

# Daniel A. Skelly

## Curriculum vitae

The Jackson Laboratory  
600 Main Street  
Bar Harbor, ME 04609  
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### EDUCATION

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- 2012                      Ph.D., Genome Sciences  
University of Washington, Seattle, WA  
Advisor: Joshua M. Akey  
Thesis: *Patterns and determinants of variation in functional genomics phenotypes in the yeast Saccharomyces cerevisiae*
- 2005                      Bachelor of Science, Zoology (with honors)  
University of Wisconsin, Madison, WI

### RESEARCH EXPERIENCE

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- 2021–current            Senior computational scientist  
2018–2021              Research scientist  
2016–2018              Associate research scientist  
The Jackson Laboratory, Bar Harbor, ME
- 2014–2016              Postdoctoral scholar  
2013–2014              Postdoctoral associate  
Laboratory of Paul M. Magwene  
Department of Biology  
Duke University, Durham, NC
- 2013                      Postdoctoral fellow  
2007–2012              Graduate student  
Laboratory of Joshua M. Akey  
Department of Genome Sciences  
University of Washington, Seattle, WA
- 2005–2007              Research assistant

- 2003–2005 Undergraduate research assistant  
Laboratory of Carol E. Lee  
Department of Zoology  
University of Wisconsin, Madison, WI
- 2003 NSF Research Experience for Undergraduates summer fellow  
Laboratory of Maria I. Klapa  
Department of Chemical Engineering  
University of Maryland, College Park, MD

## PREPRINTS & PUBLICATIONS

[Google Scholar profile](#)

30. Kuffler L, **Skelly DA**, Czechanski A, Munger SC, Baker CL, Reinholdt LG, Carter GW (2022) Imputation of 3D genome structure by genetic-epigenetic interaction modeling in mice. [bioRxiv link](#)
29. Aydin S, Pham DT, Zhang T, Keele GR, **Skelly DA**, Pankratz M, Choi T, Gygi S, Reinholdt LG, Baker CL, Churchill GA, Munger SC (2022) Genetic dissection of the pluripotent proteome through multi-omics data integration. [bioRxiv link](#)
28. Takemon Y, Chick JM, **Skelly DA**, Devuyst O, Gygi SP, Churchill GA, Korstanje R (2021) Proteomic and transcriptomic profiling reveal different aspects of aging in the kidney. *eLife* 10:e62585. doi: [10.7554/eLife.62585](#)
27. Forte E, Mclellan M, **Skelly DA**, Rosenthal NA (2021) *Ex uno, plures*—From one tissue to many cells: A review of single-cell transcriptomics in cardiovascular biology. *International Journal of Molecular Sciences* 22(4):2071. doi: [10.3390/ijms22042071](#)
26. Yang HS, Onos KD, Choi K, Keezer KJ, **Skelly DA**, Carter GW, Howell GR (2021) Natural genetic variation determines microglia heterogeneity in wild-derived mouse models of Alzheimer’s disease. *Cell Reports* 34:108739. doi: [10.1016/j.celrep.2021.108739](#)
25. Forte E, Perkins B, Sintou A, Kalkat HS, Papanikolaou A, Jenkins C, Alsubaie M, Chowdhury RA, Duffy TM, **Skelly DA**, Branca J, Bellahcene M, Schneider MD, Harding SE, Furtado MB, Ng FS, Rosenthal N, Hasham MG, Sattler S (2021) Cross-priming dendritic cells exacerbate immunopathology after ischemic tissue damage in the heart *Circulation* 143:821-836. doi: [10.1161/CIRCULATIONAHA.120.044581](#)
24. Byers C, Spruce C, Fortin HJ, Hartig EI, Czechanski A, Munger SC, Reinholdt LG, **Skelly DA**, Baker CL (2022) Genetic control of pluripotency epigenome

- determines differentiation bias in mouse embryonic stem cells *EMBO J* 41(2):e109445. doi: [10.15252/embj.2021109445](https://doi.org/10.15252/embj.2021109445)
23. **Skelly DA**, Czechanski A, Byers C, Aydin S, Spruce C, Olivier C, Choi K, Gatti DM, Raghupathy NM, Stanton A, Vincent M, Dion S, Greenstein I, Pankratz M, Porter DK, Martin W, Qin W, Harrill AH, Choi T, Churchill GA, Munger SC, Baker CL, Reinholdt LG (2020) Mapping the effects of genetic variation on chromatin state and gene expression reveals loci that control ground state pluripotency. *Cell Stem Cell* 27(3):13. doi: [10.1016/j.stem.2020.07.005](https://doi.org/10.1016/j.stem.2020.07.005)
  22. McLellan MA\* **Skelly DA\***, Dona MSI, Squiers GT, Farrugia GE, Gaynor TL, Cohen CD, Pandey R, Diep H, Vin A, Rosenthal NA, Pinto AR (2020) High-resolution transcriptomic profiling of the heart during chronic stress reveals cellular drivers of cardiac fibrosis and hypertrophy. *Circulation* 142(15):1448–1463. doi: [10.1161/CIRCULATIONAHA.119.045115](https://doi.org/10.1161/CIRCULATIONAHA.119.045115) (\*equal contribution)
  21. Forte E, **Skelly DA**, Chen M, Daigle S, Morelli KA, Hon O, Philip VM, Costa MW, Rosenthal NA, Furtado MB (2020) Dynamic interstitial cell response during myocardial infarction predicts resilience to rupture in diverse mice. *Cell Reports* 30(9):3149-3163. doi: [10.1016/j.celrep.2020.02.008](https://doi.org/10.1016/j.celrep.2020.02.008)
  20. Choi K, Chen Y, **Skelly DA**, Churchill GA (2020) Bayesian model selection reveals biological origins of zero inflation in single-cell transcriptomics. *Genome Biology* 21(1):183. doi: [10.1186/s13059-020-02103-2](https://doi.org/10.1186/s13059-020-02103-2)
  19. Hosur V, **Skelly DA**, Francis C, Low BE, Kohar V, Burzenski LM, Amiji MA, Shultz LD, Wiles MV (2020) Improved mouse models and advanced genetic and genomic technologies for the study of neutrophils. *Drug Discovery Today* 25(6):1013-1025. doi: [10.1016/j.drudis.2020.03.018](https://doi.org/10.1016/j.drudis.2020.03.018)
  18. Ortmann D, Brown S, Czechanski A, Aydin S, Muraro D, Huang Y, Tomaz RA, Osnato A, Canu G, Wesley BT, **Skelly DA**, Stegle O, Choi T, Churchill GA, Baker CL, Rugg-Gunn PJ, Munger SC, Reinholdt LG, Vallier L (2020) Naive pluripotent stem cells exhibit phenotypic variability that is driven by genetic variation *Cell Stem Cell* 27(3):1-12. doi: [10.1016/j.stem.2020.07.019](https://doi.org/10.1016/j.stem.2020.07.019)
  17. Bouvet M, Claude O, Roux M, **Skelly DA**, Masurkar N, Mougnot N, Nadaud S, Blanc C, Delacroix C, Chardonnet S, Pionneau C, Perret C, Yaniz-Galende E, Rosenthal NA, Trégouët D-A, Marazzi G, Silvestre J-S, Sassooun D, Hulot J-S (2020) Anti-integrin  $\alpha_V$  therapy improves cardiac fibrosis after myocardial infarction by blunting cardiac PW1<sup>+</sup> stromal cells. *Scientific Reports* 10:11404. doi: [10.1038/s41598-020-68223-8](https://doi.org/10.1038/s41598-020-68223-8)
  16. **Skelly DA**, Raghupathy N, Robledo RF, Graber JH, Chesler EJ (2019) Reference trait analysis reveals correlations between gene expression and quantitative traits in disjoint samples. *Genetics* 212(3):919-929. doi: [10.1534/genetics](https://doi.org/10.1534/genetics)

[netics.118.301865](https://doi.org/10.1101/185538)

15. **Skelly DA**, Squiers GT, McLellan MA, Bolisetty MT, Robson P, Rosenthal NA, Pinto AR (2018) Single cell transcriptional profiling reveals cellular diversity and intercommunication in the mouse heart. *Cell Reports* 22(3):600-610. doi: [10.1016/j.celrep.2017.12.072](https://doi.org/10.1016/j.celrep.2017.12.072)
14. Bogue MA, Grubb SC, Walton DO, Philip VM, Kolishovski G, Stearns T, Dunn MH, **Skelly DA**, Kadakkuzha B, TeHennepe G, Kunde-Ramamoorthy G, Chesler EJ (2018) Mouse Phenome Database: an integrative database and analysis suite for curated empirical phenotype data from laboratory mice. *Nucleic Acids Research* 46(D1):D843. doi: [10.1093/nar/gkx1082](https://doi.org/10.1093/nar/gkx1082)
13. Vijayraghavan S, Kozmin SG, Strobe PK, **Skelly DA**, Lin Z, Kennell J, Magwene PM, Dietrich FS, McCusker JH (2018) Mitochondrial genome variation affects multiple respiration and non-respiration phenotypes in *Saccharomyces cerevisiae*. *Genetics* doi: [10.1534/genetics.118.301546](https://doi.org/10.1534/genetics.118.301546)
12. **Skelly DA**, Magwene PM, Meeks B, Murphy HA. Known mutator alleles do not markedly increase mutation rate in clinical *Saccharomyces cerevisiae* strains (2017) *Proceedings of the Royal Society B: Biological Sciences* 284 (1852): 20162672. doi: [10.1098/rspb.2016.2672](https://doi.org/10.1098/rspb.2016.2672)
11. **Skelly DA**, McCusker JH, Stone EA, Magene PM (2017) Private haplotype barcoding facilitates inexpensive high-resolution genotyping of multiparent crosses. [bioRxiv](https://doi.org/10.1101/185538)
10. **Skelly DA**, Magwene PM, Stone EA (2016) Sporadic, global linkage disequilibrium between unlinked segregating sites. *Genetics* 202(2):427-437. doi: [10.1534/genetics.115.177816](https://doi.org/10.1534/genetics.115.177816)
9. **Skelly DA**, Magwene PM (2016) Population perspectives on functional genomic variation in yeast. *Briefings in Functional Genomics* 15(2):138-146. doi: [10.1093/bfgp/elv044](https://doi.org/10.1093/bfgp/elv044)
8. Strobe PK, Kozmin SG, **Skelly DA**, Dietrich FS, Magwene PM, McCusker JH (2015)  $2\mu$  plasmid in *Saccharomyces* species and in *Saccharomyces cerevisiae*. *FEMS Yeast Research* 15(8):fov090. doi: [10.1093/femsyr/fov090](https://doi.org/10.1093/femsyr/fov090)
7. Strobe PK, **Skelly DA**, Kozmin SG, Mahadevan G, Stone EA, Magwene PM, Dietrich FS, McCusker JH (2015) The 100-genomes strains, an *S. cerevisiae* resource that illuminates its natural phenotypic and genotypic variation and emergence as an opportunistic pathogen. *Genome Research* 25(5):762-74. doi: [10.1101/gr.185538.114](https://doi.org/10.1101/gr.185538.114)
6. **Skelly DA**, Merrihew GE, Riffle M, Connelly CF, Kerr OK, Johansson M, Jaschob J, Graczyk B, Shulman N, Wakefield J, Cooper SJ, Fields S, No-

- ble WS, Muller EGD, Davis T, Dunham MJ, MacCoss MJ, Akey JM (2013) Integrative phenomics reveals insight into the structure of phenotypic diversity in budding yeast. *Genome Research* 23(9):1496-1504. doi: [10.1101/gr.155762.113](https://doi.org/10.1101/gr.155762.113)
5. Connelly CF, **Skelly DA**, Dunham MJ, Akey JM (2013) Population genomics and transcriptional consequences of regulatory motif variation in globally diverse *Saccharomyces cerevisiae* strains. *Molecular Biology and Evolution* 30(7):1605-1613. doi: [10.1093/molbev/mst073](https://doi.org/10.1093/molbev/mst073)
  4. **Skelly DA**, Johansson M, Madeoy J, Wakefield J, Akey JM (2011) A powerful and flexible statistical framework for testing hypotheses of allele-specific gene expression from RNA-seq data. *Genome Research* 21(10):1728-1737. doi: [10.1101/gr.119784.110](https://doi.org/10.1101/gr.119784.110)
  3. Dodson SI, **Skelly DA**, Lee CE (2010) Out of Alaska: morphological diversity within the genus *Eurytemora* from its ancestral Alaskan range (Crustacea, Copepoda). *Hydrobiologia* 653(1):131-148. doi: [10.1007/978-90-481-9908-2\\_11](https://doi.org/10.1007/978-90-481-9908-2_11)
  2. **Skelly DA**, Ronald J, Akey JM (2009) Inherited variation in gene expression. *Annual Review of Genomics and Human Genetics* 10:313-332. doi: [10.1146/annurev-genom-082908-150121](https://doi.org/10.1146/annurev-genom-082908-150121)
  1. **Skelly DA**, Ronald J, Connelly CF, Akey JM (2009) Population genomics of intron splicing in 38 *Saccharomyces cerevisiae* genome sequences. *Genome Biology and Evolution* 1:466-478. doi: [10.1093/gbe/evp046](https://doi.org/10.1093/gbe/evp046)

## FUNDING

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R21 AI145383

05/2019-04/2022

Source: National Institutes of Health, National Institute of Allergy and Infectious Diseases

Project Title: Using the Collaborative Cross to understand the impact of a high-fat diet on the adipose tissue invariant natural killer T cell compartment.

Total Budget: \$467,500

Role: **Principal Investigator**

F32 GM110997

05/2014-10/2016

Source: National Institutes of Health, National Institute of General Medical Sciences

Project Title: Functional variation in a conserved pathway influencing cellular differentiation.

*Total Budget:* \$134,725

*Role:* **Principal Investigator**

ASPIRE Award

10/2019-12/2022

*Source:* The Mark Foundation for Cancer Research

*Project Title:* Dissecting the genetic control of response to immune checkpoint inhibitors in cancer.

*Total Budget:* \$2,533,684

*Role:* **Co-Investigator**

## HONORS & AWARDS

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2013–2016	NIH NIGMS Ruth L. Kirschstein National Research Service Award (F32GM110997)
2015	Duke Center for Systems Biology travel award
2009	Best graduate student poster, Society for Molecular Biology and Evolution conference
2008	Summer Institute in Statistical Genetics, tuition scholarship
2008	Honorable mention, NSF graduate research fellowship
2005	Phi Beta Kappa
2001–2005	Dean's list, University of Wisconsin
2003	NSF Research Experience for Undergraduates, University of Maryland
2001	National Merit Scholar

## SERVICE

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	Professional service:
2019	Scientific reviewer, Genetic Variation and Evolution Study Section, NIGMS (Bethesda, MD)
ongoing	Peer reviewer for <i>Annals of Applied Statistics</i> , <i>Bioinformatics</i> , <i>BMC Genomics</i> , <i>Frontiers in Genetics</i> , <i>Genes and Development</i> , <i>Genetics</i> , <i>Molecular Biology and Evolution</i> , <i>Molecular Ecology Resources</i> , <i>Nucleic Acids Research</i> , <i>PLoS Genetics</i> , <i>PNAS</i>
	Mentoring:
2019–2020	Mentor, Alan Baez (University of Maine)
2015–2016	Mentor, Kushal Byatnal (Duke University)

2014–2016	Mentor, Rosa Yang (Duke University)
2009–2010	Mentor, Northwest Association for Biomedical Research
	Teaching:
2018	Lecturer 21st Century Mammalian Genetics The Jackson Laboratory, Bar Harbor, ME
2011	Graduate teaching assistant Genome informatics (Genome 373) University of Washington, Seattle, WA
2010	Graduate teaching assistant Introductory genetics (Genome 371) University of Washington, Seattle, WA

## PRESENTATIONS

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Graham JP, Walter A, Baez A, Branca J, Rosenthal NA, **Skelly DA** (2019) Diet-driven changes in immune regulation of adipose tissue revealed by single cell transcriptomics. International Mammalian Genome Society, Strasbourg, France (selected talk).

**Skelly DA**, Byers C, Czechanski A, Spruce C, Choi K, Gatti DM, Aydin S, Stanton A, Porter D, Choi T, Churchill GA, Munger SC, Baker CL, Reinholdt LG (2018) Genetic variation influences ground state pluripotency in mouse embryonic stem cells through a hierarchy of molecular phenotypes. International Mammalian Genome Society, San Juan, Puerto Rico (selected talk).

**Skelly DA**, Byers C, Czechanski A, Spruce C, Choi K, Gatti DM, Aydin S, Stanton A, Porter D, Choi T, Churchill GA, Munger SC, Baker CL, Reinholdt LG (2018) Genetic variation influences ground state pluripotency in mouse embryonic stem cells through a hierarchy of molecular phenotypes. Poster presentation (Reviewers' Choice Award) at the American Society of Human Genetics Conference, San Diego, CA

**Skelly DA**, Raghupathy N, Choi K, Srivastava A, Churchill GA (2017) Widespread RNA splicing variation in Diversity Outbred mice. Complex Trait Community 15th Annual Meeting (selected talk).

**Skelly DA**, Aydin S, Vijayraghavan S, McCusker JH, Stone EA, Buchler NE, Magwene PM (2016) A powerful yeast mapping panel for complex trait genetics. The Allied Genetics Conference, Orlando, FL (selected talk).

**Skelly DA**, Raghupathy N, Choi K, Srivastava A, Churchill GA (2017) Widespread RNA splicing variation in Diversity Outbred mice. Poster presentation (Review-

ers' Choice Award) at the American Society of Human Genetics Conference, Orlando, FL.

**Skelly DA**, Strobe PK, Kozmin S, Dietrich FS, McCusker JH, Stone EA, Magwene PM (2015) Dissecting the genetic basis of phenotypic variation in budding yeast. Poster presentation at Gordon Research Conference in Microbial Population Biology, Andover, NH.

**Skelly DA**, Strobe PK, Kozmin S, Dietrich FS, McCusker JH, Stone EA, Magwene PM (2014) Small Eukaryotes Group seminar. North Carolina Biotechnology Center, Durham, NC.

**Skelly DA**, Strobe PK, Kozmin S, Dietrich FS, McCusker JH, Stone EA, Magwene PM (2014) Population Biology seminar. Duke University, Durham, NC.

**Skelly DA**, Strobe PK, Kozmin S, Dietrich FS, McCusker JH, Stone EA, Magwene PM (2014) Genomics of Microbial Systems seminar. Duke University, Durham, NC.

**Skelly DA**, Briceno M, Madeoy J, Connelly CF, Wakefield J, Akey JM (2010) Modeling allele-specific gene expression in yeast. Poster presentation at Society for Molecular Biology and Evolution conference, Lyon, France.

**Skelly DA**, Ronald J, Connelly CF, Akey JM (2009) Population genomics of intron splicing in *Saccharomyces cerevisiae*. Poster presentation (Best Poster Award) at Society for Molecular Biology and Evolution conference, Iowa City, IA.