# Charles G. Danko, Ph.D.

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Assistant Professor of Epigenetics & Gene Regulation

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## Education

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

## Research & Work Experience

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|---|---|---|
| *Assistant Professor* | Baker Institute/ Department of Biomedical Sciences Cornell University, Ithaca NY | July 1st 2014- |
| *Postdoctoral Fellow* | Dep. Biological Statistics & Computational Biology Cornell University, Ithaca NY | 2009-2014 |
| *Software Developer* | SUNY Microarray Core Facility Syracuse, NY | 2007-2008 |
| *Graduate Student* | Department of Pharmacology, SUNY Upstate Syracuse, NY; Dr. Arkady Pertsov, Advisor | 2003-2008 |
| *Research Assistant* | Kennedy Krieger Institute, Johns Hopkins Baltimore, MD; Dr. Walter Kaufmann, Advisor | 2002-2003 |

## Distinctions & Awards

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|---|---|
| **Searle Institutional Nominee:** Searle Scholars program, Cornell nominee | 2015 |
| **Genome Research Poster Prize:** The Biology of Genomes (Cold Spring Harbor Labs) | 2014 |
| **Best Poster:** Reproductive Genomics Retreat, 2012, Poster Session | 2012 |
| **Professional and Public Service Award:** SUNY Upstate Medical University | 2008 |
| **Judiciary and Ethical Committee**: SUNY Upstate Medical University | 2006-2008 |
| **Bausch & Lomb Honorary Science Award** | 1999 |

## Open Source Software Contributions

1. **Rtfbs-db**. Parse TF binding motifs from public databases.    2015-
   Languages: R, Shell      *GitHub*

2. **dREG**. Detection of Regulatory Elements using GRO-seq Data.    2014-
   Languages: R, C      *GitHub*

3. **GroHMM**. R package for the analysis of GRO-seq data, HMM implementation.    2009-
   Languages: R, C                *Bioconductor*

4. **Affytiling**.  Easy extraction of individual probes in Affymetrix tiling arrays.   2007-2016
   Languages: R, C                *Bioconductor*

## Publications

**(\* equal contribution)  (¥ corresponding author) (Danko lab members underlined)**

**Preprints Submitted for Peer-Review**

1. Blumberg A, Rice EJ, Kundaje A, **Danko CG**, Mishmar D (2016).  *Initiation of mtDNA transcription is followed by pausing, and diverge across human cell types and during evolution.  **bioRxiv**. doi:* [http://dx.doi.org/10.1101/054031](http://dx.doi.org/10.1101/054031)

**Peer-reviewed Publications**

2. Wang Z, Martins AL, **Danko CG**¥ (2016).  *RTFBSDB: an integrated framework for transcription factor binding site analysis. **Bioinformatics**.* In press.

3. 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**.*  In press.

4. 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.**  Apr 7;62(1):63-78. doi: 10.1016/j.molcel.2016.02.025. Epub 2016 Mar 24.*

5. 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.**  Oct 13;13(2): 337-49.*                **Cover article**

6. Chae M, **Danko CG**, Kraus WL (2015).  *groHMM: a computational tool for identifying unannotated and cell type-specific transcription units from global run-on sequencing data.  **BMC Bioinformatics**, Jul 16;16:222.*

7. Andersson R¥, Sandelin A, **Danko CG**¥ (2015).  *A Unified Architecture of Transcriptional Regulatory Elements.  **Trends in Genetics.** Jun 11. pii: S0168-9525(15)00104-3.*

8. Fuda NJ, Guertin MJ, Sharma S, **Danko CG**, Martins AL, Siepel A, Lis JT (2015).  *GAGA Factor Maintains Nucleosome-free Promoters Allowing RNA Polymerase II Recruitment and Promoter-proximal Pausing.  **PLoS Genetics**.  Mar 27;11(3):e1005108.*

9. **Danko CG**¥, Hyland SL, Core LJ, Martins AL, Waters CT, Lee HW, Cheung VG, Kraus WL, Lis JT¥, and Siepel A¥ (2015). *Accurate Identification of Active Transcriptional Regulatory Elements from Global Run-On and Sequencing Data.  **Nature Methods**.  Mar 23.*

10. Core LJ\*, Martins AL\*, **Danko CG**, Waters C, Siepel A, Lis JT (2014).  *Analysis of*

*transcription start sites from nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers.* **Nature Genetics.** Nov 10. doi: 10.1038/ng.3142. **<span style="color:red">Featured in a perspective piece</span>**

11. Luo X, Chae M, Krishnakumar R, **<u>Danko CG</u>**, Kraus WL (2014). *Dynamic reorganization of the AC16 cardiomyocyte transcriptome in response to TNFalpha signaling revealed by integrated genomic analyses.* **BMC Genomics**. Feb 24;15(1):155.

12. Oxford EM, **<u>Danko CG</u>**, 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.* **J Vet Intern Med**. Jan;28(1):92-101.

13. Hah N, Murakami S, Nagari A, **<u>Danko CG</u>**, Kraus WL (2013). *Enhancer Transcription Marks Active Estrogen Receptor Binding Sites.* **Genome Res**. May 1. PMID: 23636943.

14. **<u>Danko CG</u>**, 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**. Apr 25;50(2):212-22. **<span style="color:red">Cover article</span>**
**<span style="color:red">Featured in a perspective piece</span>**
**<span style="color:red">Recommended by Faculty of 1000</span>**

15. Zeng L, Sang Chul C, **<u>Danko CG</u>**, 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.

16. Gronau I, Hubisz MJ, Gulko B, **<u>Danko CG</u>**, Siepel A. (2011). *Bayesian inference of ancient human demography from individual genome sequences.* **Nature Genetics**, 18;43(10):1031-4.

17. Oxford EM, **<u>Danko CG</u>**, 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.* **J Vet Cardiol**, 13(2):101-13. **<span style="color:red">Cover article</span>**

18. Hah N**\***, **<u>Danko CG</u>\***, Core L, Waterfall JJ, Siepel A, Lis JT, Kraus WL (2011). *A rapid, extensive, and transient transcriptional response to estrogen signaling in breast cancer cells.* **Cell**, 13;145(4):622-34. *\* Equal Contribution*
**<span style="color:red">Featured in a perspective piece</span>**

19. Schuster SC, et. al. (2010). *Complete Khoisan and Bantu genomes from southern Africa.* **Nature**, 18;463(7283):943-7. **<span style="color:red">Cover article</span>**

20. **<u>Danko CG</u>**, Pertsov AM (2009). *Identification of co-regulatory modules and associated cis-elements involved in degenerative heart disease.* **BMC Medical Genomics**, 28;2:31.

21. **<u>Danko CG</u>**, McIlvain VA, Qin M, Knox BE, Pertsov AM (2007). *Bioinformatic identification of novel putative photoreceptor specific cis-elements.* **BMC Bioinformatics**, Oct 22;8(1):407.

22. Jarrar MH, **<u>Danko CG</u>**, 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. **J Child Neurol**, 18(10):675-82.*

## Talks & Conference Participation

**Invited Talks**

1. **<u>Danko CG</u>** (2016). Widespread stabilizing and positive selection govern primate enhancer evolution.
   Host: *Paula Cohen*　　　　　　　　　*NCTRI Male Res. Focus Group Meeting, April 2016*

2. **<u>Danko CG</u>** (2016). Glioblastoma Multiforme epigenomics through the lens of ChRO-seq.
   Host: *Lawrence Chin*　　　　　*SUNY Upstate Neuroscience Grand Rounds, Feb. 2016*

3. **<u>Danko CG</u>** (2015). Positive Selection in Regulatory Elements Drives Changes in Gene Expression in the Adaptive Immune System of Primate Species.
   Host: *Arkady Pertsov*　　　　　*SUNY Upstate Biomedical Sciences Retreat, 2015*

4. **<u>Danko CG</u>** (2014). Evolutionary Changes in Gene Expression and Regulatory Element Usage Quantified in Primate CD4$^+$ T-Cells.　　　　　*3CPG Annual Symposium*

5. **<u>Danko CG</u>** (2014). Toward a Systems Understanding of the Genetic Basis of Disease.
   *Baker Institute Advisory Council, Cornell Club, New York, NY*

6. **<u>Danko CG</u>** (2014). Transcriptional Regulation through the Lens of GRO-seq.
   *Baker Institute Faculty Search*

**Talks Selected from Abstracts**

7. **<u>Danko CG</u>** (2016). Widespread stabilizing and positive selection govern primate enhancer evolution.　　*Systems Biology: Global Regulation of Gene Expression, March 2016*

8. **<u>Danko CG</u>** (2015). Positive Selection in Regulatory Elements Drives Changes in Gene Expression in the Adaptive Immune System of Primate Species.　　　　*SMBE 2015*

9. **<u>Danko CG</u>** (2012). Variation in RNA Polymerase II Transcription Rate in Human Cells.
   *Mountain Lake Elongation and Termination Meeting*

**Selected Posters**

1. **<u>Danko CG</u>**, Martins A, Lis JT, Siepel A, Kraus WL (2014). Evolutionary Changes in Gene Expression and Active Regulatory Element Usage Quantified in Primate CD4+ T-Cells using GRO-seq.
   *Biology of Genomes; Poster*

   **<span style="color:red">Winner, Poster competition (top 3 of 324)</span>**

2. **<u>Danko CG</u>**, Hah N, Luo X, Martins A, Core L, Lis JT, Siepel A, Kraus WL (2012). Variation in the RNA Polymerase II Transcription Rate in Human Cells.
   *Reproductive Genomics Retreat; Poster*

   **<span style="color:red">Winner, Poster competition (top 1 of 30)</span>**

3. **<u>Danko CG</u>**, Hah N, Kraus WL, Siepel AS. (2009). Primate-specific expansions of putative sex-hormone response elements.

*Biology of Genomes; Poster*

<p style="text-align:center; color:red;">**Honorable Mention, Cornell Verge poster competition**</p>

## Research Support

**Current**

| | | |
|---|---|---|
| **Baker Institute Startup Funds** | Danko (PI) | 7/01/14-6/30/17 |
| **Walbridge Fund** | Chin | 1/1/16-12/31/17 |
| **NIH-NHLBI U01 (**UHL129958A**)** | Lis (co-I) | 9/01/15-8/31/20 |

*Di-Hi-C: Creating Photo-activated X-linkers to define Nuclear Architecture*

**NIH-NIA R01 (**2R01AG024425-11**)**     Lee (co-I)     9/01/15-8/31/20
*Genetic and Epigenetic Determinants of Longevity*

**Pending**

**NYS DOH Wadsworth Center**     Danko (PI)     8/01/16-7/31/17
*Genome-Wide discovery of non-coding mutations conferring resistance to tamoxifen*

**NSF DEB**     Danko (PI)     9/01/16-8/31/21
*Investigating the evolution of mtDNA transcription*

**NIH-NIGMS R01**     Danko (PI)     9/01/16-8/31/21
*Contributions of the RNA Life-Cycle to primate CD4+ T-cell evolution*

**NIH-NHGRI R01**     Danko (PI)     9/01/16-8/31/21
*Mapping RNA polymerase in tissue samples with ChRO-seq*

**NIH-NHGRI UM1**     Danko (PI)     12/01/16-11/30/20
*The Discovery of Functional Elements using Maps of Nascent Transcription*

## Teaching & Mentoring

**Student Advisees**

| | |
|---|---|
| **Tinyi Chu,** *Computational Biology* | 2014- |
| **Lauren Choate,** *Genetics Genomics & Development* | 2015- |
| **Paul Munn,** *Computational Biology* | 2016- |

**Thesis Committee**

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|---|---|
| **Wenke Wang**, *Biochemistry, Molecular & Cell Biology (Lee)* | 2014- |
| **Digbijay Mahat**, *Biochemistry, Molecular & Cell Biology (Lis)* | 2014- |
| **Joo Hyun Im**, *Genetics Genomics & Development (Lazzaro)* | 2014- |
| **Noah Dukler**, *Tri-I Computational Biology & Medicine (Siepel)* | 2015- |
| **Nate Tippens**, *Tri-I Computational Biology & Medicine (Lis, Yu)* | 2015- |
| **Anyimilehidi Mazo-Vargas**, *Entomology (Reed)* | 2015- |

**Michelle White**, *Biological & Biomedical Sciences (Boyko)* 2015-
**Lina Bagepalli**, *Biochemistry, Molecular & Cell Biology (Lis)* 2015-
**Ian Rose**, *Genetics Genomics & Development (Nikitin)* 2015-

### A-exam Committees

**Wenke Wang**, *Biochemistry, Molecular & Cell Biology* 2014
**Joo Hyun Im**, *Genetics Genomics & Development* 2014
**Noah Dukler**, *Tri-I Computational Biology & Medicine* 2015
**Ravi Patel**, *Genetics Genomics & Development* 2015
**Michelle White**, *Biological & Biomedical Sciences* 2016
**Tina Tran**, *Biochemistry, Molecular & Cell Biology* 2016

### Guest Teaching

**Problems in Genetics & Development (BioMG7810)** 10/22/2015
**Computational Genetics & Genomics (BTRY4840/6840)** 11/5/2015
**3CPG Short Read Sequencing Workshop** 2010

## Intra- & Extramural Service

### Intramural Committee Service

**Faculty Search in Computational Genomics** *Molecular Biology & Genetics* 2014-2015
**Awards Committee** Rank LPS/ Wellnitz Paper Awards (GG&D program) 2015
**Admissions Committee** *Computational Biology Graduate Program* 2015-
**Bio-IT Advisory Board** *Advisory board to the Bio-IT core facility.* 2016-
**GG&D Recruitment Faculty Coordinator** *Coordinates GG&D recruitment.* 2016-
**Bio Honors Thesis Review** *Lydia Lam.* 2016

### Reviewing Activity (Academic Journals)

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|---|---|
| *Genome Research* | *BMC Bioinformatics* |
| *Molecular Biology & Evolution* | *BMC Genomics* |
| *Nature Protocols* | *PLoS One* |
| *Nature Genetics* | *Cell* |