner. 133rd Meeting of the American Ornithologists' Union, held in conjunction with the 85th Meeting of the Cooper Ornithological Society, Norman, OK.
- 28) *Talk*, “Rapid and recent diversification of curassows, guans, and chachalacas (Galliformes: Cracidae),” co-authored with PA Hosner & RT Kimball. 133rd Meeting of the American Ornithologists' Union, held in conjunction with the 85th Meeting of the Cooper Ornithological Society, Norman, OK.
- 29) *Poster*, “Ultraconserved elements provide orthologous portals into tetrapod genomes illuminating the remarkably slow evolution of crocodylian genomes,” co-authored with TC Glenn, BC Faircloth, JE McCormack, DA Ray & RE Green. Society for Integrative and Comparative Biology Meeting, West Palm Beach, FL.
- 30) *Poster*, “Unexpected olfactory receptor gene numbers revealed in two cathartid species that demonstrate discrete sensory system reliance during foraging,” co-authored with JE Wright, A Kumar, JG Burleigh & RT Kimball. Society for Integrative and Comparative Biology Meeting, West Palm Beach, FL.

2014:

- 31) *Seminar**, “Understanding the archosaur genome: Evolutionary genomics in birds and crocodylians,” College of Life Sciences, Beijing Normal University, Beijing, China.
- 32) *Seminar**, “Using next-gen sequencing to understand the evolution of galliforms,” College of Life Sciences, Beijing Normal University, Beijing, China.

- 33) *Talk**, "Small genomes in the era of Big Data: Phylogeny and patterns of molecular evolution for mitogenomes in Galliformes," co-authored with RT Kimball, KA Meiklejohn, PA Hosner, A Kumar, TC Glenn, BC Faircloth. 132nd Meeting of the American Ornithologists' Union, held in conjunction with the 84th Annual Meeting of Cooper Ornithological Society and the Society of Canadian Ornithologists meeting, Estes Park, CO.
- 34) *Talk*, "Phylogeny and diversification of the New World quail (Odontophoridae)," co-authored with PA Hosner & RT Kimball. 132nd Meeting of the American Ornithologists' Union, held in conjunction with the 84th Annual Meeting of Cooper Ornithological Society and the Society of Canadian Ornithologists meeting, Estes Park, CO.
- 35) *Talk*, "Resolving conflicts among galliform phylogenies using ultra-conserved elements," co-authored with RT Kimball, PA Hosner, TC Glenn, & BC Faircloth. 132nd Meeting of the American Ornithologists' Union, held in conjunction with the 84th Annual Meeting of Cooper Ornithological Society and the Society of Canadian Ornithologists meeting, Estes Park, CO.
- 36) *Talk**, "Species tree methods and ultraconserved elements (UCEs): a case study in galliform birds," KA Meiklejohn, RT Kimball, BC Faircloth & TC Glenn. Evolution 2014, Raleigh, NC.
- 37) *Talk*, "Tick-tock goes the croc: Three genome drafts indicate slow molecular evolution in crocodylians and provide insight into archosaur evolution," DA Ray, RE Green, B Paten, TC Glenn, BC Faircloth, FG Hoffmann, T Gabaldón, FM McCarthy, CJ Schmidt, MK Fujita, JC Opazo & AF Smit. Evolution 2014, Raleigh, NC.
- 38) *Talk*, "Testing Darwin's hypothesis on the evolution of ornamental eyespots in peafowl and their relatives," co-authored with RT Kimball, K Sun, KA Meiklejohn, BC Faircloth & TC Glenn. Evolution 2014, Raleigh, NC.
- 39) *Talk*, "Conserved DNA elements as tools for understanding crocodylian biology," co-authored with T Glenn, B Faircloth, J Finger, T Kieran, S Isberg, C Moran, K Vliet, M Shirley, M Venegas-Anaya, L Densmore, RE Green & D Ray. 23rd Working Meeting of the IUCN-SSC Crocodile Specialist Group, Lake Charles, LA.
- 40) *Poster*, "Adaptive evolution of Cep63-CEF152 centrosome microcephaly ring in association with brain size shift in mammals," co-authored with A Kumar & TR Kimball. 22nd annual International Conference on Intelligent Systems for Molecular Biology held in Boston, MA,

2013:

- 41) *Talk**, "'Big Bird' – inferences based upon analyses of a large-scale supermatrix of avian genetic data," co-authored with JG Burleigh & RT Kimball. 131st Meeting of the American Ornithologists' Union, held in conjunction with the 83rd Annual Meeting of the Cooper Ornithological Society, Chicago, IL.
- 42) *Talk*, "'Patterns of diversification in the Phasianidae,'" co-authored with RT Kimball. 131st Meeting of the American Ornithologists' Union, held in conjunction with the 83rd Annual Meeting of the Cooper Ornithological Society, Chicago, IL.
- 43) *Talk**, "Comparison of the utility of mitochondrial DNA, nuclear introns, and ultraconserved element (UCE) data for the resolution of a recent but difficult avian radiation," co-authored with KA Meiklejohn, RT Kimball, BC Faircloth & T Glenn, Evolution 2013, Snowbird, UT.
- 44) *Talk*, "Evolution of the olfactory receptor subgenome in New World vultures," RT Kimball, J Wright & JG Burleigh, Evolution 2013, Snowbird, UT.
- 45) *Talk*, "Conflicting phylogenetic signal among mitochondrial regions: affects of taxon sampling and model choice," co-authored with KA Meiklejohn, M Danielson, B Faircloth, T Glenn & RT Kimball, Evolution 2013, Snowbird, UT.
- 46) *Talk*, "Unraveling the Evolutionary History of Nocturnality in the Nightbirds," co-authored with N White, BC Faircloth, J McCormack & M Braun, Evolution 2013, Snowbird, UT.

2012:

- 47) *Seminar**, "Biodiversity genomics: Rare genomic changes and models of evolution," Department of Biological Sciences, West Virginia University, Morgantown, WV.

- 48) *Talk*, "Independent corroboration of the avian tree of life," co-authored with RT Kimball & N Wang. North American Ornithological Conference, Vancouver, Canada.
- 49) *Talk*, "Early Bird update: The avian tree of life based on 28 genes and 203 taxa," co-authored with MJ Braun, S Mirarab & T Warnow. North American Ornithological Conference, Vancouver, Canada.
- 50) *Poster*, Sequencing, annotation, and phylogenomic analysis of Xerxes, a cluster N mycobacteriophage. co-authored with TN Larsen, MB Averkiou, LD Bean, BA Borgert, H Dharia, BM Dominguez, AGP Fernandez, JD Fitzgerald, CR Ibe, K Ivanova, S Karic, MS Kawwa, EL Kirkpatrick, O Oliver, VL Ramirez, SA Ring, A Srivastav, KL Weston, HH Yousaf, JL Sabo & WB Barbazuk. SEA Phages Symposium, HHMI Janelia Farms, Ashburn, VA.

2011:

- 51) *Talk**, "Reptilian genomics in science pedagogy." Snake Genomics and Integrative Biology meeting, Vail, CO.
- 52) *Talk*, "Impact of DNA sequence alignment on estimates of the Avian Tree of Life," co-authored with MJ Braun, K Liu, T Warnow & CR Linder. 129th Meeting of the American Ornithologists' Union, Jacksonville, FL.
- 53) *Talk*, "Increased numbers of olfactory receptors in Black and Turkey vultures," co-authored with RT Kimball & JG Burleigh. 129th Meeting of the American Ornithologists' Union, Jacksonville, FL.
- 54) *Talk*, "Testing hypotheses about the sister group of the Passeriformes using an independent 30 locus dataset," co-authored with N Wang & RT Kimball. 129th Meeting of the American Ornithologists' Union, Jacksonville, FL.
- 55) *Talk*, "Data mining and locus discover methods in the brown algae (Phaeophyceae)," co-authored with Dankwa, M, G Han, L Andersen, L Niko & N Phillips. Phycological Society of America 2011 Meeting, Seattle, WA.
- 56) *Talk**, "Challenges posed by transposable element insertions and microinversions for automated multiple sequence alignment," co-authored with RT Kimball. NESCENT meeting "Challenges for large-scale phylogeny and alignment estimation," Durham, NC.
- 57) *Talk*, "Impact of DNA sequence alignment on estimates of the Avian Tree of Life," co-authored with MJ Braun, K Liu, T Warnow & CR Linder. NESCENT meeting "Challenges for large-scale phylogeny and alignment estimation," Durham, NC.

2010:

- 58) *Seminar**, "Models, rare genomic changes, and phylogenomics," Department of Biology, Villanova University, Philadelphia, PA.
- 59) *Talk*, "Impact of DNA sequence alignment on estimates of the Avian Tree of Life," co-authored with MJ Braun, K Liu, T Warnow & CR Linder. AFO meeting, Ogden, UT.
- 60) *Talk*, "Evolution of barriers to recombination in avian sex chromosomes," co-authored with CN Ferguson & RT Kimball. CSO/AOU/SCO, San Diego, CA.
- 61) *Talk**, "Phylogenomic analyses of the brown algae and related heterokonts," co-authored with N Phillips, NR Ciemniecki, DF Kapraun, D Price & D Bhattacharya. Evolution 2010, Portland, OR.
- 62) *Talk*, "The challenges of using transposons in avian phylogenetics," co-authored with K-L Han, RT Kimball & N Wang. Evolution 2010, Portland, OR.
- 63) *Talk*, "Eight billion years of shrinkage in avian genomes," co-authored with J Harshman, MJ Braun, RCK Bowie, SJ Hackett, K-L Han, CJ Huddleston, RT Kimball, BD Marks, KJ Miglia, WS Moore, S Reddy, FH Sheldon, DW Steadman, CC Witt & T Yuri. Evolution 2010, Portland, OR.
- 64) *Talk*, "Evolution of barriers to recombination in avian sex chromosomes," co-authored with CN Ferguson & RT Kimball. Evolution 2010, Portland, OR.
- 65) *Talk*, "Molecular phylogeny provides insights into evolution of the Vermetidae," co-authored with CL Chaffee & CW Osenberg. Evolution 2010, Portland, OR.

2009:

- 66) *Seminar**, "Sequences, rare genomic changes, and the early evolution of birds," Department of Biological Sciences, George Washington University, Washington, DC.
- 67) *Talk*, "Phylogenomic analysis of a powerful and unique TGF-beta superfamily antagonist: Evolution of the inhibin alpha-subunit structural regions that regulate function," co-authored with J Zhu, S Kohno S, M Antenos, E Xu, J Lin, B Moore, LJ Guillette Jr, T Jardezky & T Woodruff. Society for the Study of Reproduction 2009.
- 68) *Talk**, "Examining the Avian Tree of Life using microinversions," co-authored with RT Kimball, K-L Han, N Iuhasz, AJ Bonilla, JL Chojnowski, JV Smith, MJ Braun, RCK Bowie, SJ Hackett, J Harshman, CJ Huddleston, BD Marks, KJ Miglia, WS Moore, S Reddy, FH Sheldon, CC Witt & T Yuri. Evolution 2009, Moscow, ID.
- 69) *Poster*, "Comparative molecular evolution and phylogenetic utility of 3'-UTRs and introns in Galliformes," co-authored with AJ Bonilla & RT Kimball. Evolution 2009, Moscow, ID.
- 70) *Poster*, "Candidate genes in temperature-dependent sex determination (TSD) in the Red-eared Slider Turtle, *Trachemys scripta*," co-authored with JL Chojnowski, SICB, Boston, MA.
- 71) *Poster*, "Next generation sequencing of the rainbow lorikeet reveals hundreds of potential microsatellite loci," co-authored with RT Kimball, 127th Meeting of the American Ornithologists' Union, Philadelphia, PA.
- 72) *Poster**, 2009. "Are we inching toward reality? Using introns and other non-coding sequences to understand the avian tree of life," co-authored with RT Kimball, K-L Han, N Iuhasz, AJ Bonilla, JL Chojnowski, JV Smith, T Yuri, RCK Bowie, MJ Braun, SJ Hackett, J Harshman, CJ Huddleston, BD Marks, KJ Miglia, WS Moore, S Reddy, FH Sheldon, DW Steadman & CC Witt. CIPRES all hands meeting, Berkeley, CA
- 73) *Poster*, "Eight billion years of shrinkage in avian introns," co-authored with J Harshman, MJ Braun, RCK Bowie, SJ Hackett, K-L Han, CJ Huddleston, RT Kimball, BD Marks, KJ Miglia, WS Moore, S Reddy, FH Sheldon, DW Steadman, CC Witt & T Yuri. CIPRES all hands meeting, Berkeley, CA

2008:

- 74) *Seminar**, "Models, rare genomic changes, and the early evolution of birds," Department of Botany and Zoology, University of Florida, Gainesville, FL.
- 75) *Symposium talk*, "Candidate genes in a turtle with temperature-dependent sex determination," co-authored with JL Chojnowski, part of the "Reptile genomics and evolutionary genetics" symposium, SICB Annual Meeting 2008, San Antonio, TX.
- 76) *Talk**, "Improved maximum likelihood analyses of protein sequences," co-authored with RT Kimball, Evolution 2008, Minneapolis, MN.
- 77) *Talk**, "Phylogenomic investigations within Brown Algae," co-authored with N Phillips, A Moustafa & D Bhattacharya, Protist 2008 (joint meeting of the International Society of Protistologists and the International Society for Evolutionary Protistology), Halifax, Nova Scotia, Canada.
- 78) *Talk*, "Who is sister group of the most speciose avian order (Passeriformes)? Analyses of over 20 nuclear loci," co-authored with RT Kimball, T Yuri, MJ Braun, RCK Bowie, JL Chojnowski, S Hackett, K-L Han, J Harshman, CJ Huddleston, BD Marks, KJ Miglia, WS Moore, S Reddy, FH Sheldon, DW Steadman & CC Witt, Evolution 2008, Minneapolis, MN.
- 79) *Talk*, "Model based phylogenetic analyses of over 12,000 insertion/deletion characters from multiple avian genes," co-authored with T Yuri, RT Kimball, MJ Braun, RCK Bowie, JL Chojnowski, S Hackett, K-L Han, J Harshman, CJ Huddleston, BD Marks, KJ Miglia, WS Moore, S Reddy, FH Sheldon, DW Steadman & CC Witt, Evolution 2008, Minneapolis, MN.
- 80) *Talk*, "Multi-locus phylogeny of Galliformes: Examining conflict among loci and with other studies," co-authored with RT Kimball, 126th Meeting of the American Ornithologists' Union (joint meeting with the Cooper Ornithological Society and Society of Canadian Ornithologists), Portland, OR.

- 81) *Talk*, “Testing monophyly of flightless paleognaths using a large-scale molecular dataset,” co-authored with JV Smith & RT Kimball, 126th Meeting of the American Ornithologists’ Union (joint with COS and SCO), Portland, OR.
- 82) *Talk*, “Phylogenomic evidence for multiple losses of flight in ratite birds,” co-authored with MJ Braun, J Harshman, CJ Huddleston, RCK Bowie, JL Chojnowski, S Hackett, K-L Han, RT Kimball, BD Marks, KJ Miglia, WS Moore, S Reddy, FH Sheldon, SJ Steppan, C Witt & T Yuri, 126th Meeting of the American Ornithologists’ Union (joint with COS and SCO), Portland, OR.

2007:

- 83) *Symposium talk**, “Phylogenomics and secondary plastids: A look back and a look ahead,” co-authored with N Phillips & D Bhattacharya, part of the “Borrowed Chloroplasts: Secondary Endosymbiosis and the Chromalveolates” symposium organized by N Phillips, D Bhattacharya & E Braun, Botany and Plant Biology 2007 Joint Congress, Chicago, IL.
- 84) *Symposium talk*, “Genomic insights into evolutionary relationships among Heterokont lineages,” co-authored with N Phillips, S Calhoun, A Moustafa & D Bhattacharya, part of the “Borrowed Chloroplasts: Secondary Endosymbiosis and the Chromalveolates” symposium organized by N Phillips, D Bhattacharya & E Braun, Botany and Plant Biology 2007 Joint Congress, Chicago, IL.
- 85) *Talk*, “Patterns of vertebrate isochore evolution revealed by comparison of expressed genes,” co-authored with JL Chojnowski, Evolution 2007, Christchurch, New Zealand.
- 86) *Talk*, “Phylogenomic evidence for multiple losses of flight in ratite birds,” co-authored with J Harshman, MJ Braun, RCK Bowie, J Chojnowski, S Hackett, K-L Han, CJ Huddleston, RT Kimball, BD Marks, KJ Miglia, WS Moore, S Reddy, FH Sheldon, DW Steadman, SJ Steppan, CC Witt, T Yuri, Association of Field Ornithologists Meeting, Orono, ME.
- 87) *Poster*, “The two AGPase subunits evolve at different rates in angiosperms, yet they are equally sensitive to activity-altering amino acid changes when expressed in bacteria,” co-authored with N Georgelis, JR Shaw & LC Hannah, Botany and Plant Biology 2007 Joint Congress, Chicago, IL.

2006:

- 88) *Seminar**, “Phylogenomic evidence for multiple losses of flight in the ratites,” Department of Biology, University of North Texas, Denton, TX.
- 89) *Talk**, “Analysis of deep avian phylogeny using alignment-free methods,” co-authored with R Kimball, S Hackett, M Braun, J Harshman, W Moore, F Sheldon, D Steadman, R Bowie, J Chojnowski, K-L Han, C Huddleston, B Marks, K Miglia, S Reddy, C Witt & T Yuri, Evolution 2006, Stony Brook, NY.
- 90) *Talk*, “Evolution of introns in galliform birds,” co-authored with RT Kimball, Evolution 2006, Stony Brook, NY.
- 91) *Talk*, “Assembling the Avian Tree of Life: Evaluating signal and conflict in a 19-gene dataset,” co-authored with S Reddy, S Hackett, R Kimball, M Braun, J Harshman, W Moore, F Sheldon, D Steadman, R Bowie, J Chojnowski, K-L Han, C Huddleston, B Marks, K Miglia, C Witt & T Yuri, Evolution 2006, Stony Brook, NY.
- 92) *Talk*, “Are raptorial birds each other’s closest relatives?” co-authored with MJ Braun, CJ Huddleston, K-L Han, S Hackett, J Harshman, R Bowie, R Kimball, J Chojnowski, B Marks, K Miglia, W Moore, S Reddy, F Sheldon, C Witt & T Yuri. North American Ornithological Congress, Veracruz, Mexico.
- 93) *Talk*, “Assembling the Avian Tree of Life: Examining signal and conflict in a 19 gene dataset,” co-authored with S Reddy, S Hackett, R Kimball, M Braun, R Bowie, K-L Han, J Harshman, C Huddleston, B Marks, K Miglia, WA Moore, FH Sheldon, D Steadman, C Witt & T Yuri. 24th International Ornithological Congress, Hamburg, Germany.
- 94) *Talk*, “Early Bird, an international collaboration in deep molecular phylogenetics of birds: can assault by masses of DNA sequences and sampled species breach the wall of death?” co-

authored with J Harshman, M Braun, R Bowie, S Hackett, K-L Han, C Huddleston, R Kimball, B Marks, K Miglia, WA Moore, S Reddy, FH Sheldon, D Steadman, C Witt & T Yuri. 24th International Ornithological Congress, Hamburg, Germany.

- 95) *Talk*, "The utility of introns and other non-coding DNA sequences for deep node phylogenetic inference," co-authored with MJ Braun, CJ Huddleston, K-L Han, T Yuri, S Hackett, J Harshman, R Bowie, S Reddy, R Kimball, J Chojnowski, W Moore, K Miglia, F Sheldon, B Marks & C Witt. 24th International Ornithological Congress, Hamburg, Germany.
- 96) *Talk*, "A molecular phylogeny of Galliformes: position of the New World Quail contradicts the Sibley-Ahlquist tapestry," co-authored with WA Cox & RT Kimball. Midwestern Ecology and Evolution Conference, St. Louis, MO.
- 97) *Poster*, "Preliminary annotation and phylogenomic characterization of the basal brown alga *Choristocarpus* EST library," co-authored with H-S Yoon, JL Chojnowski, NE Phillips & D Bhattacharya, Evolution 2006, Stony Brook, NY.
- 98) *Poster*, "Conservation and molecular evolution of 3' untranslated regions in birds," co-authored with AJ Bonilla & Kimball, RT. SICB Annual Meeting 2006, Orlando, FL.
- 99) *Poster*, "Phylogenomic analyses of gene duplication in holostean fish," co-authored with MN Burch, B Moore & LJ Guillette. SICB Annual Meeting 2006, Orlando, FL.
- 100) *Poster*, "Molecular evolution of non-canonical introns in the class Aves," co-authored with VR Heimer-Torres & Kimball, RT. SICB Annual Meeting 2006, Orlando, FL.
- 101) *Poster*, "Resolving the phylogeny of paleognathes: A novel genomic approach," co-authored with JV Smith & Kimball, RT. SICB Annual Meeting 2006, Orlando, FL.

2005:

- 102) *Seminar**, "Early Bird and beyond: Large-scale phylogeny of birds (and other organisms)," The Institute for Genomic Research (TIGR), Rockville, MD.
- 103) *Seminar**, "Avian phylogenomics: Early results from the Early Bird consortium," Department of Organismic and Evolutionary Biology, Harvard University, Boston, MA.
- 104) *Talk*, "Molecular evolutionary properties of gene regions used in the Early Bird project," co-authored with R Kimball, S Hackett, M Braun, J Harshman, W Moore, F Sheldon, D Steadman, R Bowie, J Chojnowski, K-L Han, C Huddleston, B Marks, K Miglia, S Reddy, C Witt & T Yuri, 123rd Meeting of the American Ornithologists' Union. Santa Barbara, CA.
- 105) *Talk*, "Phylogenetic relationships within the Galliformes inferred from sequences of 14 nuclear loci," co-authored with RT Kimball, B Burkley & A Cox, 123rd Meeting of the American Ornithologists' Union. Santa Barbara, CA.
- 106) *Poster*, "Getting to grips with raptors and other flighty birds," co-authored with G Gibb, O Kardailsky & D Penny, Society for Molecular Biology and Evolution conference, Auckland, New Zealand.
- 107) *Poster**, "Evolutionary Genomics of the Archosauria: Initial Results from the "Early Bird" and Alligator Genome Projects," co-authored with members of the Early Bird consortium and the Alligator Genome working group, Evolutionary Genomics Conference, Tucson, AZ.

2004:

- 108) *Talk**, "Early Bird: A large-scale approach to avian phylogeny," co-authored with S Hackett, RT Kimball, MJ Braun, J Harshman, WA Moore, FJ Sheldon, D Steadman, RCK Bowie, J Chojnowski, K-L Han, C Huddleston, BD Marks, KJ Miglia S Reddy & T Yuri, Evolution 2004, Fort Collins, CO.
- 109) *Talk*, "What, if anything, is a ratite?" co-authored with J Harshman, S Hackett, MJ Braun, RCK Bowie, K-L Han, C Huddleston, T Yuri, RT Kimball, BD Marks, FJ Sheldon, KJ Miglia, WA Moore & D Steadman, Evolution 2004, Fort Collins, CO.
- 110) *Poster*, "Phylogenomic analyses of the MYB transcription factors: What are the prospects for reconstructing ancient events?" co-authored with E Grotewold, Evolution 2004, Fort Collins, CO.

- 111) *Poster*, "A comparison of paralogous *clathrin heavy chain* genes in avian phylogenetics," co-authored with J Chojnowski & RT Kimball, Evolution 2004, Fort Collins, CO.
- 112) *Poster*, "Early Bird: Comparative study of nucleotide substitutions in introns, exons and UTRs in avian orders," co-authored with K Miglia, T Yuri, W Moore, RCK Bowie, MJ Braun, SJ Hackett, K-L Han, J Harshman, C Huddleston, RT Kimball, BD Marks, FJ Sheldon & D Steadman, Evolution 2004, Fort Collins, CO.
- 113) *Talk**, "The evolutionary history of the protein subunit of RNase P in prokaryotes provides insights into the transition from the RNA World," Bioastronomy 2004: Habitable Worlds (8th International Conference of Bioastronomy), Reykjavik, Iceland.
- 114) *Talk*, "Early Bird: Early results," co-authored with J Harshman, MJ Braun, RCK Bowie, SJ Hackett, K-L Han, C Huddleston, RT Kimball, BD Marks, KJ Miglia, WA Moore, FJ Sheldon, D Steadman, & T Yuri, 122nd Meeting of the American Ornithologists' Union. Québec City, QC, Canada.
- 115) *Seminar**, "Using evolutionary models to reconstruct and deconstruct the last universal common ancestor of life," University of Florida Genetics Institute, Gainesville, FL.
- 2003:**
- 116) *Seminar**, "Innovation from reduction: Loss and divergence in genome evolution," Department of Biochemistry, Ohio State University, Columbus, OH.
- 117) *Talk**, "The *Alligator* expressed genome project (AEGP) at the University of Florida: Steps toward the genomics of reptiles," Ecotoxicogenomics symposium, Okazaki, Japan.
- 118) *Talk**, "A genomic view of polytomies in species trees: A case study in the Avian genus *Gallus*," co-authored with R T Kimball, Evolution 2003, Chico, CA.
- 119) *Talk*, "Evolution of ornamentation in the Phasianidae: Implications from molecular phylogenetics," co-authored with R T Kimball, Evolution 2003, Chico, CA.
- 120) *Talk*, "Early Bird: A collaborative project to resolve the deep nodes of avian phylogeny," co-authored with S Hackett, M Braun, J Harshman, R Kimball, W Moore, F Sheldon, D Steadman, R Bowie, T Chesser, J Chojnowski, L Christidis, M Krosby, B Marks, K Miglia, R Page & T Yuri, 121st Meeting of the American Ornithologists' Union. Champaign-Urbana, IL.
- 2002:**
- 121) *Talk**, "The role of evolutionary model complexity and taxon sampling upon avian phylogenetic estimation," co-authored with RT Kimball, 23rd International Ornithological Congress, Beijing, China.
- 122) *Talk*, "Using molecular phylogenetics to understand evolutionary changes in morphology and behavior in the Phasianidae," co-authored with RT Kimball, JD Ligon, E Randi & V Lucchini, 23rd International Ornithological Congress, Beijing, China.
- 123) *Talk*, "Phylogeny of the Galliformes," co-authored with TM Crowe, P Bloomer, E Randi, V Lucchini, RT Kimball, & JG Groth, 23rd International Ornithological Congress, Beijing, China.
- 2001:**
- 124) *Seminar**, "Patterns of gene loss and domain loss: Insights from Evolutionary Genomics," Department of Botany, University of Florida, Gainesville, FL.
- 125) *Talk**, "Investigating the evolution of novel regulatory functions in plants," co-authored with A Dias & E Grotewold, Maize Genetics Conference, Lake Geneva, WI.
- 2000:**
- 126) *Seminar**, "Patterns of gene loss and domain loss: Insights from evolutionary genomics," Department of Zoology, University of Florida, Gainesville, FL.
- 127) *Talk**, "Uncovering complex patterns of evolution for genes encoding Myb-domain proteins," co-authored with A Dias & E Grotewold, Maize Genetics Conference, Coeur d'Alene, ID.
- 128) *Talk**, "Regulation of flavonoid metabolism by *MYB* genes," co-authored with AP Dias, TJ Matulnik, JM Hernandez & E Grotewold, Plant Molecular Biology Conference, Beltsville, MD.

- 129) *Talk**, “Examining the complex patterns of evolutionary rate variation for the *MYB* transcription factor gene family,” co-authored with E Grotewold, *Evolution* 2000, Bloomington, IN.
- 130) *Talk*, “Evolutionary relationships of galliform birds: A review of data from fossils, molecules and organisms *OR* What kind of fowl am I?” co-authored with TM Crowe, E Randi, RT Kimball, V Lucchini, J Groth & P Bloomer, *Evolution* 2000, Bloomington, IN.
- 131) *Talk*, “Comparison of nuclear intron and mitochondrial phylogenies in the avian order Galliformes,” co-authored with RT Kimball, *Evolution* 2000, Bloomington, IN.

1999:

- 132) *Seminar**, “pc-Myb: An ancient Myb protein for ancient functions?” Department of Plant Biology, Ohio State University, Columbus, OH.
- 133) *Seminar**, “Evolution and function of plant *Myb* genes,” Ohio Agriculture Research and Development Center, Wooster, OH.
- 134) *Talk**, “The maize *R2R3 Myb* gene family,” co-authored with PD Rabinowicz & E Grotewold, Maize Genetics Conference, Lake Geneva, WI.
- 135) *Poster**, “Evolution of the *Myb* gene family in plants,” co-authored with E Grotewold, *Evolution* '99, Madison, WI.

1998:

- 136) *Seminar**, “The evolution of gene families: Exploring the diversity of *Myb* genes in plants.” Department of Zoology and Genetics, Iowa State University, Ames, IA.
- 137) *Seminar**, “Comparative genomics and the *Neurospora* genome project.” Department of Plant Biology, Columbus, OH.
- 138) *Seminar**, “The *Neurospora* genome project: Molecular evolution and comparative genomics.” Laboratory of Molecular Systematics, National Museum of Natural History, Suitland, MD.
- 139) *Seminar**, “Comparative genomics for *Neurospora crassa*.” Department of Molecular Genetics and Microbiology, University of New Mexico School of Medicine (presented with AL Halpern)

Additional scholarly works (not peer-reviewed)

A total of 41 published scholarly works of various types that typically do not undergo full peer-review. This list includes some works that undergo editorial review (e.g., papers for public outreach) and works that have a direct association with peer-reviewed publications (e.g., data packages).

1. **Preprint:** Pandey, A & **EL Braun**. 2018. Why do phylogenomic analyses of early animal evolution continue to disagree? Sites in different structural environments yield different answers. *bioRxiv* <https://doi.org/10.1101/400465> (Altmetric 34; top 5%) (currently in review at *Molecular Biology and Evolution*).
2. **Data Package:** Braun, EL. 2018. Data for: Resolving the avian tree of life from top to bottom: The promise and potential boundaries of the phylogenomic era (Version 1.0) [Data set]. Zenodo. <http://doi.org/10.5281/zenodo.1419827> (for a manuscript to be submitted to *Avian Genomics in Ecology and Evolution - From the lab into the wild*).
3. **Data Package:** Pandey, A & **EL Braun**. (2018). Data for: Why do phylogenomic analyses of early animal evolution continue to disagree? Sites in different structural environments yield different answers (Version 1.0.0) [Data set]. Zenodo. <http://doi.org/10.5281/zenodo.1403225> (for the manuscript currently available from *bioRxiv* and submitted to *Molecular Biology and Evolution*).
4. **Data Package:** Reddy, S, R Kimball, A Pandey, P Hosner, M Braun, S Hackett, K Han, J Harshman, C Huddleston, S Kingston, B Marks, K Miglia, W Moore, F Sheldon, C Witt, T Yuri & **E Braun**. 2017. Data from: Why do phylogenomic data sets yield conflicting trees?

- data type influences the avian tree of life more than taxon sampling. Dryad Digital Repository, for a publication in *Systematic Biology*. <http://dx.doi.org/10.5061/dryad.6536v>
5. **Software:** Pandey, A & **EL Braun**. 2017. Extract-seq software pipeline, available from https://github.com/aakanksha12/Extract_seq, used for analyses in “Why do phylogenomic data sets yield conflicting trees? data type influences the avian tree of life more than taxon sampling,” used in Reddy et al. 2017, *Systematic Biology*.
 6. **Mitogenome announcement:** Eimanifar, A, RT Kimball, **EL Braun** & JD Ellis. 2016. The complete mitochondrial genome of the hybrid honey bee, *Apis mellifera capensis* × *Apis mellifera scutellata*, from South Africa. *Mitochondrial DNA Part B*. 1:1, 856-857, DOI: 10.1080/23802359.2016.1250132.
 7. **Mitogenome announcement:** Eimanifar, A, RT Kimball, **EL Braun** & JD Ellis. 2016. The complete mitochondrial genome of the Cape honey bee, *Apis mellifera capensis* Esch. (Insecta: Hymenoptera: Apidae), *Mitochondrial DNA Part B*, 1:1, 817-819, DOI: 10.1080/23802359.2016.1241682.
 8. **Data Package:** Ascunce, MS, JC Hugueta-Tapia, **EL Braun**, A Ortiz-Urquiza, NO Keyhani & EM Goss. 2016. Whole genome sequence of the emerging oomycete pathogen *Pythium insidiosum* strain CDC-B5653 isolated from an infected human in the USA. *Genomics Data*, 7:60-61. doi:10.1016/j.gdata.2015.11.019 <http://dx.doi.org/10.1016/j.gdata.2015.11.019>
 9. **Data Package and Software:** Meiklejohn, KA, BC Faircloth, TC Glenn, RT Kimball & EL Braun. 2016. Data from: Analysis of a rapid evolutionary radiation using ultraconserved elements (UCEs): Evidence for a bias in some multi-species coalescent methods. Dryad Digital Repository. <http://dx.doi.org/10.5061/dryad.p1m52>; includes Braun, EL. 2016. SMRT-raxMRP.pl, software for supermatrix rooted triples analysis.
 10. **Meeting Abstract:** Goss, E, M Ascunce, J Hugueta-Tapia, **E Braun**, A Ortiz-Urquiza & N Keyhani. Phylogenomic analysis supports polyphyly in *Pythium sensu lato*. *Phytopathology*, **106**: S4.143.
 11. **Meeting Abstract:** Glenn, TC, BC Faircloth, JE McCormack, DA Ray, **EL Braun** & RE Green. 2015. Ultraconserved elements provide orthologous portals into tetrapod genomes illuminating the remarkably slow evolution of crocodylian genomes. *Integrative and Comparative Biology*, **55**: E67.
 12. **Meeting Abstract:** Wright, JE, A Kumar, JG Burleigh, **EL Braun** & RT Kimball. 2015. Unexpected olfactory receptor gene numbers revealed in two cathartid species that demonstrate discrete sensory system reliance during foraging. *Integrative and Comparative Biology*, **55**: E67.
 13. **Data Package:** Burleigh, JG, RT Kimball & EL Braun. 2014. Data from: Building the avian tree of life using a large-scale, sparse supermatrix. Dryad Digital Repository, for a publication in *Molecular Phylogenetics and Evolution*, <http://dx.doi.org/10.5061/dryad.r6b87>
 14. **Meeting Poster:** Kumar, A, **EL Braun** & RT Kimball. 2014. Adaptive evolution of Cep63-CEF152 centrosome microcephaly ring in association with brain size shift in mammals. Presented at the 2014 ISCB student council symposium at the 22nd annual International Conference on Intelligent Systems for Molecular Biology held in Boston, MA, available from <http://f1000research.com/posters/1096500>
 15. **Data Package:** Sun, K, KA Meiklejohn, BC Faircloth, TC Glenn, EL Braun & RT Kimball. 2014. Data from: The evolution of peafowl and other taxa with ocelli (eyespot): a phylogenomic approach. Dryad Digital Repository, for a publication in *Proceedings of the Royal Society B: Biological Sciences*, <http://dx.doi.org/10.5061/dryad.66942>
 16. **Preprint:** Kimball, RT & **EL Braun**. 2013. Does more sequence data improve estimates of galliform phylogeny? Analyses of a rapid radiation using a complete data matrix. PeerJ PrePrints, 1:e131v1 (available from <http://dx.doi.org/10.7287/peerj.preprints.131v1>; now published after peer-review)
 17. **Community Dialog:** Castoe, TA, **EL Braun**, AM Bronikowski, CL Cox, AR Davis Rabosky,

- APJ de Koning, J Dobry, MK Fujita, MW Giorgianni, A Hargreaves, CV. Henkel, SP Mackessy, D O'Meally, DR Rokyta, SM Secor, JW Streicher, KP Wray, KD Yokoyama & DD Pollock. 2012. Report from the first Snake Genomics and Integrative Biology meeting. *Standards in Genomic Sciences* 7:1.
18. **Data Package:** Ponciano, JM, JG Burleigh, **EL Braun** & M Taper. 2012. Data from: Assessing parameter identifiability in phylogenetic models using Data Cloning. Dryad Digital Repository, for a publication in *Systematic Biology*, <http://dx.doi.org/10.5061/dryad.rr6400b4>
 19. **Data Package:** Smith, JV, **EL Braun** & RT Kimball. 2012. Data from: Ratite non-monophyly: independent evidence from 40 novel loci. For paper published in *Systematic Biology*, <http://dx.doi.org/10.5061/dryad.5vd2560f>
 20. **Meeting Abstract:** Dankwa, M, G Han, L Andersen, L Niko, N Phillips & **EL Braun**. 2011. Data mining and locus discover methods in the brown algae (Phaeophyceae). *Journal of Phycology*, **47**(Supplement 2):S28-S29.
 21. **Meeting Abstract:** Phillips, N, D Kapraun, D, AG Garreta, AR Siguan, JL Rull, NS Soler, **E Braun**, R Lewis, H Kawai. 2011. Sizing the heterokont: Phaeopycean genome. *Journal of Phycology*, **47**(Supplement 1):52.
 22. **Article for Public Outreach:** **Braun, EL** & RT Kimball. 2010. Early Bird — The Bird Tree of Life. *American Paleontologist*, **18**(number 3): 11-12. Part of the “Why Study the Tree of Life? — The Scientists Speak” feature in the Fall 2010 issue edited by Paula Mikkelsen.
 23. **Meeting Abstract:** Zhu, J, S Kohno S, M Antenos, **EL Braun**, E Xu, J Lin, B Moore, LJ Guillette Jr, T Jardezky & T Woodruff. 2009. Phylogenomic analysis of a powerful and unique TGF-beta superfamily antagonist: Evolution of the inhibin alpha-subunit structural regions that regulate function. *Biology of Reproduction*, **81**(1 Supplement):148.
 24. **Meeting Abstract:** Chojnowski, JL & **EL Braun**. 2009. Candidate genes in a turtle with temperature-dependent sex determination. *Integrative and Comparative Biology*, **49**:E212.
 25. **United States Patent:** Grotewold, E, AP Dias & **EL Braun**. 2009. Transgenic plants with altered levels of phenolic compounds. Patent number 7,592,506 B2, issued 22 Sept 2009.
 26. **United States Patent Application Publication:** Grotewold, E, AP Dias & **EL Braun**. 2008. Transgenic plants with altered levels of phenolic compounds. Publication number US 2008/0235829, published 25 Sept 2008.
 27. **Meeting Abstract:** Harshman, J, **EL Braun**, MJ Braun, SJ Hackett, K-L Han, CJ Huddleston, RT Kimball, BD Marks, KJ Miglia, WA Moore, S Reddy, FH Sheldon, D Steadman, T Yuri & C Witt. 2006. Early Bird, an international collaboration in deep molecular phylogenetics of birds: Can four million bases resolve the tree? *Journal of Ornithology*, **147**:42. (cited twice in Science Citation Index and Google Scholar)
 28. **Meeting Abstract:** Bonilla, AJ, RT Kimball & **EL Braun**. 2005. Conservation and molecular evolution of 3' untranslated regions in birds. *Integrative and Comparative Biology*, **45**:1112.
 29. **Meeting Abstract:** Burch, MN, B Moore, LJ Guillette & **EL Braun**. 2005. Phylogenomic analyses of gene duplication in holostean fish. *Integrative and Comparative Biology*, **45**:1114.
 30. **Meeting Abstract:** Heimer-Torres, VR, **EL Braun**, RT Kimball. 2005. Molecular evolution of non-canonical introns in the class Aves. *Integrative and Comparative Biology*, **45**:1143.
 31. **Meeting Abstract:** Smith, JV, RT Kimball & **EL Braun**. 2005. Resolving the phylogeny of paleognathes: A novel genomic approach. *Integrative and Comparative Biology*, **45**:1196.
 32. **Meeting Abstract:** **Braun, EL**, M Jovanovic & V Gopalan. 2004. The evolutionary history of the protein subunit of RNase P in prokaryotes provides insights into the transition from the RNA world. *Astrobiology*, **4**:241 (Bioastronomy 2004 Abstract 26B).
 33. **Meeting Abstract:** Dias, A, **EL Braun**, MD McMullen & E Grotewold. 2002. Duplication and functional divergence of *R2R3 Myb* regulatory genes in the grasses. *Maize Genetics Conference Abstracts*, **44**: T9.
 34. **Meeting Abstract:** **Braun, EL**, A Dias & E Grotewold. 2000. Uncovering complex patterns

- of evolution for genes encoding Myb-domain proteins. *Maize Genetics Conference Abstracts*, **42**: T20.
35. **International Patent Application:** Werner-Washburne, M, P Padilla, E Fuge & **EL Braun**. 2000. Detection using Snz and Sno genes and proteins. Patent number WO/2000/022169, published 20 April 2000.
 36. **Professional Newsletter:** **Braun, EL** & E Grotewold. 1999. Diversification of the *R2R3 Myb* gene family and the segmental allotetraploid origin of the maize genome. *Maize Genetics Cooperation Newsletter*, **73**: 26-27 (cited 7 times in Google Scholar; available online from <http://www.maizegdb.org/mnl/73/47braun.html>)
 37. **Meeting Abstract:** **Braun, EL**, P Rabinowicz & E Grotewold. 1999. The maize *R2R3 Myb* gene family. *Maize Genetics Conference Abstracts*, 41: T43.
 38. **Meeting Abstract:** Padilla, PA, EK Fuge, **EL Braun**, SR Atencio, M Werner-Washburne. 1995. Identification of a highly conserved novel gene family in *Saccharomyces cerevisiae*. *Molecular Biology of the Cell*, supplement to volume **6**: 1785.
 39. **Meeting Abstract:** Werner-Washburne, M, DR Caprioglio, **E Braun**, BL Butler, PO Doherty, C Padilla, ME Crawford, H Yazzie, VM Peck. 1993. Characterization of entry into stationary phase in the yeast *Saccharomyces cerevisiae*. *Journal of Cellular Biochemistry* **17C**: 144.
 40. **Meeting Abstract:** **Braun, EL**, BL Butler & M Werner-Washburne. 1992. Gene expression during stationary phase in yeast. *Molecular Biology of the Cell*, supplement to volume **3**: A246.
 41. **Meeting Abstract:** Caprioglio, DE, R Maldonado, **E Braun** & M Werner-Washburne. 1990. Isolation and characterization of yeast mutants constitutive for transcription from a stationary phase promoter *SSA3*. *Journal of Cell Biology*, **11** (issue 5 part 2): 353A.

Publications in progress (submitted, in revision, and in preparation)

Complete and nearly-complete manuscripts.

1. Ryder, TB, C Alfonso, CN Balakrishnan, J Barske, M Bosholn, WA Boyle, **EL Braun**, I Chiver, R Dakin, L Day, R Driver, L Fusani, B Horton, RT Kimball, S Lipshutz, C Mello, MC Miles, E Miller, I Moore, G Cardenas-Posada, BA Schlinger, B Vernasco, M Webster, M Wirthlin & MJ Fuxjager. *Submitted to Behavioral Ecology*. Physiological regulatory networks and the evolution of the integrated behavioral phenotype
2. Houde, P, **EL Braun** & S Mirarab. *In preparation*. Species tree analyses of the avian species tree using indels (insertions and deletions) and sequence data reveals congruence and conflicts.
3. Kimball, RT, CH Oliveros, N Wang, ND White, FK Barker, DJ Field, DT Ksepka, MJ Braun, RT Chesser, RG Moyle, RT Brumfield, BC Faircloth, BT Smith & **EL Braun**. *In preparation*. Sequence capture: the key to the phylogenomic (super) tree of birds (and other organisms). (manuscript invited by the journal *Diversity*).
4. Ksepka, DT, AM Balanoff, NA Smith, GS Bever, B-AS Bhullar, E Bourdon, **EL Braun**, G Burleigh, JA Clarke, MW Colbert, JR Corfield, FJ Degrange, VL De Pietri, CM Early, DJ Field, PM Gignac, MEL Gold, ED Jarvis, RT Kimball, S Kawabe, L Lefebvre, J Marugán-Lobón, A Morhardt, MA Norell, RC Ridgely Paul Scofield, CP Tambussi, CR Torres, M van Tuinen, SA Walsh, A Watanabe, LM Witmer, AK Wright, LE Zanno, & JB Smaers. *In preparation*. Tempo and pattern of avian brain size evolution.
5. Kumar, A, RT Kimball & **EL Braun**. *In preparation*. Tracing the molecular signals underlying brain size evolution in eutherian mammals.
6. Leite, RN, RT Kimball, **EL Braun**, EP Derryberry, PA Hosner, GE Derryberry, M Anciães, J McKay, D Meyer, A Aleixo, CC Ribas, RT Brumfield, J Cracraft. *In preparation*. Exploring locus filtering strategies brings light to the phylogenomics of neotropical manakins (Aves: Pipridae).

