

## 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, Comp. Bioscience Program, CU 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**, (2017)

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

72. S. Hunter, R. Sigauke, J. Stanley, M. Allen, **R.D. Dowell**. Protocol Variations in Run-On Transcription Dataset Preparation Produce Detectable Signatures in Sequencing Libraries. (*accepted*, BMC Genomics) 2022. Preprint available: <https://www.researchsquare.com/article/rs-571377/v1>
71. A. Gupta, S.K. Sasse, M.A. Gruca, L. Sanford, **R.D. Dowell**, A.N. Gerber. Deconvolution of multiplexed transcriptional responses to wood smoke particles defines rapid aryl hydrocarbon receptor signaling dynamics. J. Biol. Chem., 297(4):101147, 2021.
70. L.N. Janiszewski, M. Minson, M.A. Allen, **R.D. Dowell**, A.E. Palmer. Characterization of global gene expression, regulation of metal ions, and infection outcomes in immune competent 129S6 mouse macrophages. Infection and Immunity, 89(11):e00273-21, 2021.
69. A. Pouikli, S. Parekh, M. Maleszewska, M. Baghdadi, I. Tripodi, C. Nikopoulou, K. Folz-Donahue, Y. Hintze, A. Mesaros, P. Giavalisco, **R. Dowell**, L. Partridge, P. Tessarz. Chromatin remodeling due to degradation of citrate carrier impairs osteogenesis of aged mesenchymal stem cells. Nature Aging. 1:810-825, 2021.
68. C. Zhang, Dongmei Wang, Li Wang, **Robin Dowell** and Rui Yi. Escape of hair follicle stem cells causes stem cell exhaustion during ageing. Nature Aging. 1:889-903, 2021.
67. R. Sigauke, M. Gruca, M. Gohde‡, **R.D. Dowell**. Annotation agnostic approaches to nascent transcription analysis. Meth. Enzymology. (*accepted*)
66. C.B. Levandowski, T. Jones, M. Gruca, S. Ramamoorthy, **R.D. Dowell**#, D.J. Taatjes#, The naturally occurring  $\Delta 40p53$  isoform inhibits eRNA transcription and enables context-specific regulation during p53 activation. PLoS Biology 19(8):e3001364
65. M. Melnick, P. Gonzales, T.J. LaRocca, Y. Song, J. Wu, M. Benatar, B. Oskarsson, L. Petrucelli, **R.D. Dowell**, C.D. Link, M. Prudencio, Application of a bioinformatic pipeline to RNA-seq data identifies novel viruslike sequence in human blood, G3 Genes—Genomes—Genetics, 11(9):jkab141, 2021.
64. J.D. Rubin, J.T. Stanely, R.S. Sigauke, C.B. Levandowski, Z.L. Maas‡, J. Westfall, D.J. Taatjes, **R.D. Dowell**. Transcription factor enrichment analysis (TFEA) quantifies the activity of multiple transcription factors from a single experiment. Commun. Biol. 2;4(1):661, 2021
63. Q. Yang, T.K. Saldi, E. Lasda, C.J. Decker, C.L. Paige, D. Muhrad, P.K. Gonzales, M.R. Fink, K.L. Tat, C.R. Hager, J.C. Davis, C.D. Ozeroff, N.R. Meyerson, S.K. Clark, W.T. Fattor, A.R. Gilchrist, A. Barbachano-Guerrero, E.R. Worden-Sapper, S.S. Wu, G.R. Brisson, M.B. McQueen, **R.D. Dowell**, L. Leinwand, R. Parker, S.L. Sawyer. Just 2% of SARS-CoV-2-positive individuals carry 90% of the virus circulating in communities. PNAS 118(21):e2104547118, 2021 (*Highlighted in PNAS Commentary* <https://www.pnas.org/content/118/26/e2108044118>)
62. C.J. Walker, C. Crocini, D. Ramirez, A.R. Killaars, J.C. Grim, B.A. Aguado, S.K. Clark, M. Allen, **R.D. Dowell**, L.A. Leinwand, K.S. Anseth. Nuclear

- mechanosensing drives chromatin remodelling in persistently activated fibroblasts. *Nat Biomed Eng.* <https://doi.org/10.1038/s41551-021-00709-w>, 2021
61. D.T. Youmans, A.R. Gooding, **R.D. Dowell**, T.R. Cech. Competition between PRC2.1 and 2.2 subcomplexes regulates PRC2 chromatin occupancy in human stem cells. *Molecular Cell*. 81(3):P488-501.E9, 2021
60. F.S. Gally, S.K. Sasse, J.S. Kurche, M.A. Gruca, J.H. Cardwell, T. Okamoto, H.W. Chu, X. Hou, O.B. Poirion, J. Buchanan, S.P. Colgan, **R.D. Dowell**, I.V. Yang, D.A. Schwartz, A.N. Gerber. Epigenetic priming and RNA polymerase 2 loading at the-3kB MUC5B enhancer region that is genetically associated with idiopathic pulmonary fibrosis (IPF).” *JCI Insight* 6(2):e144294, 2021
59. J.K. Rimel, Z.C. Posselt, B. Erickson, Z.L. Maas, C.C. Ebmeier, J.L. Johnson, T.O. Yaron, M.J. Bradley, K.B. Hamman, S. Hu, G. Malojcic, J.J. Marineau, P.W. Whiate, M. Brault, L. Tao, P. DeRoy, C. Clavette, S. Nayak, T-M. Decker, I.H. Kalthheuner, H. Bunch, L.C. Cantley, M. Geyer, J. Iwasa, **R.D. Dowell**, D.L. Bentley, W.M. Old, D.J. Taatjes. Selective inhibition of CDK7 reveals high-confidence targets and new models for TFIID function in transcription. *Genes & Development* 34:21-22, 2020
58. R.A. Radcliffe, **R. Dowell**, A. Odell, P. Richmond, B. Bennett, C. Larson, K. Kechris, L. Saba, P. Rudra, S. When. RNA-seq analysis of the LXS recombinant inbred mouse strains: Genetic and molecular insights into acute functional tolerance. *PLoS ONE* <https://doi.org/10.1371/journal.pone.0240253>, 2020
57. I.J. Tripodi, T.J. Callahan, J.T.V. Westfall, N.S. Meitzer, **R.D. Dowell**, L.E. Hunter. Mechanistic inference from knowledge representation: a toxicogenomics case study. *Toxicology In Vivo* 66:104877, 2020 (Named one of 2020’s Top Translational Bioinformatics Publications by Yearbook of Biomedical Informatics)
56. I.J. Tripodi, M. Chowdhury, **R.D. Dowell**. ATAC-seq signal processing and recurrent neural networks can identify RNA polymerase activity. *PLoS ONE* 15(4):e0232332, 2020
55. C.B. Fant, C. Levandowski, K. Gupta, Z.L. Maas, J. Moir, J.D. Rubin, A. Sawyer, M.N. Esbin, J.K. Rimel, O. Luyties, M.T.Marr, I. Berger, **R.D. Dowell**, D.J. Taatjes. TFIID Enables RNA polymerase II promoter-proximal pausing. *Molecular Cell* 78(4):785-793, 2020
54. Y. Han, L. Sanford, D.M. Simpson, **R.D. Dowell**, A.E. Palmer. Remodeling of Zn<sup>2+</sup> homeostasis upon differentiation of mammary epithelial cells. *Metallomics* 12:346-362 doi:10.1039/c9mt00301k, 2020
53. J.F. Cardiello, G.J. Sanchez, M.A. Allen, **R.D. Dowell**. Lessons from eRNAs: understanding transcriptional regulation through the lens of nascent RNAs. *Transcription* 11(1):3-18 2020 doi:10.1080/21541264.2019.1704128, 2020. (A peer reviewed review article)
52. J.T. Stanley, A.R. Gilchrist, A.C. Stabell, M.A. Allen, S.L. Sawyer, **R.D. Dowell**. Two-stage ML classifier for identifying host protein targets of the dengue protease. *Pac Symp Biocomput. (PSB)*. 25:487-498, 2020
51. S.K. Sasse, M. Gruca, M.A. Allen, V. Kadiyala, T. Song, F. Gally, A. Gupta, M.A. Pufall, **R.D. Dowell**, A.N. Gerber. Nascent transcription analysis defines

- glucocorticoid-induced inflammatory response. *Genome Research* 29(11):1753-1765, 2019
50. I. Steinparzer, V. Sedlyarov, J.D. Rubin, K. Eislmayr, M.D. Galbraith, C.B. Levandowski, T. Vcelkova, L. Sneezum, F. Wascher, F. Amman, R. Kleinova, J.M. Espinosa, G. Superti-Furga, **R.D. Dowell**, D.J. Taatjes, P. Kovarik. Transcriptional responses to interferon require Mediator kinase-dependent pause release and mechanistically distinct functions of CDK8 and CDK19. *Mol. Cell* 76(3):485-499, 2019
  49. M. Melnick, P. Gonzales, J. Cabral, M.A. Allen, **R.D. Dowell**, C.D. Link. Heat shock in *C. elegans* induces downstream of gene transcript accumulation of double-stranded RNA. *PLoS ONE* 14(4):e0206715, 2019
  48. D. Smith, R. Martinelli, G.S. Besra, P.A. Illarionov, I. Szatmari, P. Brazda, M.A. Allen, W. Xu, X. Wang, L. Nagy, **R.D. Dowell**, G.A.W. Rook, L.R. Brunet, C.A. Lowry. Identification and characterization of a novel anti-inflammatory lipid isolated from *Mycobacterium vaccae*, a soil-derived bacterium with immunoregulatory and stress resilience properties. *Psychopharmacology* 236(5):1653-1670, 2019
  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. Merkenschlager. 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(13):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 Vázquez-Baeza, Antonio González, James T. Morton, Siavash Mirarab, Zhen jiang Zech Xu, Lingjing Jiang, Mohamed F. Haroon, Jad Kanbar, Qiyun Zhu, Se Jin Song, Tomasz Kosciolk, Nicholas A. Bokulich, Joshua Lefler, 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 (**Dowell part of Consortium**)

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 TFIIF kinase CDK7 regulates transcription-associated epigenetic modifications. *Cell Reports* 20(5):1173-1186, 2017
38. J. Azofeifa, 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* 34(10):2690-2703, 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. Azofeifa, 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. Azofeifa 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.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  $\alpha$ -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):1327–1339, 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. **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)  
  
===== *Postdoctoral and Predoctoral publications* =====
12. 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
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

SUBMITTED  
MANUSCRIPTS

B.L. Allen, K. Quach, T. Jones, C.B. Levandowski, J.D. Rubin, T. Read, **R.D. Dowell**, A. Schepartz, D.J. Taatjes. Suppression of p53 response by targeting p53-Mediator binding with a stapled peptide. (*resubmitted in response to reviewers*) bioRxiv: <https://doi.org/10.1101/757401>

J.V. Kurland, A. Van Deusen, B. Pawlikowski, M. Hall, N.D. Betta, T. Antwine, A. Cutler, A. Russell, M.A. Allen, **R. Dowell**#, B. Olwin#. Myonuclear maturation dynamics in aged and adult regenerating mouse skeletal muscle. (*preparing response to reviewers*) bioRxiv <https://doi.org/10.1101/2021.07.13.452218>

C.J. Walker, C. Bishop, D. Ramirez, B.A. Aguado, M. Schroeder, C. Crocini, J. Schwisow, K. Moulton, L. Macdougall, R. Weiss, M. Allen, **R. Dowell**, L.A. Leinwand, K.S. Anseth. Extracellular matrix stiffness controls cardiac valvular myofibroblast activation through epigenetic remodeling. (*submitted*)

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**

Instructor

MCDB 3450 Biological Data Science (Spring 2020-2021)

MCDB 4520/5520; CSCI 4830/7000 Bioinformatics and Genomics (Spring 2016-19, Fall 2010)

MCDB 4521/5521 Bioinformatics and Genomics Laboratory (Spring 2016-19)

MCDB 2150 Principles of Genetics (Spring 2013-2015)

APPM 4720/5720; CSCI 4830/7000; MCDB 6440; CHEM 4921/5921 Statistics & Computation for Genomics and Metagenomics (Spring 2012; co-taught Manuel Lladser)

MCDB 5520 Methods and Logic (Spring 2012; co-taught Tom Blumenthal)

Independent Study Mentor



MCDB 7840 (Fall 2021: 3 hours) Samuel Hunter  
BCHM 6901 (Fall 2018: 5 hours) Martin Fenk  
MCDB 4840 (Fall 2014; Spring 2016) Josphephina Hendrix; Jon DeMassi  
Lecturer in Team Taught Classes  
MCDB 5240 Graduate Core 2 (Spring 2019-2021; 5 lectures/year)  
GRAD 5000 Responsible Conduct of Research (Fall 2018-2020; Spring 2018: 1 lecture/term)  
CBPS 7711 Methods and Tools in Biomedical Informatics (Fall 2010-20: 2 lectures/year)  
CBPS 7712 Research Methods in Biomedical Informatics (Spring 2010-21: 2 lectures/year)  
MCDB 5230 Graduate Core 1 (Fall 2012-2017; 2 lectures/year)  
Guest Lecturer  
CSCI 3352 Biological Networks (Spring 2020: 2 lectures)  
CHEM 5801 Advanced Topics in Signal Transduction and Cell Cycle Regulation (Spring 2020, 2016: 1 lecture)  
CSCI 7000-009 Computational Genomics Seminar (Fall 2018: 1 lecture)  
CSCI 3434 Theory of Computation (Spring 2011-2012: 1 lecture)  
CSCI 4810 Seminar in Computational Biology (Spring 2010: 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**

Short Read Sequence Analysis Workshop (Summer 2021, 2014-2019; 2 weeks/year, reverse classroom)  
Nascent Transcription Workshop (Rocky Mountain Genomics HackCon 2018; 1.5 days)  
Global Run-on Protocol Workshop (April 2016, March 2019; 1 week)  
Online Course in Python Programming (Winter 2013: 2 weeks; now MOOC)

**ICAR-Indian Agricultural Research Institute, New Delhi**

NAHEP-CAAST “Next Generation Sequencing and Computational Biology for Agriculture” March 2020 (1 day)

**CURRICULUM  
DEVELOPMENT**

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

Integrated Data Science Certificate Development (2020-2021)  
Computational Biology Minor Development (2018-2021)  
Interdisciplinary Quantitative Biology Program Development (2010-2012)  
Course Creation and Development  
MCDB 3450 Biological Data Science (first offered Spring 2020)  
MCDB 4521/5521 Bioinformatics and Genomics Laboratory (first offered Spring 2016)  
APPM 4720/5720; CSCI 4830/7000; MCDB 6440; CHEM 4921/5921 Statistics &

Computation for Genomics and Metagenomics (first offered Spring 2012)  
Math 1310 Redesign (2010)

REFeree

Boettcher Foundation Webb-Waring Award Review Panel (2014-2021)  
National Institute Health F series Panel (2020,2021)  
ISMB Proceedings Program Committee (2018-2021)  
UK Medical Research Council (MRC) Grants program (2021)  
German Cancer Research Center (DKFZ) Grant program (2020, 2021)  
Austrian FWF grants program (Der Wissenschaftsfonds) (2020)  
National Science Foundation *ad hoc* grant reviewer (2013-2020)  
National Institute Health GCAT grant reviewer (2019)  
Wellcome Trust Grants Program (2017)  
National Institute of Health *ENCODE* Grant Panel (2016)  
National Institute Health NHGRI Grant Panel (2016)  
Linda Crnic Institute Seed Grants Program (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 Journals:** Bioinformatics, BMC Bioinformatics, BMC Genomics, Cell Reports, eLife, Genome Biology, Genome Research, Molecular Cell, NAR, Nature, Nature Genetics, PLoS Computational Biology, PLoS Genetics, Transcription

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