Charles G. Danko, Ph.D.

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Associate Professor
Baker Institute for Animal Health
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Education

SUNY Upstate Medical University	Syracuse, NY	2009
Ph.D.	Department of Pharmacology	
Dissertation Title:	*Bioinformatic Identification of Putative Regulatory Motifs*	
Johns Hopkins University	Baltimore, MD	2003
B.S.	Biomedical Engineering	

Research & Work Experience

Associate Professor 2021-
Baker Institute of Animal Health, College of Veterinary Medicine, Cornell University, Ithaca NY

Robert N. Noyce Assistant Professor in Life Science and Technology 2019-2021
Baker Institute of Animal Health, College of Veterinary Medicine, Cornell University, Ithaca NY

Assistant Professor 2014-2019
Baker Institute of Animal Health, College of Veterinary Medicine, Cornell University, Ithaca NY

Postdoctoral Fellow 2009-2014
Biological Statistics & Computational Biology, Cornell University, Ithaca NY

Software Developer 2007-2008
SUNY Microarray Core Facility, Syracuse, NY

Distinctions & Awards

Robert N. Noyce Assistant Professorship in Life Science and Technology	2019
Genome Research Poster Prize: The Biology of Genomes, Cold Spring Harbor Labs	2014
Best Poster: Reproductive Genomics Retreat, Cornell University, Ithaca, NY	2012
Honorable Mention, CVG/ Verge Poster Competition	2009
Professional and Public Service Award: SUNY Upstate Medical University, Syracuse, NY	2008
Judiciary and Ethical Committee: SUNY Upstate Medical University, Syracuse, NY	2006-2008
Bausch & Lomb Honorary Science Award: Rochester, NY	1999

Open Source Software Contributions

1. Rgtsvm. GPU implementation for SVMs in R (led by Zhong Wang). 2016-
   Languages: R, C/ C++ GitHub
2. Rtfbs-db. Parse TF binding motifs from public databases. 2015-
   Languages: R, Shell GitHub

3. dREG. Detection of Regulatory Elements using GRO-seq Data. 2014-
   Languages: R, C GitHub/ http://dreg.dnasequence.org
4. GroHMM. R package for GRO-seq data analysis, HMM implementation. 2009-
   Languages: R, C Bioconductor
5. Affytiling. Easy extraction of individual probes in Affymetrix tiling arrays. 2007-2016
   Languages: R, C Bioconductor

Publications

** equal contribution, ¥ corresponding/ senior author, Danko lab members*

Preprints

1. Villanueva JW, Kwong L, Han T, Martinez SA, Pan FC, Shanahan MT, Kanke M, Chen S, Dow LE, **Danko CG¥**, Sethupathy P¥ (2021). Genome edited colorectal cancer organoid models reveal distinct microRNA activity patterns across different mutation profiles. *bioRxiv*: https://doi.org/10.1101/2021.12.13.472432
2. Chou SP, Alexander AK, Rice EJ, Choate LA, Cohen PE, **Danko CG¥** (2021). Genetic Dissection of the RNA Polymerase II Transcription Cycle. *bioRxiv*: https://doi.org/10.1101/2021.05.23.445279
3. Judd J, Wojenski LA, Wainman LM, Tippens ND, Rice EJ, Dziubek A, Villafano GJ, Wissink EW, Versluis P, Bagepalli L, Shah SR, Mahat DB, Tome JM, **Danko CG**, Lis JT¥, Core LJ¥ (2020). A rapid, sensitive, scalable method for Precision Run-On sequencing (PRO-seq). *bioRxiv*: https://doi.org/10.1101/2020.05.18.102277
4. Chu T¥, **Danko CG¥** (2020). Bayesian Inference of Cell Composition and Gene Expression Reveals Tumor-Microenvironment Interactions. *bioRxiv:* https://doi.org/10.1101/2020.01.07.897900.

Journal Articles

5. Wang Z*, Chivu AG*, Choate LA, Rice EJ, Miller DC, Chu T, Chou SP, Kingsley NB, Petersen JL, Finno CJ, Bellone RR, Antczak DF, Lis JT, and **Danko CG¥** (2022). Prediction of histone post-translational modification patterns based on nascent transcription data. *Nat Genet. Mar;54(3):295-305. doi: 10.1038/s41588-022-01026-x. bioRxiv:* https://doi.org/10.1101/2020.04.08.032730 Featured in a perspective piece.
6. Barshad G*, Webb LM*, Ting HA, Oyesola OO, Onyekwere OG, Lewis JJ, Rice EJ, Matheson MK, Sun XH, von Moltke J, **Danko CG**, Tait Wojno ED¥ (2022). E-Protein Inhibition in ILC2 Development Shapes the Function of Mature ILC2s during Allergic Airway Inflammation. *J Immunol* Mar 1;208(5):1007-1020. doi: 10.4049/jimmunol.2100414. Epub 2022 Feb 18.
7. Stephan T, Burgess SM, Cheng H, **Danko CG**, Gill CA, Jarvis ED, Koepfli KP, Koltes JE, Lyons E, Ronald P, Ryder OA, Schriml LM, Soltis P, VandeWoude S, Zhou H, Ostrander EA, Karlsson EK (2022). Darwinian genomics and diversity in the tree of life. *Proc Natl Acad Sci U S A*. Jan 25;119(4):e2115644119.
8. Choate LA, Barshad G, McMahon PW, Said I, Rice EJ, Munn PR, Lewis JJ¥, **Danko CG¥** (2021). Multiple stages of evolutionary change in anthrax toxin receptor expression in humans. *Nat Commun.* Nov 15;12(1):6590. *bioRxiv*: https://doi.org/10.1101/2020.07.29.227660

9. Arenas-Mena C¥, Miljovska S, Rice EJ, Gurges J, Shashikant T, Ercan S, **Danko CG** (2021). Identification and prediction of developmental enhancers in sea urchin embryos. *BMC Genomics*. Oct 19;22(1):751.
10. Zhao Y, Dukler N, Barshad G, Toneyan S, **Danko CG**, Siepel A¥ (2021). Deconvolution of Expression for Nascent RNA sequencing data (DENR) highlights pre-RNA isoform diversity in human cells. *Bioinformatics.* Aug 11:btab582.
11. Cicconardi F*, Lewis JJ*, Martin SH, Reed RD, **Danko CG**, Montgomery SH¥ (2021). Chromosome fusion affects genetic diversity and evolutionary turnover of functional loci, but consistently depends on chromosome size. *Mol Biol Evol.* Jun 19:msab185.
12. Lewis JJ¥, Cicconardi F, Martin SH, Reed RD, **Danko CG**, Montgomery SH¥ (2021). The Dryas iulia genome supports multiple gains of a W chromosome from a B chromosome in butterflies. *Genome Biol Evol.* Jun 12;evab128. doi: 10.1093/gbe/evab128.
13. Wang MFZ, Mantri M, Chou SP, Scuderi GJ, McKellar DW, Butcher JT, **Danko CG**, De Vlaminck I¥ (2021). Uncovering transcriptional dark matter via gene annotation independent single-cell RNA sequencing analysis. *Nat Commun* Apr 12;12(1):2158. doi: 10.1038/s41467-021-22496-3.
14. Blumberg A, Zhao Y, Huang YF, Dukler N, Rice EJ, Chivu AG, Krumholz K, **Danko CG**, Siepel A¥ (2021). Characterizing RNA stability genome-wide through combined analysis of PRO-seq and RNA-seq data. *BMC Biology.* Feb 15;19(1):30.
15. Saikia M, Holter MM, Donahue LR, Lee IS, Zheng QC, Wise JL, Todero JE, Phuong DJ, Garibay D, Coch R, Sloop KW, Garcia-Ocana A, **Danko CG**, Cummings BP¥ (2021). GLP-1 receptor signaling increases PCSK1 and β cell features in human α cells. *JCI Insight.* Feb 8;6(3):141851.
16. Lewis JJ¥, Van Belleghem SM, Papa R, **Danko CG¥**, Reed RD¥ (2020). Many functionally connected loci foster adaptive diversification along a neotropical hybrid zone. *Science Advances*. Sep 25;6(39):eabb8617.
17. Wan YCE, Liu J, Zhu L, Kang TZE, Zhu X, Ramakrishnan S, Tai SK, Yang D, Chan SY, Chan LL, Li Q, Lis J, Ishibashi T, Han J, **Danko CG¥**, Wang X¥, Chan KM¥ (2020). The H2BG53D oncohistone directly upregulates ANXA3 transcription and enhances cell migration in Pancreatic Ductal Adenocarcinoma. *Signal Transduct Target Ther.* Jun 30;5(1):106.
18. Mukai C, Choi E, Sams KL, Klampen EZ, Anguish L, Marks BA, Rice EJ, Wang Z, Choate LA, Chou SP, Kato Y, Miller AD, **Danko CG**, Coonrod SA¥ (2020). Chromatin Run-On Sequencing Analysis Finds That ECM Remodeling Plays an Important Role in Canine Hemangiosarcoma Pathogenesis. *BMC Vet Res.* Jun 22;16(1):206.
19. Dinh TA, Sritharan R, Smith FD, Francisco AB, Ma RK, Bunaciu RP, Kanke M, **Danko CG**, Massa AP, Scott JD, Sethupathy P¥ (2020). Hotspots of aberrant enhancer activity in fibrolamellar carcinoma reveal molecular mechanisms of oncogenesis and intrinsic drug resistance. *Cell Reports*. Apr 14;31(2):107509.
20. Früh SP, Saikia M, Eule J, Mazulis CA, Miller JE, Cowulich JM, Oyesola OO, Webb LM, Peng SA, Cubitt RL, **Danko CG**, Miller WH, Tait Wojno ED¥ (2020). Elevated circulating Th2 but not group 2 innate lymphoid cell responses characterize canine atopic dermatitis. *Vet Immunol Immunopathol*. Jan 24;221:110015.
21. Lewis JJ¥, Geltman RC, Pollak PC, Rondem KE, Van Belleghem SM, Hubisz MJ, Munn PR, Zhang L, Benson C, Mazo-Vargas A, **Danko CG**, Counterman BA, Papa R, Reed RD (2019). Parallel evolution of ancient, pleiotropic enhancers underlies butterfly wing pattern mimicry. *Proc Natl Acad Sci U S A*. Nov 11. pii: 201907068. doi: 10.1073/pnas.1907068116.

22. Ray J*, Munn PR*, Vihervaara A, Lewis JJ, Ozer A¥, **Danko CG¥**, Lis JT¥ (2019). Chromatin conformation remains stable upon extensive transcriptional changes driven by heat shock. *Proc Natl Acad Sci U S A*. 2019 Sep 10. pii: 201901244. doi: 10.1073/pnas.1901244116.
23. Lu YC, Chu T, Hall MS, Fu DJ, Shi Q, Chiu A, An D, Wang L, Pardo Y, Southard T, **Danko CG**, Liphardt J, Nikitin AY, Wu M, Fischbach C, Coonrod S¥, Ma M¥ (2019). Physical confinement induces malignant transformation in mammary epithelial cells. *Biomaterials*. Jun 26;217:119307.
24. van der Burg KRL, Lewis JJ, Martin A, Nijhout HF, **Danko CG**, Reed RD¥ (2019). Contrasting roles of transcription factors spineless and EcR in the highly dynamic chromatin landscape of butterfly wing metamorphosis. *Cell Reports*. Apr 23;27(4):1027-1038.e3.
25. Webb LM, Oyesola OO, Fruh SP, Kamynina E, Still KM, Patel RK, Peng SA, Cubitt RL, Grimson AW, Grenier JK, Harris TH, **Danko CG**, Tait Wojno E¥ (2019). The Notch signaling pathway promotes basophil responses during helminth induced - type 2 inflammation. *Journal of Experimental Medicine.* Apr 11. pii: jem.20180131.
26. Chou S, **Danko CG¥** (2019). AlleleHMM: a data-driven method to identify allele-specific differences in distributed functional genomic marks. *Nucleic Acids Research.* Mar 28. pii: gkz176. doi: 10.1093/nar/gkz176.
27. Wang Z, Chu T, Choate LA, **Danko CG¥** (2019). Identification of regulatory elements from nascent transcription using dREG. *Genome Research.* Feb;29(2):293-303. doi: 10.1101/gr.238279.118.
28. Saikia M, Burnham P, Keshavjee SH, Wang MFZ, Moral-Lopez P, Hinchman MM, **Danko CG**, Parker JSL, De Vlaminck I¥ (2019). Simultaneous multiplexed amplicon sequencing and transcriptome profiling in single cells. *Nature Methods*. Jan;16(1):59-62.
29. Chu T, Rice EJ, Booth GT, Salamanca HH, Wang Z, Core LJ, Longo SL, Corona RJ, Chin LS, Lis JT, Kwak H¥, **Danko CG¥** (2018). Chromatin run-on and sequencing maps the transcriptional regulatory landscape of glioblastoma multiforme. *Nature Genetics.* Nov;50(11):1553-1564.
30. Blumberg A, **Danko CG**, Kundaje A, Mishmar D¥ (2018). A common pattern of DNase-I footprinting throughout the human mtDNA unveils clues for a chromatin-like organization. *Genome Research*. Aug;28(8):1158-1168.
31. Horibata S, Rice EJ, Zheng H, Mukai C, Chu T, Marks BA, Coonrod SA¥, **Danko CG¥** (2018). A bi-stable feedback loop between GDNF, EGR1, and ERα contributes to endocrine resistant breast cancer. *PLoS One.* Apr 3;13(4):e0194522.
32. Horibata S, Rice EJ, Mukai C, Marks BA, Sams LK, Zheng H, Anguish LJ, Coonrod SA¥, **Danko CG¥** (2018). ER-positive breast cancer cells are poised for RET-mediated endocrine resistance. *PLoS One.* Apr 2;13(4):e0194023.
33. Birkenheuer CH, **Danko CG**, Baines JD¥ (2018). Herpes Simplex Virus 1 Dramatically Alters Loading and Positioning of RNA Polymerase II on Host Genes Early in Infection. *J Virol.* 2018 Feb 7. pii: JVI.02184-17. doi: 10.1128/JVI.02184-17.
34. **Danko CG¥**, Choate LA, Marks BA, Rice EJ, Wang Z, Chu T, Martins AL, Dukler N, Coonrod SA, Tait-Wojno E, Lis JT, Kraus WL, Siepel A¥ (2018). Dynamic Evolution of Regulatory Element Ensembles in Primate CD4+ T Cells. *Nature Ecology & Evolution*. Mar;2(3):537-548. Featured in a perspective piece
35. Meyers-Wallen VN¥, Boyko AR, **Danko CG**, Grenier JK, Mezey JG, Hayward JJ, Shannon LM, Gao C, Shafquat A, Rice EJ, Pujar S, Eggers S, Ohnesorg T, Sinclair AH (2017) XX Disorder of Sex Development is associated with an insertion on chromosome 9 and downregulation of RSPO1 in dogs (Canis lupus familiaris). *PLoS One*. Oct 20;12(10):e0186331.

36. Dukler N, Booth GT, Huang YF, Tippens N, **Danko CG**, Lis JT¥, Siepel A¥ (2017). Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol. *Genome Research*, Oct 12. doi: 10.1101/gr.222935.117.
37. Vihervaara A, Mahat DB, Guertin MJ, Chu T, **Danko CG**, Lis JT, Sistonen L¥ (2017). Transcriptional response to stress is pre-wired by promoter and enhancer architecture. *Nature communications*, Aug 15;8(1):255.
38. Blumberg A, Rice EJ, Kundaje A, **Danko CG**, Mishmar D¥ (2017). Initiation of mtDNA transcription is followed by pausing, and diverge across human cell types and during evolution. *Genome research, 27*(3):362-373.
39. Wang Z, Chu T, Choate LA, **Danko CG¥** (2017). Rgtsvm: Support Vector Machines on a GPU in R. *arXiv*: https://arxiv.org/abs/1706.05544
40. Mahat DB, Kwak H, Booth GT, Jonkers I, **Danko CG**, Patel R, Waters CT, Munson K, Core LC, Lis JT¥ (2016). Base-Pair Resolution Genome-Wide Mapping Of Active RNA polymerases using Precision Nuclear Run-On (PRO-seq). *Nature protocols, 11*(8):1455-1476.
41. Choate LA, **Danko CG¥** (2016). Poised for development. *Nature genetics, 48*(8):822-823. Invited by the editor
42. Wang Z, Martins AL, **Danko CG¥** (2016). RTFBSDB: an integrated framework for transcription factor binding site analysis. *Bioinformatics, 32*(19):3024-3026.
43. Mahat DB, Salamanca H, Duarte FM, **Danko CG**, Lis JT¥ (2016). Mammalian heat shock response and mechanisms underlying its genome-wide transcriptional regulation. *Molecular cell, 62*(1):63-78. Mar 24.
44. Welsh IC, Kwak H, Chen FL, Werner M, Shopland LS, **Danko CG**, Lis JT, Zhang M, Martin JF, Kurpios NA¥ (2015). Embryonic gut laterality is mirrored by asymmetric chromatin architecture at the Pitx2 locus dependent on Pitx2 and CTCF. *Cell reports, 13*(2): 337-349. Cover article
45. Chae M, **Danko CG**, and Kraus WL¥ (2015). groHMM: a computational tool for identifying unannotated and cell type-specific transcription units from global run-on sequencing data. *BMC Bioinformatics, 16*: 222.
46. Andersson R¥, Sandelin A, **Danko CG¥** (2015). A unified architecture of transcriptional regulatory elements. *Trends in genetics, Aug;31(8):426-33.*
47. Fuda NJ, Guertin MJ, Sharma S, **Danko CG**, Martins AL, Siepel A, Lis JT¥ (2015). GAGA factor maintains nucleosome-free regions and has a role in RNA polymerase II recruitment to promoters. *PLoS genetics, 11*(3):e1005108.
48. **Danko CG¥**, Hyland SL, Core LJ, Martins AL, Waters CT, Lee HW, Cheung VG, Kraus WL, Lis JT¥, Siepel A¥ (2015). Accurate identification of active transcriptional regulatory elements from global run-on and sequencing data. *Nature Methods*. P.011353.
49. Core LJ*, Martins AL*, **Danko CG**, Waters C, Siepel A¥, Lis JT¥ (2014). Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. *Nature genetics, 46*(12):1311-1320. Featured in a perspective piece
50. Luo X, Chae M, Krishnakumar R, **Danko CG**, Kraus WL¥ (2014). Dynamic reorganization of the AC16 cardiomyocyte transcriptome in response to TNFalpha signaling revealed by integrated genomic analyses. *BMC genomics, 15*(1):155.
51. Oxford EM¥, **Danko CG**, Fox P, Kornreich B, Moise NS¥ (2014). Change in β-catenin localization suggests involvement of the canonical Wnt pathway in Boxer dogs with arrhythmogenic cardiomyopathy. *Journal of veterinary internal medicine, 28*(1):92-101.

52. Hah N, Murakami S, Nagari A, **Danko CG**, Kraus WL¥ (2013). Enhancer Transcription Marks Active Estrogen Receptor Binding Sites. *Genome Research*.
53. **Danko CG**, Hah N, Luo X, Martins AL, Core L, Lis JT, Siepel A, Kraus WL¥ (2013). Signaling pathways differentially affect RNA polymerase II initiation, pausing, and elongation rate in cells. *Molecular Cell, 50*(2):212-222. Cover article; Featured in a perspective piece; Recommended by Faculty of 1000
54. Zeng L, Sang Chul C, **Danko CG**, Siepel A, Stanhope MJ, Burne RA¥ (2013). Gene Regulation by CcpA and Catabolite Repression Explored by RNA-Seq in Streptococcus mutans. *PLoS One, 8*(3):e60465.
55. Gronau I, Hubisz MJ, Gulko B, **Danko CG**, Siepel A¥ (2011). Bayesian inference of ancient human demography from individual genome sequences. *Nature Genetics, 43*(10):1031-1034.
56. Oxford EM, **Danko CG**, Kornreich BG, Maass K, Hemsley SA, Raskolnikov D, Fox PR, Delmar M, Moïse NS¥ (2011). Ultrastructural changes in cardiac myocytes from Boxer dogs with arrhythmogenic right ventricular cardiomyopathy. *Journal of veterinary cardiology, 13*(2):101-113. Cover article
57. Hah N*, **Danko CG***, Core L, Waterfall JJ, Siepel A, Lis JT, and Kraus WL¥ (2011). A rapid, extensive, and transient transcriptional response to estrogen signaling in breast cancer cells. *Cell, 145*(4):622-634. Featured in a perspective piece
58. Schuster SC¥, et al. (2010). Complete Khoisan and Bantu genomes from southern Africa. *Nature, 463*(7283):943-947. Cover article
59. **Danko CG**, Pertsov AM¥ (2009). Identification of gene co-regulatory modules and associated cis-elements involved in degenerative heart disease. *BMC medical genomics, 2*(1):31.
60. **Danko CG**, McIlvain VA, Qin M, Knox BE, Pertsov AM¥ (2007). Bioinformatic identification of novel putative photoreceptor specific cis-elements. *BMC bioinformatics, 8*(1):407.
61. Jarrar MH, **Danko CG**, Reddy S, Lee YJ, Bibat G, Kaufmann WE¥ (2003). MeCP2 expression in human cerebral cortex and lymphoid cells: immunochemical characterization of a novel higher-molecular-weight form. *Journal of child neurology, 18*(10):675-682.

Protocol Papers, Invited by the Editor

62. Chu T, Wang Z, Chou S, **Danko CG¥** (2019). Discovering transcriptional regulatory elements from run-on and sequencing data using the web-based dREG gateway. *Current Protocols in Bioinformatics.* e70. doi: 10.1002/cpbi.70

Refereed Conference Papers

63. Wang Z, Christie M, Abeysinghe E, Chu T, Marru S, Pierce M, **Danko CG** (2018). Building a Science Gateway for processing and modeling sequencing data via Apache Airavata. Proceedings of the Practice and Experience on Advanced Research Computing (PEARC '18). ISBN #: 978-1-4503-6446-1. doi: 10.1145/3219104.3219141.

Seminars & Talks

Invited Seminars

2021 "Transcription as a lens for interpreting genome sequence", Distinguished Speaker Seminar series, Max Planck in Tübingen.

2020 “ChRO-seq: a new lens for interpreting genome sequence”, Functional Genomics Workshop, National Academy of Sciences, Washington DC.

2020 “Bayesian Inference of Cell Composition and Gene Expression Reveals Tumor-Microenvironment Interactions”, Stem Cell Seminar Series WIP, Cornell University, Ithaca, NY.

2019 “ChRO-seq: a new lens for interpreting genome sequence”, Department of Molecular Biology & Genetics, Cornell University, Ithaca, NY.

2019 “ChRO-seq: a new lens for interpreting genome sequence”, Department of Genetics, Yale University, New Haven, CT.

2019 “ChRO-seq: a new lens for interpreting genome sequence”, Rochester Epigenetic Symposium, University of Rochester, Rochester, NY.

2019 “Gene Regulatory Control through the Lens of ChRO-seq”, Skirball Institute of Biomolecular Medicine, NYU Langone Health Center, New York, NY.

2018 “Positive Selection Drives Changes in the Primate Immune System”, Cornell Center for Vertebrate Genomics, Cornell University, Ithaca, NY.

2018 “Glioblastoma multiforme through the lens of ChRO-seq”, Institute for Computational Biology, Weill Cornell Medical Center, New York, NY.

2018 “Glioblastoma multiforme through the lens of ChRO-seq”, Baker Advisory Council, New York, NY.

2017 “Chromatin Run-on Reveals Nascent RNAs That Differentiate Normal and Malignant Brain Tissue”, RNA Symposium, Cornell University, Ithaca, NY.

2017 “Transcriptional regulation through the lens of ChRO-seq”, Baker Institute Seminar Series, Cornell University, Ithaca, NY. 3rd year review seminar

2017 “Mapping transcriptional regulation at multiple layers using ChRO-seq”, International Society for Animal Genetics, Dublin, Ireland. Workshop keynote

2017 “Widespread stabilizing and positive selection govern primate enhancer evolution”, Department of Ecology & Evolutionary Biology, Cornell University, Ithaca, NY.

2017 “Natural Selection has Shaped Coding and Non-coding Transcription in Primate CD4+ T-cells”, Enhanceropathies, Banbury Center of Cold Spring Harbor laboratory, NY.

2016 “Mapping multiple ‘layers’ of gene regulation using ChRO-seq”, LisFest, Cornell University, Ithaca, NY.

2016 “Widespread stabilizing and positive selection govern primate enhancer evolution”, National Centers for Translational Research in Reproduction and Infertility Male Research Focus Group Meeting, Cornell University, Ithaca, NY.

2016 “Glioblastoma Multiforme epigenomics through the lens of ChRO-seq”, SUNY Upstate Neuroscience Grand Rounds, Syracuse, NY.

2015 “Positive Selection in Regulatory Elements Drives Changes in Gene Expression in the Adaptive Immune System of Primate Species”, SUNY Upstate Biomedical Sciences Retreat, Syracuse, NY.

2014 “Evolutionary Changes in Gene Expression and Regulatory Element Usage Quantified in Primate CD4+ T-Cells”, 3CPG Annual Symposium, Cornell University, Ithaca, NY.

2014 “Toward a Systems Understanding of the Genetic Basis of Disease”, Baker Institute Advisory Council, New York, NY.

2014 “Transcriptional Regulation through the Lens of GRO-seq”, Baker Institute Faculty Search, Ithaca, NY.

Selected from Abstracts

2017 “Chromatin run-on reveals nascent RNAs that differentiate normal and malignant brain tissue”, Mechanisms of Eukaryotic Transcription, Cold Spring Harbor Laboratory, NY.

2016 “Widespread stabilizing and positive selection govern primate enhancer evolution”, Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor Laboratory, NY.

2015 “Positive Selection in Regulatory Elements Drives Changes in Gene Expression in the Adaptive Immune System of Primate Species”. Society for Molecular Biology and Evolution, Vienna, Austria.

2012 “Variation in RNA Polymerase II Transcription Rate in Human Cells”, Post-initiation Activities of RNA Polymerases: 2012 Transcription meeting, Mountain Lake, VA.

Research Support

Active

P50 HD104454 (Cohen) 05/01/21-04/30/26
Spermatogenic Gene Regulation and Infertility
National Institute of Child Health and Human Development (NICHD)

The primary goal of our project is to understand the role of testes specific bromodomain proteins in regulating transcription during spermatogenesis.
Role: Project I co-PI

R01 HG010346 (Danko, Siepel) 05/01/19-04/30/23
Evolution of Chromatin Architecture and Transcriptional Regulation in Mammals
National Human Genome Research Institute (NHGRI)

The primary goal of this proposal is to understand how distinct layers of gene regulation evolve in concert to maintain, and sometimes change, organism phenotypes.
Role: contact PI
Project Direct costs: $2,115,464

17-EXO-17-2-0112 (Danko) 05/01/18-04/30/21
POL II Pausing as a Milestone on the Road to Complex Animals
National Aeronautics and Space Administration (NASA)

The primary goal of this proposal is to determine when and how paused RNA polymerase evolved.
Role: PI
Project Direct costs: $791,393

R01 AI130379-01A1 (Tait Wojno) 09/25/17-08/31/22
Role of the Prostaglandin D2 Receptor CRTH2 in Helminth-Induced Type2 Inflammation in the Intestine
National Institutions of Allergy and Infectious Disease (NIH/NIAID)

The goal of this project is to study how the PGD2-CRTH2 pathway regulates IECs and integrates with cytokine networks during helminth infection, expanding our understanding of intestinal type 2 inflammation and informing the development and use of therapies that target CRTH2 to treat type 2 inflammatory diseases.
Role: Co-I
Danko Lab Direct Costs: $45,240

R01 HG009309-01 (Danko) 02/01/17-01/31/22
Mapping RNA polymerase in tissue samples with ChRO-seq
National Human Genome Research Institute (NHGRI)
The major goal of this project is to develop a suite of molecular and computational technologies that allow researchers to directly measure transcriptional regulation of genes, enhancers, and lincRNAs in limited clinical isolates.
Role: PI
Project Direct costs: $1,225,000

U01HL129958 (Lis, Henning, Zipfel) 09/01/15-08/31/20
Di-Hi-C: Creating Photo-activated X-linkers to define Nuclear Architecture
National Institutes of Health
The goal of this proposal is to develop a method that can reveal the organization of DNA in nucleus with unprecedented resolution, and thus inform us about the mechanics of how genes are mis-regulated to produce disease conditions and how effective therapies could be developed.
Role: Co-I
Danko Lab Direct Costs: $340,000

2R01AG024425-11 (Lee, Danko) 09/01/15-08/31/20
Genetic and Epigenetic Determinants of Longevity
National Institutes of Health
The goal of this project is to understand the genetic and epigenetic determents of longevity in the C. elegans model.
Role: Co-I
Danko Lab Direct Costs: $45,161

Completed

I3110 Cornell Research Grants Program in Animal Health (Danko) 07/1/16-06/30/18
Genetic Mapping of Canine ARVC in the English Bulldog
Cornell University College of Veterinary Medicine
The goal is to identify the genetic basis of canine ARVC in the English bulldog and Boxer
Role: PI
Direct costs: $100,000

Harry N. Zweig Memorial Fund (Antczak, Danko) 01/01/17-12/31/18
Functional Gene Annotation in the Horse
Harry N. Zweig Memorial Fund for Equine Research

The major goal is to identify the functional genes in horses.
Role: Co-PI
Project Direct costs: $124,746
Danko Lab Direct costs: $64,633

I3203 Canine Research Grants in Animal Health (multiple Baker PIs) 07/01/16-06/30/18
Development of Single Cell Sequencing Technology to Identify Paired Variable Regions of Canine B- and T-cell Receptors during Viral Infection
Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University
The goal is to development single-cell sequencing in dogs.
Role: PI
Project Direct costs: $240,000

I3080 Canine Research Grants in Animal Health (multiple Baker PIs) 01/01/16-12/31/17
Development of Novel Targeted Therapies for Treating Malignant Solid Tumors in Dogs
Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University
The major goal of this project is to identify novel mediators of malignant solid tumors in dogs; carry out pre-clinical trials to test the ability of targeted inhibitors in preventing progression of these tumors; and to use Tethered Enzyme Technology (TET) to develop a Point of Care testing device for screening/early diagnosis and monitoring of disease progression via the analysis of known tumor biomarkers and those identified through this project.
Role: Co-PI
Project Direct costs: $240,000

I3081 Canine Research Grants in Animal Health (multiple Baker PIs) 12/01/15-11/30/17
Identifying the Molecular Basis of Canine Genetic Disorders and Developing Preventative Therapies
Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University
The major goal of this project is to develop research resources that aid in mapping DNA sequences causally responsible for genetic diseases in the domestic dog, and to develop strategies to prevent diseases by selective breeding or genetic engineering.
Role: Co-PI
Project Direct costs: $216,173

CLL-13977 PO#4001955607 (Danko) 10/01/16-09/30/17
Understanding Resistance to Endocrine Agents in Breast Cancer Cells
Genentech, Inc.
The goal of this project is to examine RNA Polymerase II distribution on genes in the breast cancer cell line MCF7 after a variety of different treatments.
Role: PI
Project Direct costs: $46,016

Active (Compute time/ resources)

TG-BIO160048 (Danko) 04/01/19-03/31/20
dREG Science Gateway

Extreme Science and Engineering Discovery Environment (XSEDE)

This project is a grant for time on the XSEDE high performance computing resources which provides the community with a web-based interface for our dREG software package.

Role: PI

Computer time. Resources: 16,560 GPU hours. Estimated value: $6,341.12.

TG-MCB160061 (Danko) 04/01/19-03/31/20

Discovery of genomic control elements using machine learning

Extreme Science and Engineering Discovery Environment (XSEDE)

This project is a grant for time on the XSEDE high performance computing resources. The goal of this project is to use machine learning tools to identify the genomic location of active functional elements in mammalian genomes.

Role: PI

Computer time. Resources: 5,872 GPU hours. Estimated value: $1,415.12.

Completed (Compute time/ resources)

TG-BIO160048 (Danko) 02/14/17-03/31/19

dREG Science Gateway

Extreme Science and Engineering Discovery Environment (XSEDE)

This project is a grant for time on the XSEDE high performance computing resources which provides the community with a web-based interface for our dREG software package.

Role: PI

Computer time. Resources: 50,000 service units (SUs). Estimated value: $12,100.38

TG-MCB160061 (Danko) 07/20/16-03/31/19

Discovery of genomic control elements using machine learning

Extreme Science and Engineering Discovery Environment (XSEDE)

This project is a grant for time on the XSEDE high performance computing resources. The goal of this project is to use machine learning tools to identify the genomic location of active functional elements in mammalian genomes.

Role: PI

Computer time. Resources: 419,968 service units (SUs). Estimated value: $3,531.14.

Teaching & Mentoring

Cornell Graduate Field Memberships

Biochemistry, Molecular, and Cell Biology (BMCB)	2020-
Ecology & Evolutionary Biology (EEB)	2018-
Tri-Institutional Program for Computational Biology & Medicine (Tri-I CBM)	2016-
Comparative Biomedical Sciences (CBS)	2014-
Computational Biology (CB)	2014-
Genetics, Genomics, and Development (GG&D)	2014-

Technical Staff

Edward J. Rice (laboratory manager) 2014-
Zhong Wang, Ph.D. (programmer) 2015-2019
  Current: Professor, Dalian University, China

Postdoctoral Fellows

Jyoti Lama, Ph.D. 2021-
Blaine Harlan, Ph.D. 2021-
Gilad Barshad, Ph.D. 2019-
James Lewis, Ph.D. 2016-2021
  Reproductive Genomics T32
  Current: Postdoc, Judith Mank
Mridusmita Saikia, Ph.D. 2016-2020
  Current: Lecturer, Biomedical Engineering, Cornell University

Graduate Students

Adam He, Computational Biology 2019-
Alexandra Chivu, Genetics, Genomics & Development (joint with John Lis) 2019-
  Center for Vertebrate Genomics fellowship
Jonathan Villanueva, Biological and Biomedical Sciences (joint with Praveen Sethupathy) 2018-
  SUNY McNair Diversity Fellowship
Adriana Alexander, Comparative Biomedical Sciences (joint with Paula Cohen) 2017-2021
  SUNY McNair Diversity Fellowship
  NSF Predoctoral Fellowship
  Thesis: Temporal Control of Transcription During Prophase I of Male Meiosis
  Current: Postdoctoral Associate, Humphrey Yao (NIH)
Shao-Pei Chou, Genetics, Genomics & Development 2016-2021
  Thesis: Computational Exploration of the Genetic Factors behind Transcriptional Regulation
  Current: Computational Biologist, Ginko Bioworks
Paul Munn, Computational Biology 2016-2020
  Thesis: Computational Approaches to Understanding Transcriptional Regulation
  Current: Computational Biologist, TREx Core, Cornell University
Lauren Choate, Genetics, Genomics & Development 2015-2020
  Center for Vertebrate Genomics fellowship
  National Institutes of Health, F31, NIAID
  Thesis: Cis-Regulatory Adaptation in the Primate Immune System
  Current: Mayo Clinic Laboratory Genetics and Genomics Fellow
Tin Yi Chu, Computational Biology 2014-2019
  Croucher Foundation Predoctoral Fellowship
  Thesis: Bayesian Statistical Inference for Tumor Microenvironment Compositions
  Current: Postdoctoral Associate, Dana Pe'er (MSKCC)

Rotation Students

Wilfred Wong, Tri-Institutional Program for Computational Biology & Medicine	2020
David Iu, Genetics, Genomics & Development	2020
Kuang-Tse Wang, Genetics, Genomics & Development	2019
Adam He, Computational Biology	2019
Iskander Said, Genetics, Genomics & Development	2019
Lauren Walter, Genetics, Genomics & Development	2019
Alexandra Chivu, Genetics, Genomics & Development	2018
Jonathan Villanueva, Biological and Biomedical Sciences	2018
Minsoo Kim, Tri-Institutional Program for Computational Biology & Medicine	2017
Albert Vill, Genetics, Genomics & Development	2016
Charles Liang, Computational Biology	2016
Eamon Collins, Biomedical Engineering	2016
Kofi Gyan, Tri-Institutional Program for Computational Biology & Medicine	2016
Coryandar Gilvary, Tri-Institutional Program for Computational Biology & Medicine	2016
Andrew Wiens, Computer Science	2016
Dania Villarnovo, Comparative Biomedical Sciences	2015
Blaine Harlan, Genetics, Genomics & Development	2015
Ian Rose, Genetics, Genomics & Development	2015
Xiatong Yao, Tri-Institutional Program for Computational Biology & Medicine	2015
Yu-Ling (Linda) Lan, Genetics, Genomics & Development	2015
Alyssa Wetterau, Comparative Biomedical Sciences	2014

Undergraduate/ Post Baccalaureate Students

Honoria Brown, Leadership student	2019
Pierce McMahon, Undergraduate	2018-2020
Jay Chia, Undergraduate	2018
Samantha Lin, Leadership student	2018
Hedda Somsen, Exchange student	2018
Zilu Wang, Ithaca High school student	2017-2018
Connor Musick, Undergraduate	2017-2018
Vianne Gao, Undergraduate summer intern from Carleton College	2017
Marlena Holter, VIP Student	2017
Gavisha Waidyaratne, Postbac	2017
Maria Dalby, Exchange student	2017
Madison Ramsey, Undergraduate	2017
Kai Chun “Katie” Lin, Cornell Abroad	2016
Shuting Jin, Leadership student	2015
Alice Wang, Undergraduate	2015-2016

Thesis Committee Membership

Sarah Saddoris, Biological & Biomedical Sciences (Schang)	2021-
Keith Ou, Animal Sciences (Lei)	2021-
Shobhita Gupta, Biophysics (Yu)	2021-
Madhav Mantri, Computational Biology (De Vlaminck)	2021-

Eti Sinha, Biomedical Engineering (Elemento, Guzman)	2020-
Alaa Farghli, Genetics Genomics & Development (Sethupathy)	2020-
Olivia Lang, Computational Biology (Pugh)	2020-
Blaine Harlan, Genetics, Genomics & Development (Soloway)	2020-2021
Zhou Zhou, Biochemistry, Molecular & Cell Biology (Lis)	2019-
Mauricio Paramo, Genetics Genomics & Development (Yu)	2019-
Alexis Dziubek, Genetics Genomics & Development (Grimson)	2019-
Thomas Roberts, Chemical Engineering (Zipfel)	2019-
Rosanna Ma, Biological & Biomedical Sciences (Sethupathy)	2019-
Philip Versluis, Biochemistry, Molecular & Cell Biology (Lis)	2019-
Yingying Zhang, Biophysics (Yu)	2019-
Alexa Bracci, Genetics Genomics & Development (Koren)	2018-
Tommy Carter, Genetics Genomics & Development (Feschotte)	2017-2021
Michael DeBerardine, Genetics Genomics & Development (Lis)	2017-
Yeonui Kwak, Genetics Genomics & Development (Grimson)	2017-
Debadrita Bhattacharya, Biochemistry, Molecular & Cell Biology (Simoes-Costa)	2017-2020
Dashiell Massey, Genetics Genomics & Development (Koren)	2017-
Ellie Larson, Biological & Biomedical Sciences (Wagner)	2017-2021
Simon Frueh, Biological & Biomedical Sciences (Tait Wojno)	2017-2021
Alex Cheng, Biomedical Engineering (De Vlaminck)	2017-2021
Andrea Slavney, Genetics Genomics & Development (Clark)	2016-2017
Kara Rode, Biochemistry, Molecular & Cell Biology (Lis)	2016-
Shing Hu, Comparative Biomedical Sciences (Kurpios)	2016-2022
Brooke Marks, Biological & Biomedical Sciences (Coonrod)	2016-2022
Charles Liang, Computational Biology (Yu)	2016-2021
Ian Rose, Genetics Genomics & Development (Nikitin)	2015-2020
Lina Bagepalli, Biochemistry, Molecular & Cell Biology (Lis)	2015-2020
Michelle White, Biological & Biomedical Sciences (Boyko)	2015-2019
Anyimilehidi Mazo-Vargas, Entomology (Reed)	2015-2020
Nate Tippens, Tri-I Computational Biology & Medicine (Lis, Yu)	2015-2020
Noah Dukler, Tri-I Computational Biology & Medicine (Siepel)	2015-2018
Digbijay Mahat, Biochemistry, Molecular & Cell Biology (Lis)	2014-2017
Joo Hyun Im, Genetics Genomics & Development (Lazzaro)	2014-2018
Wenke Wang, Biochemistry, Molecular & Cell Biology (Lee)	2014-2017

A-exam Committee Membership

Madhav Mantri, Computational Biology (De Vlaminck)	2021
Olivia Lang, Computational Biology (Pugh)	2021
Philip Versluis, Biochemistry, Molecular & Cell Biology (Lis)	2020
Jonathan Villanueva, Biological and Biomedical Sciences (Danko)	2020
Alexa Bracci, Genetics Genomics & Development (Koren)	2019
Simon Frueh, Biological & Biomedical Sciences (Tait Wojno)	2018
Ellie Larson, Biological & Biomedical Sciences (Wagner)	2018
Yeonui Kwak, Genetics Genomics & Development (Kwak)	2018

Sylvia Chang, Genetics Genomics & Development (Feschotte)	2018
Debadrita Bhattacharya, Biochemistry, Molecular & Cell Biology (Simoes-Costa)	2018
Dashiell Massey, Genetics Genomics & Development (Koren)	2018
Brooke Marks, Biological & Biomedical Sciences (Coonrod)	2017
Tinyi Chu, Computational Biology (Danko)	2017
Kara Rode, Biochemistry, Molecular & Cell Biology (Lis)	2017
Paul Munn, Computational Biology (Danko)	2017
Charles Liang, Computational Biology (Yu)	2017
Qiliang "Andy" Ding, Genetics Genomics & Development (Kroen, Clark)	2017
Anyimilehidi Mazo-Vargas, Entomology (Reed)	2016
Ian Rose, Genetics Genomics & Development (Nikitin)	2016
Tina Tran, Biochemistry, Molecular & Cell Biology (Schimenti)	2016
Jacob Merle, Genetics Genomics & Development (Grimson)	2016
Lina Bagepalli, Biochemistry, Molecular & Cell Biology (Lis)	2016
Lauren Choate, Genetics Genomics & Development (Danko)	2016
Michelle White, Biological & Biomedical Sciences (Boyko)	2016
Noah Dukler, Tri-I Computational Biology & Medicine (Siepel)	2015
Ravi Patel, Genetics Genomics & Development (Grimson)	2015
Joo Hyun Im, Genetics Genomics & Development (Lazzaro)	2014
Wenke Wang, Biochemistry, Molecular & Cell Biology (Lee)	2014

Workshops/ Short Courses

3CPG Short Read Sequencing Workshop	2010

Undergraduate Curriculum

Molecular Basis of Disease (BioMG4390, Danko, Kwak)	2017-
Cellular Physiology (BioAP3160, White, Yen)	2018-

Veterinary Curriculum

Block 2, guest lecture on new tools in genomics and epigenetics	2018

Graduate Curriculum

Development and Evolution (BioMG4610) – guest lecture	2019
Critical Thinking in Genetics & Development (BioMG7810) – genomics workshop	2018
Precision and Genomic Medicine (BME6120, De Vlaminck) – guest lecture	2016, 2018
Problems in Genetics & Development (BioMG7810)	2015-2017
Computational Genetics & Genomics (BTRY4840/6840, Williams) – guest lecture	2015

Administrative Experience

Intramural Service

Genomics Core, Faculty Advisory Board	2021-
BBS3 Seminar Series, committee	2021-

Faculty search committee, Dept. Biomedical Science, reproductive biology position	2021
Center for Vertebrate Genomics, Director of Communications	2020-2022
Bioinformatics Facility, Faculty Advisory Board	2020-
Undergraduate Thesis Review, Bio Honors Michael Zelko (Kwak)	2019
Undergraduate Thesis Review, Bio Honors Alex Friefeld (Cohen)	2019
Center for Comparative and Population Genomics (3CPG), Executive Committee	2018-
Genetics Genomics & Development graduate program, Steering Committee	2018-
Institute of Biotechnology, Core facilities @ Cornell, Advisory Board Member	2017-2022
Bio-IT Core Facility, Chair of the Advisory Board	2017
Graduate field of Computational Biology, Membership Committee	2017
Tri-I Graduate Program in Computational Biology & Medicine, Member of Admissions Committee	2016-
Genetics Genomics & Development graduate program, Member of Admissions Committee	2016-2022
CVM Strategic Planning, Member of Research & Graduate Education Committee	2016-2017
Bio-IT Core Facility, Member of Advisory Board	2016-2017
Center for Vertebrate Genomics, Shared Resources Committee Member	2016-2018
GG&D graduate program, Faculty Coordinator for Recruitment	2016
Undergraduate Thesis Review, Bio Honors Lydia Lam	2016
BBS Recruitment, Co-Organizer Baker visit	2016
Computational Biology Graduate Program, Member Admissions Committee	2015-2016
LPS/ Wellnitz Paper Awards (GG&D program), Awards Committee Rank	2015
Computational Genomics Molecular Biology & Genetics, Faculty Search Committee	2014-2015

Extramural Service

Organizing Committee, *Next steps for functional genomics*, National Academy of Sciences	2019-2020
Session moderator: Systems Biology, Perspectives in Comparative Genomics & Evolution	2019
Session moderator: Mechanism & Function, Perspectives in Comparative Genomics & Evolution	2019
Organizing Committee, *Comparative Genomics & Evolution*, NHGRI Strategic Planning	2019
4DN Consortium Annual Meeting, Abstract Reviewer	2017-2018
4DN Consortium Annual Meeting, Organizing Committee	2017-2019
4DN Consortium, Data Analysis Working Group	2016-2020
Canine Longevity Consortium, phenotype working group	2015
Canine Longevity Consortium, advisory committee meeting	2014-2015

Journal Editorial Boards

Genome Research	2020-

Ad Hoc Journal Reviews

Genome Research (14)
Nature Communications (4)
Molecular Biology & Evolution (3)
Cell (3)
Nucleic Acids Research (4)
Genome Biology & Evolution (2)
Molecular Systems Biology (2)
Nature (5)
Nature Genetics (3)
Nature Protocols (3)
eLife (3)
Bioinformatics (3)
PLoS Genetics (2)
G3 (2)

BMC Genomics
PCI Evolutionary Biology
PLoS Computational Biology
Cell Reports
Human Molecular Genetics
The EMBO Journal
Cancer Letters
Epigenetics & Chromatin
PLoS One
Trends in Genetics
Science
BMC Bioinformatics
Nature Methods
Mol. Cancer Research
Cancer Research
PNAS