

Robin D. Dowell

CONTACT INFORMATION BioFrontiers Institute
University of Colorado *Office:* (303) 492-8204
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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**, Founder (founded 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

ACTIVE SUPPORT
(GRANTS)

PI

- NIH R01 GM125871: A Technique for Measuring Transcription Factor Activity (Dowell) 2018-2023
- NSF ABI: ABI Innovation: Data driven model of polymerase activity (Dowell) 2018-2021
- DTRA: Double-stranded RNA as a non-invasive biomarker of infection (Sawyer/Dowell/Parker/Poeschla) 2018-2021
- NIH R03 AG061466: How does the naturally-occurring delta-Np53 isoform influence aging? (Dowell/Taatjes) 2019-2021
- MCDB-UCCC Joint Multi-PI Pilot Project: Structural mapping of nascent transcription in H3K27M+ diffuse intrinsic pontine glioma (Vibhakar, Dowell) 2020-2021
- NIH R03 HD103995: Measuring global, loci-specific RNA degradation to interrogate RNA dysregulation in Down syndrome during development (Dowell) 2020-2022

PEER-REVIEWED
PUBLICATIONS

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

61. F.S. Gally, S. Sasse, M. Gruca, S.P. Colgan, **R.D. Dowell**, 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)." *Amer. J. Respiratory and Critical Care Medicine*. Jan 2021 (*accepted*)
60. J.K. Rimel, Z.C. Poss, 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. Kaltheuner, 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.
59. 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>
58. 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.
57. 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.
56. 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
55. M. Gruca, M. Gohde†, **R.D. Dowell**. Annotation agnostic approaches to nascent transcription analysis: Fast Read Stitcher and Transcription Fit. (*accepted*) *Meth. Enzymology*.

54. Y. Han, L. Sanford, D.M. Simpson, **R.D. Dowell**, A.E. Palmer. Remodeling of Zn²⁺ homeostasis upon differentiation of mammary epithelial cells. *Metallomics* 12:346-362 2020 doi:10.1039/c9mt00301k
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 (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. Eismayr, 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 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. (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 TFIIH 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 -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. Andrysiak, 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.

SUBMITTED
PUBLICATIONS

C. Zhang, Dongmei Wang, Li Wang, **Robin Dowell** and Rui Yi. Escape of hair follicle stem cells from a defective niche. (*submitted*)

J.D. Rubin, J.T. Stanely, R.S. Sigauke, **R.D. Dowell**. Transcription factor enrichment analysis (TFEA) measures colocalization of transcription factor motifs with regulatory regions. (*submitted*) bioRxiv: <https://doi.org/10.1101/2020.01.25.919738>

C.B. Levandowski, T. Jones, M. Gruca, S. Ramamoorthy, **R.D. Dowell***, D.J. Taatjes*, The naturally occurring 40p53 isoform inhibits eRNA transcription and enables context-specific regulation during p53 activation. (*submitted*)

B.L. Allen, K. Quach, 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. (*submitted*) bioRxiv: <https://doi.org/10.1101/757401>

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. Citrate carrier links intermediate metabolism to chromatin architecture and regulates osteogenesis in mesenchymal stem cells upon ageing. (*submitted*) bioRxiv: <https://doi.org/10.1101/2020.04.02.022293>

C.J. Walker, C. Crocini, D. Ramirez, A.R. Killaars, J.C. Grim, B.A. Aguado, S.K. Clark, M.A. Allen, **R.D. Dowell**, L.A. Leinwand, K.S. Anseth. Nuclear mechanosensing drives epigenetic remodeling of persistently activated myofibroblasts (*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.

PATENTS

University of Colorado, Boulder, Colorado USA

R.D. Dowell, J. Azofeifa and M.A. Allen. Assessment of Transcription Factor Activity (*Filed Feb 14, 2018*)

PCT Application No. PCT/US2018/018230

CU TTO File No. CU4226B-PCT1

S. Sawyer, N. Myerson, Q. Yang, and R.D. Dowell. Systems, Methods, And Compositions For The Rapid Early-Detection of Host RNA Biomarkers of Infection (*Filed Nov 13, 2019*)

CU TTO File No. 62934754

MENTORING

University of Colorado, Boulder, Colorado USA

Current Postdocs (year joined lab)

Jacob Stanley (2018)

Gilson Sanchez (2019)

Lynn Sanford (2020)

Current Graduate Students (year joined lab)

Daniel Ramirez (2017) (IQ/MCDB)

Chi Zhang (2017) (MCDB; joint R. Yi)

Jessica Westfall (2018) (MCDB)

Samuel Hunter (2018) (MCDB)

Rutendo Sigauke (2018) (CBP)

Qing Yang (2018) (MCDB; joint S. Sawyer)

Marko Melnick (2018) (Iphy; joint C. Link)

Kendra Meer (2019) (CBP)

Taylor Jones (2019) (Biochem; joint D. Taatjes)

Jesse Kurland (2019) (MCDB; joint with B. Olwin)

Current Undergraduate Students

Niketna Vivek (MCDB)

Antonio Salcido-Alcantar Jr. (CHEM)

William Sherlock (MCDB)

Colin Moore (MCDB,CSCI)

Simeon Petrov (PSYC, NEUR)

REFEREE

National Institute Health F series grant reviewer (2020)

National Science Foundation *ad hoc* grant reviewer (2013 – 2020)

Boettcher Foundation Webb-Waring Award Review Panel (2014 – 2020)
ISMB Proceedings Program Committee (2018-2020)
National Institute Health GCAT grant reviewer (2019)
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 a dozen 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