

## Robin D. Dowell

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CONTACT INFORMATION BioFrontiers Institute  
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ACADEMIC POSITIONS **University of Colorado**  
Associate Professor, Molecular, Cellular and Developmental Biology (2017-Present)  
BioFrontiers Institute Core Faculty (2009-Present)  
Affiliated Faculty, Computer Science (2009-Present)  
Core Faculty, Computational Bioscience Program, Univ. Colorado Med. School (2009-Present)  
Assistant Professor, Molecular, Cellular and Developmental Biology (2009-2017)

**Massachusetts Institute of Technology**  
Postdoctoral Fellow; 2005-2009  
Adviser: David K. Gifford

FOUNDER **Arpeggio Biosciences**, Scientific Advisor

EDUCATION **Washington University in St. Louis**  
D.Sc. Biomedical Engineering, December 2004  
“Stochastic Context-Free Grammars for RNA Secondary Structure Prediction”  
Adviser: Sean R. Eddy  
M.S. Computer Science, May 2001  
Advisers: Lincoln Stein, Sean R. Eddy, Michael R. Brent  
Project: “A Distributed Annotation System” (Tech report wucs-01-07)

**Texas A&M University**  
B.S. Computer Engineering, May 1997, *cum laude*, Engineering Scholar  
B.S. Genetics, May 1997, University Honors, Foundation Honors  
Honors Thesis: “A Graphical User Interface for Contig Mapping”

HONORS Kavli Foundation Fellow, National Academy of Sciences, 2014 and 2015  
Linda Crnic Institute Investigator, 2013  
Boulder Faculty Assembly Recognition, 2013  
Alfred P. Sloan Foundation Research Fellow, 2012  
Boettcher Foundation Webb-Waring Investigator, 2010  
Spencer T. and Ann W. Olin Medical Scientist Fellow, 2005  
Mr. and Mrs. Spencer T. Olin Fellowship, 2002-2004  
Association of Women Faculty Graduate Student Award, 1999  
Howard Hughes Predoctoral Fellowship, 1997-2002  
National Science Foundation Fellowship (declined), 1997

University Undergraduate Research Fellow (Best Presentation Award), 1997

PEER-REVIEWED \* these authors contributed equally to this work; # co-corresponding author  
PUBLICATIONS underline indicates students; † indicates undergraduates

47. S Cuartero, F.D. Weiss, G. Dharmalingam, Y. Guo, E. Ing-Simmons, S. Masella, I. Robles-Rebollo, X. Xiao, Y.F. Wang, I. Barozzi, D. Djeghloul, M.T. Amano, H. Niskanen, E. Petretto, **R.D. Dowell**, K. Tachibana, M.U. Kaikkonen, K.A. Nasmyth, B. Lenhard, G. Natoli, A.G. Fisher, M. Merckenschlager. Control of inducible gene expression links cohesin to hematopoietic progenitor self-renewal and differentiation. *Nat. Immunol* 19(9):932-941 2018.
46. Z.N. Wilson, A.L. Scott, **R.D. Dowell**, G. Odorizzi. PI(3,5)P2 Controls Vacuole Potassium Transport to Support Cellular Osmoregulation. *Molecular Biology of the Cell* 29(14):1718-1731 2018.
45. I.J. Tripodi, M.A. Allen, **R.D. Dowell**. Detecting differential transcription factor activity from ATAC-seq data. *Molecules Special Issue Transcription Factors as Therapeutic Targets*. 23(5): 1136 2018.
44. P. Russell, B. Vestal, W. Shi, P. Rudra, **R. Dowell**, R. Radcliffe, L. Saba, K. Kechris. miR-MaGiC improves quantification accuracy for small RNA-seq. *BMC Research Notes* 11:296 2018.
43. J. Azofeifa, M.A. Allen, J. Hendrix†, J. Rubin, T. Read, **R.D. Dowell**. Enhancer RNA Profiles Predict Transcription Factor Activity. *Genome Research* 28:334-344 2018. **featured on cover**
42. G. Sanchez, P. Richmond, E. Bunker, S. Karman, J. Azofeifa, A. Garnett, Q. Xu, G. Wheeler, C. Toomey, Q. Zhang, **R. Dowell**, X. Liu. Genome-wide Dose-dependent Inhibition of Histone Deacetylases Reveals Their Roles in Enhancer Remodeling and Suppression of Oncogenic Super-enhancers. *Nucleic Acids Research* 45(4): 1756-1776 2018.
41. Luke R. Thompson, Jon G. Sanders, Daniel McDonald, Amnon Amir, Joshua Ladau, Kenneth J. Locey, Robert J. Prill, Anupriya Tripathi, Sean M. Gibbons, Gail Ackermann, Jose A. Navas-Molina, Stefan Janssen, Evguenia Kopylova, Yoshiki Vazquez-Baeza, Antonio Gonzalez, James T. Morton, Siavash Mirarab, Zhenjiang Zech Xu, Lingjing Jiang, Mohamed F. Haroon, Jad Kanbar, Qiyun Zhu, Se Jin Song, Tomasz Kosciolk, Nicholas A. Bokulich, Joshua Leffler, Colin J. Brislawn, Gregory Humphrey, Sarah M. Owens, Jarrad Hampton-Marcell, Donna Berg-Lyons, Valerie McKenzie, Noah Fierer, Jed A. Fuhrman, Aaron Clauset, Rick L. Stevens, Ashley Shade, Katherine S. Pollard, Kelly D. Goodwin, Janet K. Jansson, Jack A. Gilbert, Rob Knight, and The Earth Microbiome Project Consortium. A communal catalogue reveals Earth's multiscale microbial diversity. *Nature* 551(7681):457-463, 2017.
40. C.L. Trexler, A.T. Odell, M.Y. Jeong, **R.D. Dowell**, L.A. Leinwand. The transcriptome and functional profile of cardiac myocytes is influenced by biological sex. *Circulation:Cardiovascular Genetics* 10:e001770, 2017.
39. C. Ebmeier, B. Erickson, B.L. Allen, M.A. Allen, H. Kim, N. Fong, J.R. Jacobsen. K. Liang, A. Shilatifard, **R.D. Dowell**, W.M. Old, D.L. Bentley, D. Taatjes.

Human TFIIH kinase CDK7 regulates transcription-associated epigenetic modifications. *Cell Reports* 20(5):1173-1186, 2017.

38. J. Azoifeifa, M. Lladser, M.A. Allen, **R.D. Dowell**. An annotation agnostic algorithm for detecting nascent RNA transcripts in GRO-seq *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 14(5):1070-1081, ISSN: 1545-5963, 2017.
37. A.L. Scott, P. Richmond, **R.D. Dowell** and A. Selmecki. The influence of polyploidy on the evolution of yeast grown in sub-optimal carbon source. *Molecular Biology and Evolution* msx205, 2017.
36. K.A. Audetat, A.T. Odell, T. Lee, J.M. Espinosa, **R.D. Dowell**, and D. Taatjes. A kinase-independent role for CDK19 in p53 response. *Molecular and Cellular Biology* MCB.00626-16, 2017.
35. S. Bhandare, D. Goldberg, and **R.D. Dowell**. Discriminating between HuR and TTP binding sites using the k-spectrum kernel method. *PLoS ONE* 12(3):e0174052, 2017.
34. P. Rudra, W.J. Shi, B. Vestal, P.H. Russell, A. Odell, **R.D. Dowell**, R.A. Radcliffe, L.M. Saba, K. Kechris. Model based heritability scores for high-throughput sequencing data. *BMC Bioinformatics* 18:143, 2017.
33. M.E. Lladser, J.G. Azoifeifa, M.A. Allen, **R.D. Dowell**. RNA Pol II transcription model and interpretation of GRO-seq data. *Journal of Mathematical Biology*, 74:77, 2017.
32. J. Azoifeifa and **R.D. Dowell**. A generative model for the behavior of RNA polymerase. *Bioinformatics*, 33(2):227-234, 2017.
31. **R.D. Dowell**, A. Odell, P. Richmond, D. Malmer, E. Harper-Stromberg, B. Bennett, C. Larson, S. Leach, and R. Radcliffe. Genome Characterization of the Selected Long and Short Sleep Mouse Lines. *Mammalian Genome*, 27:574, 2016.
30. H.M. Kamens, R.P. Corley, P.A. Richmond, T.M. Darlington, **R.D. Dowell**, C.J. Hopfer, M.C. Stallings, J.K. Hewitt, S.A. Brown, Marissa A. Ehringer. Evidence for Association Between Low Frequency Variants in CHRNA6/CHRNA3 and Antisocial Drug Dependence. *Behavior Genetics*, Sep;46(5):693-704, 2016
29. J.Vera and **R.D. Dowell**. Survey of cryptic unstable transcript in yeast. *BMC Genomics* 17:305, 2016.
28. Z.C. Poss, C.C. Ebmeier, A. Odell, A. Tangpeerachaikul, T. Lee, H. E. Pelish, M.D. Shair, **R.D. Dowell**, W. Old, D.J. Taatjes. Identification of Mediator kinase substrates in human cells using cortistatin A and quantitative phosphoproteomics. *Cell Reports* 15(2):436-450, 2016.
27. Li Wang, J.A. Siegenthaler, **R.D. Dowell**, and R. Yi. Foxc1 reinforces quiescence in self-renewing hair follicle stem cells. *Science* 351(6273): 613-617, 2016.
26. T. Read, P. Richmond, **R.D. Dowell**. Genetic background controls the regulatory capacity of a polymorphic transcription factor. *PLoS Genetics* 12(1): e1005746. doi: 10.1371/journal.pgen.1005746, 2016.
25. D. Knox and **R.D. Dowell**. A simulation model to study transcriptional regulation through the dynamic changes in configuration of DNA binding factors. *IEEE/ACM*

*Transactions on Computational Biology and Bioinformatics*. May-June  
13(3):459–71; ISSN: 1545-5963, 2016.

24. E.K. Pugach, P.A. Richmond, J.G. Azofeifa, **R.D. Dowell**, L.A. Leinwand. Prolonged Cre expression driven by the -myosin heavy chain promoter can be cardiotoxic. *Journal of Molecular and Cellular Cardiology* 86:54–61, 2015.
23. B. Bennett, C. Larson, P.A. Richmond, A. Odell, L. Saba, B. Tabakoff, **R.D. Dowell**, R. Radcliffe. QTL Mapping of Acute Functional Tolerance in the LXS Recombinant Inbred Strains. *Alcoholism: Clinical and Experimental Research* 39(4):611-620, 2015.
22. A. Selmecki, Y.E. Maruvka, P.A. Richmond, M. Gullet, N. Shores, A. Sorenson, S. De, R. Kishony, F. Michor, **R.D. Dowell**, and D. Pellman. Polyploidy can drive rapid adaptation in yeast. *Nature* 519:349–352, 2015.
21. J. Hendrix, T. Read, J-F. Lalonde, P.K Jensen, W. Heymann, E.Z. Lovelace, S.A. Zimmermann, M. Brasino, J. Rokicki, **R.D. Dowell**. An Engineered Calcium-Precipitable Restriction Enzyme. *ACS Synthetic Biology* 3(12):969-971, 2014.
20. J. Azofeifa, M. Lladser, M.A. Allen, **R.D. Dowell**. FStitch: A fast and simple algorithm for detecting nascent RNA transcripts. *5th ACM Conference on Bioinformatics, Computational Biology and Health Informatics* Sept 2014.
19. M.A. Allen, Z. Andrysik, V.L. Dengler, H.S. Mellert, A. Guarnieri, J.A. Freeman, K.D. Sullivan, M.D. Galbraith, X. Luo, W.L. Kraus, **R.D. Dowell**, and J.M. Espinosa. Global analysis of p53-regulated transcription identifies its direct targets and unexpected regulatory mechanisms. *eLife* 3:e02200, 2014.
18. J. Rokicki, D. Knox, **R.D. Dowell** and S. Copley. Chodachrome: A Tool for visualizing protein evolution across bacteria. *BMC Genomics* 15:65, 2014.
17. M.A. Allen and **R.D. Dowell**. Retrospective reflections of a whistleblower-Opinions on misconduct responses. *Accountability in Research* 20:339-348, 2013.
16. M.D. Galbraith, M. Allen, X. Wang, M. Scwhinn, D. Daniels, W. Hahn, **R.D. Dowell** and J.M. Espinosa. HIF1A activates transcriptional elongation via recruitment of CDK8-Mediator. *Cell* 153(6):13271339, 2013.
15. L. Wang, **R.D. Dowell**, and R. Yi. Genome-wide maps of polyadenylation reveal dynamic mRNA 3'end formation in mammalian skin lineages. *RNA* 19:413-425, 2013.
14. J. Shi, H. Zhang, **R.D. Dowell** and M.W. Klymkowsky. *sizzled* function and secreted factor network dynamics. *Biology Open*. 1, 286-294. 2012.
13. T.W. Danford, **R.D. Dowell**, S. Agarwala, P. Grisafi, G.R. Fink, D.K. Gifford. Discovering Regulatory Overlapping RNA Transcripts. *Journal of Computational Biology* 18(3):295-303, 2011.
12. **R.D. Dowell**. Transcription factor binding variations in the evolution of gene regulation. *Trends in Genetics* 26(11):468-475, 2010. (A peer reviewed review article)
11. T. Danford, **R.D. Dowell**, S. Agarwala, P. Grisafi, G.R. Fink, and D.K. Gifford. Discovering regulatory overlapping RNA transcripts. *Fourteenth International*

*Conference on Research in Computational Molecular Biology*. Lisbon, Portugal, August 2010.

10. J. Wolf, **R.D. Dowell**, S. Mahony, M. Rabani, D.K. Gifford, and G.R. Fink. Dual transcriptional-translational regulation of *FLO11* by Khd1p implements a developmental switch. *Genetics* 185:513-522, 2010.
9. **R.D. Dowell\***, O. Ryan\*, A. Jansen, D. Cheung, S. Agarwala, T. Danford, D.A. Bernstein, P.A. Rolfe, L.E. Heisler, B. Chin, P.C. Phillips, G.R. Fink, D.K. Gifford and C. Boone. Genotype to phenotype: A complex problem. *Science* 328(5977):469, 2010.
8. S.L. Bumgarner, **R.D. Dowell**, P. Grisafi, D.K. Gifford, and G.R. Fink. Toggle involving *cis*-interfering noncoding RNAs controls variegated gene expression in yeast. *PNAS*, 106(43):18321-18326, 2009.
7. G.K. Gerber, **R.D. Dowell**, T.S. Jaakkola, and D.K. Gifford. Automated discovery of functional generality of human gene expression programs. *PLoS Computational Biology*, 3(8):e148, 2007.
6. D.T. Odom\*, **R.D. Dowell\***, E.S. Jacobsen, W. Gordon, T.W. Danford, K.D. MacIsaac, P.A. Rolfe, C.M. Conboy, D.K. Gifford, and E. Fraenkel. Tissue-specific transcriptional regulation has diverged significantly between human and mouse. *Nature Genetics*, 39(6):730-2, 2007.
5. **R.D. Dowell** and S.R. Eddy. Efficient Pairwise RNA Structure Prediction and alignment using sequence alignment constraints. *BMC Bioinformatics*, 7:400, 2006.
4. Y. Qi, P.A. Rolfe, K.D. MacIsaac, G.K. Gerber, D. Pokholok, J. Zeitlinger, T.W. Danford, **R.D. Dowell**, T.S. Jaakkola, R.A. Young, and D.K. Gifford. High-resolution computational models of genome binding events. *Nature Biotechnology*, 24(8):963-970, 2006.
3. D.T. Odom, **R.D. Dowell**, E.S. Jacobsen, L. Nekludova, P.A. Rolfe, T.W. Danford, D.K. Gifford, E. Fraenkel, G.I. Bell, and R.A. Young. Core transcriptional regulatory circuitry in human hepatocytes. *Nature/EMBO Molecular Systems Biology*, 2:2006.0017, 2006.
2. **R.D. Dowell** and S.R. Eddy. Evaluation of Several Lightweight Stochastic context-free grammars for RNA secondary structure prediction. *BMC Bioinformatics*, 5:71, 2004.
1. **R.D. Dowell**, R.M. Jokerst, A. Day, S.R. Eddy, and L. Stein. The distributed annotation system. *BMC Bioinformatics*, 2:7, 2001.

PUBLISHED  
ABSTRACTS

M.A. Ehringer, H.M. Kamens, R.P. Corley, M. Simonson, A. Poole, P. Richmond, J.A. Stitzel, **R.D. Dowell**, K. Krauter, M.B. McQueen, M.C. Stallings, C. Hopfer, T. Crowley, J.K. Hewitt. Behavioral Disinhibition: Sequencing *CHRN* genes in a selected sample to identify novel variants. *Alcohol Clin Exp Res.* 37(S2), 256A, 2013.

H.M. Kamens, A. Poole, R.P. Corley, M.B. McQueen, M.C. Stallings, C. Hopfer, J. Stitzel, J.K. Hewitt, **R.D. Dowell**, M.A. Ehringer. Sequencing nicotinic acetylcholine receptor subunits for association with dependence vulnerability. Society for Research on Nicotine and Tobacco, Abstract Book PA17-1, p.38, 2012.

R.A. Radcliffe, A.W. Poole, C.J. Larson, **R.D. Dowell**, B. Bennett. Genetic influences on alternative splicing in a mouse model of differential alcohol sensitivity. *Alcohol Clin Exp Res* 36:S158, 2012.

**R.D. Dowell.** A graphical user interface for contig mapping (an abstract). *Texas A&M University Undergraduate Journal of Science*, Spring 1997.

CLASSROOM  
TEACHING

**University of Colorado, Boulder, Colorado USA**

MCDB 4520/5520;CSCI 4830/7000 Bioinformatics and Genomics (Spring 2016-18, Fall 2010: Instructor)  
MCDB 4521/5521 Bioinformatics and Genomics Laboratory (Spring 2016-18: Instructor)  
GRAD 5000 Responsible Conduct of Research (Fall 2018; Spring 2018: Lecture on Collaboration)  
CBPS 7711 Methods and Tools in Biomedical Informatics (Fall 2010-16: 2 lectures/year)  
CBPS 7712 Research Methods in Biomedical Informatics (Spring 2010-17: 2 lectures/year)  
MCDB 2150 Principles of Genetics (Spring 2013, 2014, 2015: Instructor)  
APPM 4720/5720; CSCI 4830/7000; MCDB 6440; CHEM 4921/5921 Statistics & Computation for Genomics and Metagenomics (Spring 2012: Instructor)  
CSCI 4810 Seminar in Computational Biology (Spring 2010: 1 lecture)  
CSCI 3434 Theory of Computation (Spring 2011-2012: 1 lecture)

**Massachusetts Institute of Technology, Cambridge, Massachusetts USA**

6.874;7.90 Computational Systems Biology (Spring 2008-2009: 2 lectures)

**Washington University in St. Louis, St. Louis, Missouri USA**

BME 140 Introduction to Biomedical Engineering (Fall 2001-2004: 1 lecture)  
Bio 5495;BME 537 Computational Molecular Biology (Spring 1999: Teaching Assistant)

WORKSHOP  
INSTRUCTION

**University of Colorado, Boulder, Colorado USA**

Nascent Transcription Workshop (Rocky Mountain Genomics HackCon 2018; 1.5 days)  
Short Read Sequence Analysis Workshop (Summer 2014-2018; 2 weeks/year)  
Global Run-on Protocol Workshop (April 2016; 1 week)  
Online Course in Python Programming (Winter 2013: 2 weeks; now massively open online course)

REFEREE

National Institute Health GCAT grant reviewer (2019)  
Boettcher Foundation Webb-Waring Biomedical Research Award Review Panel (2014 – 2019)  
National Science Foundation *ad hoc* grant reviewer (2013 – 2018)  
National Institute of Health *ENCODE* grant reviewer (2016)  
National Institute Health NHGRI grant reviewer (2016)  
CCTSI Pilot Grant Reviewer (2012 – 2018)  
iGEM Jamboree Judge (2012, 2013, 2015, 2018)  
Rocky Mountain Celebration of Women in Computing Conference Paper Reviewer (2012)

Manuscript Reviewer for multiple journals (e.g. eLife, PLoS Genetics, PLoS Computational Biology)

PROFESSIONAL  
MEMBERSHIPS

- Association of Computing Machinery
- Biomedical Engineering Society
- Institute of Electrical and Electronics Engineers
- International Society for Computational Biology
- Genetics Society of America
- Trisomy 21 Research Society