

Curriculum vitae

Carol J. Bult, Ph.D.

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The primary theme of my research program is "Bridging the Digital Biology Divide," reflecting the critical role that informatics and computational biology play in advancing biomedical research. Highlights of my research program include the early use of high-throughput DNA sequencing for the discovery of novel human genes (*Nature* 377:3-174, 1995), sequencing and annotating the first three complete genomes of cellular organisms (*Science* 269:496-512, 1995; *Science* 270:397-403, 1995; *Science* 273:1058-1073, 1996), sequencing and annotation of the mouse genome (*Nature* 420:520-562, 2002; *PLoS Biology* 7(5), 2009), and genome-scale assessment of transcriptional diversity and dynamics in the mouse genome (*Nature* 409:685-690, 2001; *Nature* 420: 563-573, 2002; *Science* 309:1559-1563, 2005). Recent research initiatives in my research group include computational prediction of gene function in the mouse (*PLOS Computational Biology*, 4(9):e1000165, 2008) and the use of the mouse to understand genetic pathways in normal lung development and disease (*Genome Biology*, 9:R108, 2008; *PeerJ*, 4:e2318, 2016).

Education

- 1989 Ph.D., Genetics
University of New Hampshire, Durham, N.H.
Dissertation title: "Isozyme and quantitative trait variation within and among local natural populations of the wild soybean, *Glycine soja* (Sieb. & Zucc.)."
- 1984 B.S. with Distinction and with Recognition of a Distinguished Senior Project, Biology
George Mason University, Fairfax, VA
Thesis title: "Allozyme variation at five loci in low salinity populations of the hard-shell clam, *Mercenaria mercenaria*."

Professional Experience

- 1997 - present **The Jackson Laboratory**, Bar Harbor, ME
- Knowlton Family Chair (2015 – present)
 - Deputy Directory, The Jackson Laboratory Cancer Center (2014 – 2019)
 - Scientific Director, Patient Derived Xenograft and Cancer Avatar Program (2012 – 2019)
 - Senior Advisor for Research IT (2011 –2014)
 - Jackson Laboratory Cancer Center Deputy Director for Planning and Evaluation (interim) (2010 – 2011)
 - Professor (2009- present)
 - Associate Professor (2003-2009)
 - Assistant Professor (2000-2003)
 - Research Scientist (1999-2000)
 - Visiting Investigator (1997-1999)
- 2014-present **Tufts University**, Boston, MA
- Professor of Medicine, School of Graduate Biomedical Sciences
- 1996 - present **University of Maine**, Orono, ME
- Graduate Faculty, Graduate School of Biomedical Sciences and Engineering (1999 – present)
 - Research Faculty/Program Manager (1997-1999)
 - Visiting Scholar, Department of Spatial Information and Engineering (1996)
- 1993 -1996 **The Institute for Genomic Research** (TIGR), Rockville, MD
- Research Faculty, Department of Gene Discovery and Comparative Genomics
 - Director, Molecular Systematics Laboratory
- 1991 - 1996 **Smithsonian Institution**, Laboratory of Molecular Systematics, Washington, D.C.
- Research Associate (1993-1996)
 - Postdoctoral Fellow (1991 -1993)
- 1990 - 1991 **Louisiana State University**, Baton Rouge, Louisiana
- Postdoctoral Fellow, Department of Biochemistry
- 1984 - 1989 **University of New Hampshire**, Durham, N.H.
- Graduate Research Associate, Genetics Program

Publications

- Neuhauser S, Begley D, Krupke D, **Bult CJ**. PDX Like Me: A query language for identifying PDX models that match complex genomic profiles. *J Clinical Oncology*, submitted.
- Koc S, Lloyd MW, Gover J, Seepo S, Lakshmi S..... **Bult CJ**, Davis-Dusenbery B, Dean DA, Chuang JH, for the PDXNet Consortium Members. 2021. PDXNet Portal: Patient-Derived Xenograft model, data, workflow, and tool discovery. *bioRxiv* doi: <https://doi.org/10.1101/2021.10.15.464537>
- Petit F, Longoni M, Wells J, Maser R, Dysart MJ.....**Bult CJ**, Donahoe PK, High FA. 2021. Missense variants affecting the actin-binding domains of *PLS3* cause X-linked congenital diaphragmatic hernia and body wall defects. *medRxiv* doi: <https://doi.org/10.1101/2021.07.07.21259278>
- Foxworth N, Wells J, Ocana-Lopez S, Muller S, Denegre J....**Bult CJ**, Loscertales M. 2021. The extracellular matrix gene, *Svep1*, orchestrates airway patterning and the transition from lung branching morphogenesis to alveolar maturation in the mouse. *bioRxiv* doi: <https://doi.org/10.1101/2021.07.26.453586>
- Ravanmehr V, Blau H, Cappelletti L, Fontana T, Carmody L.....Bult C, Rueter J, Casiraghi E, Valentini G, Mungall C, Oprea T, Robinson PN. 2021. Supervised learning with word embeddings derived from PubMed captures latent knowledge about protein kinases and cancer. *bioRxiv* doi: <https://doi.org/10.1101/2021.06.11.447943>
- Richardson JE, Baldarelli RM, **Bult CJ**. 2021. Multiple genome viewer (MGV): a new tool for visualization and comparison of multiple annotated genomes. *Mamm Genome* doi: 10.1007/s00335-021-09904-1
- Ringwald M, Richardson JE, Baldarelli RM, Blake JA, Kadin JA, Smith C, **Bult CJ**. 2021. Mouse Genome Informatics (MG): latest news from MGD and GXD. *Mamm Genome* doi: 10.1007/s00335-021-09921-0
- Hamosh A, Amberger JS, Bocchini CA, Bodurtha J, **Bult CJ**, Chute CG, Cutting GR, Dietz HC, Firth HV, Gibbs RA, Grody WW, Haendel MA, Lupski JR, Posey JE, Robinson PN, Schriml LM, Scott AF, Sobreira NL, Valle D, Wu N, Rasmussen SA. 2021. *Am J Hum Genet* 108(9):1807-1808.
- Manolio TA, **Bult CJ**, Chisholm RL, Deverka PA, Ginsburg GS, Goldrich M, Jarvik GP, Mensah GA, Ramos EM, Relling MV, Roden DM, Rowley R, Williams MS, Green ED. 2021. Genomic medicine year in review: 2021. *Am J Hum Genet* 108(12):2210-2214.
- Sun H, Cao S, Mashl RJ, Mo CK, Zaccaria S, Wendl MC, Davies SR, Bailey MH, Primeau TM, Hoog J, Mudd JL, Dean DA 2nd, Patidar R, Chen L, Wyczalkowski MA, Jayasinghe RG, Rodrigues FM, Terekhanova NV, Li Y, Lim KH, Wang-Gillam A, Van Tine BA, Ma CX, Aft R, Fuh KC, Schwarz JK, Zevallos JP, Puram SV, Dipersio JF; **NCI PDXNet Consortium**, Davis-Dusenbery B, Ellis MJ, Lewis MT, Davies MA, Herlyn M, Fang B, Roth JA, Welm AL, Welm BE, Meric-Bernstam F, Chen F, Fields RC, Li S, Govindan R, Doroshow JH, Moscow JA, Evrard YA, Chuang JH, Raphael BJ, Ding L. 2021. Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidates for targeted treatment. *Nat Commun* 12(1):5086.
- Berlow NE, Crawford KA, **Bult C**, Noakes C, Sloma I, Rudzinski ER, Keller C. 2021. RET in Alveolar Rhabdomyosarcoma, *CSHL Molecular Case Studies*. doi: 10.1101/mcs.a006049
- Woo XY, Giordano J, Srivastava A, Zhao ZM, Lloyd MW.....**Bult CJ**, Medico E, Chuang JH, PDXNet Consortium, EuroPDX Consortium. Conservation of copy number profiles during engraftment and passaging of patient-derived cancer xenografts. 2021. *Nature Genetics*, 53(1):86-99.
- Manolio TA, **Bult CJ**, Chisholm RL, Deverka PA, Ginsburg GS, Goldrich M, Jarvik GP, Mensah GA, Relling MV, Roden DM, Rowley R, Tamburro C, Williams MS, Green ED. 2020. Genomic Medicine Year in Review: 2020. *Am J Hum Genet*. 107(6):1007-1010. doi: 10.1016/j.ajhg.2020.11.005.
- Blake JA, Baldarelli R, Kadin JA, Richardson JE, Smith CL, **Bult CJ**. 2020. Mouse Genome Database (MGD): Knowledgebase for mouse-human comparative biology. *Nucleic Acids Res*. 4:gkaa1083. doi: 10.1093/nar/gkaa1083.
- Alliance of Genome Resources Consortium. 2020. Alliance of Genome Resources Portal: unified model organism research platform. *Nucleic Acids Res*. 48(D1):D650-D658. doi: 10.1093/nar/gkz813.

Stripecke R, Munz C, Schuringa JJ, Bissig KD, Soper B, Meehan T, Yao LC, Di Santo JP, Brehm M, Rogriguez E, Wege AK, Bonnet D, Guionaud S, Howard KE, Kitchen S, Klein F, Saeb-Parsy K, Sam J, Sharma AD, Tump A, Trusolino L, **Bult C**, Shultz L. 2020. Innovations, challenges, and minimal information for standardization of humanized mice. *EMBO Mol Med* 12:e8662. <https://doi.org/10.15252/emmm.201708662>

Manolio TA, **Bult CJ**, Chisholm RL, Deverka PA, Ginsburg GS, Jarvik GP, McLeod HL, Mensah GA, Relling MV, Roden DM, Rowley R, Tamburro C, Williams MS, Green ED. 2019. Genomic Medicine Year in Review: 2019. *Am Soc Human Genet* 105:1072-1075.

Evrard YA, Srivastava A, Randjelovic J, Arunachalam S, **Bult CJ**.....Chuang JH. 2019. Systematic establishment of robustness and standards in Patient-Derived Xenograft experiments and analysis. *bioRxiv* doi: <https://doi.org/10.1101/790246>.

Wood XY, Giordano J, Srivastava A, Zhao ZM, Lloyd MW...**Bult CJ**, Medico E, Chuang JH. 2019. Conservation of copy number profiles during engraftment and passaging of patient-derived cancer xenografts. *bioRxiv* doi: <https://doi.org/10.1101/861393>.

Kolishovski G, Lamoureux A, Hale P, Richardson J, Recla J, Adesanya O, Simons A, Ramamoorthy G, **Bult CJ**. The JAX Synteny Browser for Mouse-Human Comparative Genomics. 2019. *Mammalian Genome*, 30:353-361.

Alliance of Genome Resources Consortium. 2019. The Alliance of Genome Resources: Building a modern data ecosystem for model organism databases. *Genetics*, doi: 10.1534/genetics.119.302523.

Hill DP, Harper A, Malcolm J, McAndrews MS, Mockus SM, Patterson SE, Reynolds T, **Bult CJ**, Chesler EJ, Blake JA. 2019. Cisplatin-Interacting Genes Differentially Regulated in Triple Negative Breast Cancer Subtypes. *BMC Cancer*, 19:1039.

Alliance of Genome Resources Consortium. 2019. Alliance of Genome Resources Portal: unified model organism research platform. *Nucl Acids Res* doi: 10.1093/nar/gkz813

Woo XY, Srivastava A, Graber JH, Yadav V, Sarsani VK, Simons A, Beane G, Grubb S, Ananda G, Liu R, Stafford G, Chuang JH, Airhart SD, Karuturi RKM, George J, **Bult CJ**. 2019. Genomic data analysis workflows for tumors from patient-derived xenografts (PDXs): challenges and guidelines. *BMC Med Genomics* 12:92

Berlow NE, Rikhi R, Geltzeiler M, Abraham J, Svalina MN, Davis LE, Wise E, Mancini M, Noujaim J, Mansoor A, Quist MJ, Matlock KL, Goros MW, Hernandez BS, Doung YC, Thway K, Tsukahara T, Nishio J, Huang ET, Airhart S, **Bult CJ**, Gandour-Edwards R, Maki RG, Jones RL, Michalek JE, Milovancev M, Ghosh S, Pal R, Keller C. 2019. Probabilistic modeling of personalized drug combinations from integrated chemical screen and molecular data in sarcoma. *BMC Cancer* 19:593.

Malcolm JE, Stearns TM, Airhart SD, Graber JH, **Bult CJ**. 2019. Factors that influence response classifications in chemotherapy treated patient derived xenografts PDX). *PeerJ* doi: 10.7717/peerj.6586

Zhang WC, Wells J, Chow KH, Huang H, Yuan M, Saxena T, Melnick MA, Politi K, Costa D, **Bult CJ**, Slack F. 2019. miR-147b-mediated TCA cycle dysfunction and pseudohypoxia initiate drug tolerance to EGFR inhibitors in lung adenocarcinoma. *Nat Metab* 4:460-474.

Recla JM, Bubier JA, Gatti DM, Ryan JL, Long KH, Robledo RF, Glidden N, Hou G, Churchill GA, Maser RS, Zhang ZW, Young EE, Chesler EJ, **Bult CJ**. 2019. Genetic mapping in Diversity Outbred mice identifies a *Trpa1* variant influencing late phase formalin response. *Pain*, 160:1740-1753.

Manolio TA, Rowley R, Williams MS, Roden D, Ginsburg GS, **Bult C**, Chisholm RL, Deverka PA, McLeod HL, Mensah GA, Relling MV, Rodriguez LL, Tamburro C, Green ED. 2019. Opportunities, Resources, and Techniques for Implementing Genomics in Clinical Care. *The Lancet* (invited contribution), 394:511-520.

Kim H, Kumar P, Menghi F, Noorbakhsh J, Cerveira E, Ryan M, Zhu Q, Ananda G, George J, Chen HC, Mockus S, Zhang C, Yang Y, Keck J, Karuturi RKM, **Bult CJ**, Lee C, Liu ET, Chuang JH. 2018. High-resolution deconstruction of evolution induced by chemotherapy treatments in breast cancer xenografts. *Sci Rep*. Dec 18;8(1):17937. PMID:30560892

The RNAcentral Consortium. 2018. RNAcentral: a hub of information for non-coding RNA sequences. *Nucleic Acids Res.* 2018 Dec 8. doi: 10.1093/nar/gky1206. PMID:30535383

Conte N, Mason JC, Halmagyi C, Neuhauser S, Mosaku A, Yordanova G, Chatzipli A, Begley DA, Krupke DM, Parkinson H, Meehan TF, **Bult CJ**. 2018. PDX Finder: A portal for patient-derived tumor xenograft model discovery. *Nucleic Acids Res.* doi: 10.1093/nar/gky984. PMID:30535239

Bult CJ, Blake JA, Smith CL, Kadin JA, Richardson JE. Mouse Genome Database Group. 2018. Mouse Genome Database (MGD) 2019. *Nucleic Acids Res.* doi: 10.1093/nar/gky1056. PMID:30407599

Howe DG, Blake JA, Bradford YM, **Bult CJ**, Calvi BR, Engel SR, Kadin JA, Kaufman TC, Kishore R, Laulederkind SJF, Lewis SE, Moxon SAT, Richardson JE, Smith C. 2018. Model organism data evolving in support of translational medicine. *Lab Anim (NY)*. Oct;47(10):277-289. PMID:30224793

Woo XY, Srivastava A, Graber JH, Yadav V, Sarsani VK, Simons A, Beane G, Grubb S, Ananda G, Liu R, Stafford G, Chuang JH, Airhart SD, Karuturi RKM, George J, **Bult CJ**. 2018. Bioinformatics workflows for genomic analysis of tumors from Patient Derived Xenografts (PDX): challenges and guidelines. *BioRxiv* doi: <https://doi.org/10.1101/414946>

Volpi S, **Bult CJ**, Chisholm RL, Deverka PA, Ginsburg GS, Jacob HJ, Kasapi M, McLeod HL, Roden DM, Williams MS, Green ED, Rodriguez LL, Aronson S, Cavallari LH, Denny JC, Dressler LG, Johnson JA, Klein TE, Leeder JS, Piquette-Miller M, Perera M, Rasmussen-Torvik LJ, Rehm HL, Ritchie MD, Skaar TC, Wagle N, Weinshilboum R, Weitzel KW, Wildin R, Wilson J, Manolio TA, Relling MV. Research Directions in the Clinical Implementation of Pharmacogenomics: An Overview of US Programs and Projects. *Clin Pharmacol Ther.* 2018 May;103(5):778-786. PMID:29460415

Berlow NE, Rikhi R, Geltzeiler MN, Abraham J, Svalina MN, Davis LE, Wise E, Mancini M, Noujaim J, Mansoor A, Quist MJ, Matlock KL, Goros MW, Hernandez BS, Duong YC, Thway K, Tsukahara T, Nishio J, Huang EC, Airhart S, **Bult CJ**, Gandour-Edwards R, Maki RG, Jones RL, Michalek JE, Milovancev M, Ghosh S, Pal R, Keller C. Probabilistic modeling of personalized drug combinations from integrated chemical screen and molecular data in sarcoma. *BioRxiv* doi: <https://doi.org/10.1101/396358>

Pujar S, O'Leary NA, Farrell CM, Loveland JE, Mudge JM, Wallin C, Girón CG, Diekhans M, Barnes I, Bennett R, Berry AE, Cox E, Davidson C, Goldfarb T, Gonzalez JM, Hunt T, Jackson J, Joardar V, Kay MP, Kodali VK, Martin FJ, McAndrews M, McGarvey KM, Murphy M, Rajput B, Rangwala SH, Riddick LD, Seal RL, Suner MM, Webb D, Zhu S, Aken BL, Bruford EA, **Bult CJ**, Frankish A, Murphy T, Pruitt KD. 2018. Consensus coding sequence (CCDS) database: a standardized set of human and mouse protein-coding regions supported by expert curation. *Nucleic Acids Res.* 46(D1):D221-D228. PMID:29126148

Krupke, DM, Begley DA, Sundberg JP, Richardson JE, Neuhauser SB, **Bult CJ**. 2017. The Mouse Tumor Biology Database: A Comprehensive Resource for Mouse Models of Human Cancer. *Cancer Research* 77:e67-e70.

Meehan TF, Conte N, Goldstein T, Inghirami, G, Murakama MA....**Bult CJ**. 2017. PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. *Cancer Research* 77:e62-e66.

Smith CL, Blake JA, Kadin JA, Richardson JE, Bult CJ. 2017. Mouse Genome Database (MGD)-2018: knowledgebase for the laboratory mouse. *Nucleic Acids Res* doi: 10.1093/nar/gkx1006.

Pujar S, O'Leary NA, Farrell CM, Loveland, JE...**Bult CJ**, Frankish A, Murphy T, Pruitt KD. 2017. Consensus coding sequence (CCDS) database: a standardized set of human and mouse protein-coding regions supported by expert curation. *Nucleic Acids Res.* doi: 10.1093/nar/gkx1031

Randolph ME, Cleary MM, Bajwa Z, Svalina MN, Young MC, Mansoor A, Kaur P, **Bult CJ**, Goros MW, Michalek JE, Xiang S, Keck J, Krasnoperov V, Gill P, Keller C. 2017. EphB4/EphrinB2 therapeutics in Rhabdomyosarcoma. *PloS One* 12(8):e0183161. doi: 10.1371/journal.pone.0183161.

Delattre O, **Bult CJ**. 2017. Editorial overview: Characterizing the cancer genome: mechanistic insights and translational opportunities. *Curr Opin Genet Dev* 42:78-80.

Manolio, TA, Fowler DM, Starita LM, Haendel MA, MacArthur DG..., **Bult C**. 2017. Bedside Back to Bench: Building bridges between basic and clinical genomic research. *Cell* 169(1):6-12.

Longoni M, High FA, Qi H, Joy MP, Hila R, Coleti CM, Synn J, Loscertales M, Shan L, **Bult CJ**, Wilson JM, Shen Y, Chung WK, Donahoe PK. 2017. Genome-wide enrichment of damaging de novo variants in patients with isolated and complex congenital diaphragmatic hernia. *Hum Genet* 136(6):679-691. doi: 10.1007/s00439-017-1774-y.

Eppig JT, Smith CL, Blake JA, Ringwald M, Kadin JA, Richardson JE, **Bult CJ**. 2017. Mouse Genome Informatics (MGI): Resources for mining mouse genetic, genomic and biological data in support of primary and translational research. *Methods Mol Biol*. 1488:47-73.

Beauchemin KJ, Wells JM, Kho AT, Philip VM, Kamir D, Kohane IS, Graber JH, **Bult CJ**. 2106. Temporal dynamics of the developing lung transcriptome in three common inbred strains of laboratory mice reveals multiple stages of postnatal alveolar development. *PeerJ*. 4:e2318. doi: 10.7717/peerj.2318 PMID:27602285

Blake JA, Eppig JT, Kadin JA, Richardson JE, Smith CL, **Bult CJ**; the Mouse Genome Database Group. 2016. Mouse Genome Database (MGD) – 2017: community knowledge resource for the laboratory mouse. *Nucleic Acids Res* pii: gkw1040 PMID:27899570

High FA, Bhayani P, Wilson JM, **Bult CJ**, Donahoe PK, Longoni M. 2016. De novo frameshift mutation in COUP-TFII (NR2F2) in human congenital diaphragmatic hernia. *Am J Med Genet A* 170(9):2457-61. doi: 10.1002/ajmg.a.37830. PMID: 27363585

Dobrolecki LE, Airhart SD, Alferez DG, Aparicio S, Behbod F, Bentires-Alj M, Brisken C, **Bult CJ**, Cai S, Clarke RB, Dowst H, Ellis MJ, Gonzalez-Suarez E, Iggo RD, Kabos P, Li S, Lindeman GJ, Marangoni E, McCoy A, Meric-Bernstam F, Piwnica-Worms H, Poupon MF, Reis-Filho J, Sartorius CA, Scabia V, Sflomos G, Tu Y, Vaillant F, Visvader JE, Welm A, Wicha MS, Lewis MT. 2016. Patient-derived xenograft (PDX) models in basic and translational breast cancer research. *Cancer Metastasis Rev*. doi: 10.1007/s10555-016-9653-x. PMID: 28025748

Bais P, Beebe K, Morelli KH, Currie ME, Norberg SN, Evsikov AV, Miers KE, Seburn KL, Guergueltcheva V, Kremensky I, Jordanova A, **Bult CJ**, Burgess RW. 2016. Metabolite profile of a mouse model of Charcot-Marie-Tooth type 2D neuropathy: implications for disease mechanisms and interventions. *Bio Open* 5(7):908-20. doi: 10.1242/bio.019273. PMID:27288508

Mockus SM, Patterson SE, Statz C, **Bult CJ**, Tsongalis GJ. 2016. Clinical trials in precision oncology. *Clin Chem*. 62(3):442-8. doi: 10.1373/clinchem.2015.247437. PMID: 26607725

Hingorani P, Janeway K, Crompton BD, Kadoch C, Mackall CL, Khan J, Shern JF, Schiffman J, Mirabello L, Savage SA, Ladanyi M, Meltzer P, **Bult CJ**, Adamson PC, Lupo PJ, Mody R, DuBois SG, Parsons DW, Khanna C, Lau C, Hawkins DS, Randall RL, Smith M, Sorensen PH, Plon SE, Skapek SX, Lessnick S, Gorlick R, Reed DR. Current State of Pediatric Sarcoma Biology and Opportunities for Future Discovery: A Report from the Sarcoma Translational Research Workshop. 2016. *Cancer Genetics* doi:10.1016/j.cancergen.2016.03.004 PMID: 27132463

Liu E, **Bult CJ**, Shultz, L. 2016. Patient Derived Xenografts: Why Now? *JAMA Oncol*. doi:10.1001/jamaoncol.2016.0193 PMID:27055176

Didion JP, Morgan AP, Yadgary L, Bell TA, McMullan RC, Ortiz de Solorzano L, Britton-Davidian J, **Bult CJ**, Campbell KJ, Castiglia R, Ching YH, Chunco AJ, Crowley JJ, Chesler EJ, Förster DW, French JE, Gabriel SI, Gatti DM, Garland T Jr, Giagia-Athanasopoulou EB, Giménez MD, Grize SA, Gündüz İ, Holmes A, Hauffe HC, Herman JS, Holt JM, Hua K, Jolley WJ, Lindholm AK, López-Fuster MJ, Mitsainas G, da Luz Mathias M, McMillan L, Ramalhinho MD, Rehermann B, Rosshart SP, Searle JB, Shiao MS, Solano E, Svenson KL, Thomas-Laemont P, Threadgill DW, Ventura J, Weinstock GM, Pomp D, Churchill GA, Pardo-Manuel de Villena F. 2016. R2d2 drives selfish sweeps in the house mouse. *Molecular Biology and Evolution* pii: msw036 PMID:26882987

Bult CJ, Eppig JT, Blake JA, Kadin JA, Richardson JE; Mouse Genome Database Group. 2016. Mouse genome database 2016. *Nucleic Acids Res*. 44(D1):D840-7.

Begley DA, Sundberg JP, Krupke DM, Neuhauser SB, **Bult CJ**, Eppig JT, Morse HC 3rd, Ward JM. 2015. Finding mouse models of human lymphomas and leukemia's using The Jackson Laboratory Mouse Tumor Biology database. *Exp Mol Pathol.* 99(3):533-6.

Eppig JT, Richardson JE, Kadin JA, Ringwald M, Blake JA, **Bult CJ**. 2015. Mouse Genome Informatics (MGI): reflecting on 25 years. *Mamm Genome.* 26(7-8):272-84.

Dolan ME, Baldarelli RM, Bello SM, Ni L, McAndrews MS, **Bult CJ**, Kadin JA, Richardson JE, Ringwald M, Eppig JT, Blake JA. 2015. Orthology for comparative genomics in the Mouse Genome Database. *Mamm Genome.* 26(7-8):305-13.

Richardson JE, **Bult CJ**. 2015. Visual Annotation Display (VLAD): A Tool for Finding Functional Themes in Lists of Genes. *Mamm Genome* 26(7-8):567-73.

Zhu Y, Richardson JE, Hale P, Baldarelli RM, Reed DJ, Recla JM, Sinclair R, Reddy TBK, **Bult CJ**. 2015. A unified gene catalog for the laboratory mouse reference genome. *Mamm Genome* 26(7-8):295-304.

Eppig JT, Richardson JE, Kadin JA, Smith CL, Blake JA, **Bult CJ**; MGD Team. 2015. Mouse Genome Database: From sequence to phenotypes and disease models. *Genesis* 53(8):458-73.

Gandara DR, Mack PC, **Bult C**, Li T, Lara PN Jr, Riess JW, Astrow SH, Gandour-Edwards R, Cooke DT, Yoneda KY, Moore EH, Pan CX, Burich RA, David EA, Keck JG, Airhart S, Goodwin N, de Vere White RW, Liu ET. 2015. Bridging tumor genomics to patient outcomes through an integrated patient-derived xenograft platform. *Clin Lung Cancer* 16:165-72.

Mockus SM, Patterson SE, Statz C, **Bult CJ**, Tsongalis GJ. 2015. Clinical trials in precision oncology. *Clin Chem pii: clinchem.2015.247437.*

Hooper JE, Cantor EL, Ehlen MS, Banerjee A, Malempati S, Stenzel P, Woltjer RL, Gandour-Edwards R, Goodwin NC, Yang Y, Kaur P, **Bult CJ**, Airhart SD, Keller C. 2015. A Patient-Derived Xenograft Model of Parameningeal Embryonal Rhabdomyosarcoma for preclinical studies. *Sarcoma* doi: 10.1155/2015/826124. Epub 2015 Nov 30.

Pan, C, Zhang H, Tepper, CG, Lin T, Davis RR, Keck J, Ghosh PM, Gill P, Airhart S, **Bult CJ**, Gandara DR, Liu E, de Vere White RW, Development and characterization of bladder cancer patient-derived xenografts for precision medicine in bladder cancer. *PLoS ONE*, 10(8):e0134346.

Ananda G, Mockus S, Lundquist M, Spoltow V, Simons A, Mitchell T, Stafford G, Philip V, Stearns T, Srivastava A, Barter M, Rowe L, Malcol J, **Bult C**, Karuturi RK, Rasmussen K, Hinerfeld D. 2015. Development and validation of the JAX Cancer Therapy Profile for detection of clinically actionable mutations in solid tumors. *Exp Mol Pathol.* 98:106-12.

Bult CJ, Krupke DM, Begley DA, Richardson JE, Neuhauser SB, Sundberg, JP, Eppig JT. 2015. Mouse Tumor Biology (MTB): a database of mouse models for human cancer. *Nucleic Acids Res* doi: 10.1093/nar/gku987

Eppig, JT, Blake JA, **Bult CJ**, Kadin JA, Richardson JE. 2014. The Mouse Genome Database (MGD): facilitating mouse as a model for human biology and disease. *Nucleic Acids Res.* Doi: 10.1093/nar/gku967

Longoni M, High FA, Russell MK, Kashani A, Tracy AA, Coletti CM, Hila R, Shamia A, Wells J, Ackerman KG, Wilson JM, **Bult C**, Lee C, Lage K, Pober BR, Donahoe, PK. 2014. Molecular pathogenesis of congenital diaphragmatic hernia revealed by exome sequencing, developmental data, and bioinformatics. *PNAS* doi: 10.1073/pnas.1412509111

Recla J, Robledo RF, Gatt DM, **Bult CJ**, Churchill GA, Chesler EJ. Precise genetic mapping and integrative bioinformatics in Diversity Outbred mice reveals *Hydin* as a novel pain gene. 2014. *Mammalian Genome* 25:211-22.

Natale DA, Arighi CN, Blake JA, **Bult CJ**, Christie KR, Cowart J, D'Eustachio P, Diehl AD, Drabkin HJ, Helfer O, Huang H, Masci AM, Ren J, Roberts NV, Ross K, Ruttenberg A, Shamovsky V, Smith B, Yerramalla MS, Zhang J, Aljanahi A, Celen I, Gan C, Lv M, Schuster-Lezell E, Wu CH. 2014. Protein Ontology: a controlled structured network of protein entities. *Nucleic Acids Res* 42:D415-21.

Grubb SC, **Bult CJ**, Bogue MA. 2014. Mouse phenome database. *Nucleic Acids Res.* 42:D825-34.

Begley DA, Krupke DM, Neuhauser SB, Richardson JE, Schofield PN, **Bult CJ**, Eppig JT, Sundberg JP. 2014. Identifying mouse models for skin cancer using the Mouse Tumor Biology Database. *Exp Dermatol.* 23(10):761-3.

Blake JA, **Bult CJ**, Eppig JT, Kadin JA, Richardson JE, Mouse Genome Database Group. 2014. The Mouse Genome Database: integration of and access to knowledge about the laboratory mouse. *Nucleic Acids Res* 42:D810-17.

Logan RW, Robledo RF, Recla JM, Philip VM, Bubier JA, Jay JJ, Harwood C, Wilcox T, Gatti DM, **Bult CJ**, Churchill GA, Chesler EJ. 2013. High-precision genetic mapping of behavioral traits in the diversity outbred mouse population. *Genes Brain Behav.* doi: 10.1111/gbb.12029.

Bult CJ, Eppig JT, Blake JA, Kadin JA, Richardson JE, Mouse Genome Database Group. 2013. The mouse genome database: genotypes, phenotypes, and models of human disease. *Nucleic Acids Res.* 41:D885-91.

Bult CJ. 2012. Bioinformatics resources for behavior studies in the laboratory mouse. *Int. Rev Neurobiol.* 104:71-90.

Russell MK, Longoni M, Wells J, Maalouf FI, Tracy AA, Loscertales m, Ackerman KG, Pober BR, Lage K, **Bult CJ**, Donahoe PK. 2012. Congenital diaphragmatic hernia candidate genes derived from embryonic transcriptomes. *Proc Natl Acad Sci USA* 109:2978-83. (Bult and Donahoe are co-senior authors)

Guan Y, Gorenshiteyn D, Burmeister M, Wong AK, Schimenti JC, Handel MA, **Bult CJ**, Hibbs MA, Troyanskaya OG. 2012. Tissue-specific functional networks for prioritizing phenotype and disease genes. *PLoS Comput Biol* 8:e1002694.

Bradley A, Anastassiadis K, Ayadi A, Battey JF, Bell C, Birling MC, Bottomley J, Brown SD, Bürger A, **Bult CJ**, Bushell W, Collins FS, Desaintes C, Doe B, Economides A, Eppig JT, Finnell RH, Fletcher C, Fray M, Friendewey D, Friedel RH, Grosveld FG, Hansen J, Héroult Y, Hicks G, Hörlein A, Houghton R, Hrabé de Angelis M, Huylebroeck D, Iyer V, de Jong PJ, Kadin JA, Kaloff C, Kennedy K, Koutsourakis M, Lloyd KC, Marschall S, Mason J, McKerlie C, McLeod MP, von Melchner H, Moore M, Mujica AO, Nagy A, Nefedov M, Nutter LM, Pavlovic G, Peterson JL, Pollock J, Ramirez-Solis R, Rancourt DE, Raspa M, Remacle JE, Ringwald M, Rosen B, Rosenthal N, Rossant J, Ruiz Noppinger P, Ryder E, Schick JZ, Schnütgen F, Schofield P, Seisenberger C, Selloum M, Simpson EM, Skarnes WC, Smedley D, Stanford WL, Stewart AF, Stone K, Swan K, Tadepally H, Teboul L, Tocchini-Valentini GP, Valenzuela D, West AP, Yamamura K, Yoshinaga Y, Wurst W. 2012. The mammalian gene function resource: the International Knockout Mouse Consortium. *Mamm Genome* 23(9-10):580-6.

Maddatu TP, Grubb SC, **Bult CJ**, Bogue MA. 2012. Mouse Phenome Database. *Nucleic Acids Res.* 40:D887-94.

Eppig JT, Blake JA, **Bult CJ**, Kadin JA, Richardson JE, Mouse Genome Database Group. 2012. The Mouse Genome Database (MGD): comprehensive resource for genetics and genomics of the laboratory mouse. *Nucleic Acids Res.* 40:D881-6.

Fairfield H, Gilbert GJ, Barter M, Corrigan RR, Curtain M, Ding Y, D'Ascenzo M, Gerhardt DJ, He C, Huang W, Richmond T, Rowe L, Probst FJ, Bergstrom DE, Murray SA, **Bult C**, Richardson J, Kile B, Gut I, Hager J, Sigurdsson S, Mauceli E, Di Palma F, Lindblad-Toh K, Cunningham ML, Cox TC, Justice MJ, Spector MS, Lowe SW, Albert T, Donahue LR, Jeddeloh J, Shendure J, Reinholdt LG. 2011. Mutation discovery in mice by whole exome sequencing. *Genome Biol.* 12(9):R86.

Meehan TF, Carr CJ, Jay JJ, **Bult CJ**, Chesler EJ, Blake JA. 2011. Autism candidate genes via mouse phenomics. *J Biomed Inform.* 44 Suppl 1:S5-11.

Bult CJ, Drabkin HJ, Evsikov A, Natale D, Arighi C, Roberts N, Ruttenberg A, D'Eustachio P, Smith B, Blake JA, Wu C. 2011. The representation of protein complexes in the Protein Ontology (PRO). *BMC Bioinformatics* 12:371.

Blake JA, **Bult CJ**, Kadin JA, Richardson JE, Eppig JT. 2011. The Mouse Genome Database (MGD): Premier model organism resource for mammalian genomics and genetics. *Nucleic Acids Res.* 10.1093/nar/gkq1008.

- Ringwald M, Iyer V, Mason J, Stone K, Tadepally H, Kadin J, **Bult C**, Eppig J, Oakley D, Briois S, Stupka E, Macelli V, Smedley D, Liu S, Handwen JM, Ballabio A, Baldock R, Wurst W, Hicks G, Skarnes B. 2011. The IKMC Web Portal: a central point of entry to data and resources from the International Knockout Mouse Consortium. *Nucleic Acids Res*, 10.1093/nar/gkq879.
- Begley DA, Krupke DM, Neuhauser SB, Richardson JE, **Bult CJ**, Eppig JT, Sundberg JP. The Mouse Tumor Biology Database (MTB): A central electronic resource for locating and integrating mouse tumor pathology data. *Vet Pathol* PMID:21282667
- Natale, DA, Arighi CN, Barker WC, Blake JA, **Bult CJ**, Caudy M, Drabkin HJ, D'Eustachio P, Evsikov, AV, Huang H, Nchoutmboube J, Robersts NV, Smith B, Wu CH. 2011. The Protein Ontology (PRO): A structured representations of protein forms and complexes. *Nucleic Acids Res*, 10.1093/nar/gkq907.
- Gaudet P, Bairoch A, Field D, Sansone S-A, Taylor C, Attwood TK, Bateman A, Blake JA, **Bult CJ**, et al. 2010. Towards a BioDBcore: a community-defined information specification for biological databases. *Nucleic Acids Res* doi.10.1093/nar/gkq1173.
- Doore SA, Beard K, **Bult CJ**. An ontology based personal exposure history. 2010. *Proceedings from the 1st ACM International Health Informatics Symposium*, November 2010.
- Bult CJ**. The laboratory mouse as a model system for human biology and disease: an introduction to the Mouse Genome Informatics (MGI) Database. 2010. *NCI-Nature Pathway Interaction Database*, doi:10.1038/pid.2010.2.
- Donnelly CJ, McFarland M, Ames A, Sundberg BA, Springer D, Blauth P, and **Bult CJ**. 2010. JAX Colony Management System (JCMS): An extensible colony and phenotype data management system. *Mammalian Genome* DOI: 10.1007/s00335-010-9250-1
- Fijalkowska I, Shamma D, **Bult CJ**, Danoff SK. 2010. Expression of the transcription factor, TFII-I, during post implantation mouse embryonic development. *BMC Research Notes* 3:203.
- Bult CJ**, Kadin, JA, Richardson, JE, Blake JA, Eppig JT, Mouse Genome Database Group. 2010. The Mouse Genome Database: enhancements and updates. *Nucleic Acids Res*. 38:D586-92.
- Gene Ontology Consortium. The Gene Ontology in 2010: extensions and refinements. *Nucleic Acids Res* 38:D331-5.
- Evsikov AV, Dolan ME, Genrich MP, Patek E, **Bult CJ**. 2009. MouseCyc: a curated biochemical pathways database for the laboratory mouse. *Genome Biol* 10(8):R84.
- Yuan R, Tsaih SW, Petkova SB, de Evsikova CM, Xing S, Marion MA, Bogue MA, Mills KD, Peters LL, **Bult CJ**, Rosen CJ, Sundberg JP, Harrison DE, Churchill GA, Paigen B. 2009. Aging in inbred strains of mice: study design and interim report on median lifespans and circulating IGF1 levels. *Aging Cell* 8(3):277-87.
- Cox A, Ackert-Bicknell CL, Dumont BL, Ding Y, Bell JT, Brockmann GA, Wergedal JE, **Bult C**, Paigen B, Flint J, Tsaih SW, Churchill GA, Broman KW. 2009. A new standard genetic map for the laboratory mouse. *Genetics* 182(4):1335-44.
- Church DM, Goodstadt L, Hillier LW, Zody MC, Goldstein S, She X, **Bult CJ**, Agarwala R, Cherry JL, DiCuccio M, Hlavina W, Kapustin Y, Meric P, Maglott D, Birtle Z, Marques AC, Graves T, Zhou S, Teague B, Potamousis K, Churas C, Place M, Herschleb J, Runnheim R, Forrest D, Amos-Landgraf J, Schwartz DC, Cheng Z, Lindblad-Toh K, Eichler EE, Ponting CP; Mouse Genome Sequencing Consortium. 2009. Lineage-specific biology revealed by a finished genome assembly of the mouse. *PLoS Biol* 7(5).
- Guan Y, Myers CL, **Bult CJ**, Troyanskaya O. 2008. A genome-wide functional network for the laboratory mouse. *PLOS Computational Biology*, 4(9):e1000165.
- Naxerova K, **Bult CJ**, Peaston A, Fancher K, Knowles B, Kasif S, Kohane I. 2008. Analysis of gene expression in a developmental context emphasizes distinct biological leitmotifs in human cancers. *Genome Biology*, 9:R108.

Blake J, **Bult C**, Eppig J, Kadin J, Richardson JE. 2008. The Mouse Genome Database (MGD): Genotypes:Phenotypes. *Nucleic Acids Research*, doi:10.1093/nar/gkn886.

Grubb S, Maddatu T, **Bult C**, Bogue M. Mouse Phenome Database (MPD). 2008. *Nucleic Acids Research*, doi: 10.1093/nar/gkn778.

Bult CJ, Eppig JT, Kadin JA, Richardson JE, Blake JA; Mouse Genome Database Group. 2008. The Mouse Genome Database (MGD): mouse biology and model systems. *Nucleic Acids Res.* 36(Database):D724-8.

Krupke DM, Begley DA, Sundberg JP, **Bult CJ**, Eppig JT. 2008. The Mouse Tumor Biology Database. *Nature Rev Cancer* 8:459-65.

Peters LL, Robledo RF, **Bult CJ**, Churchill GA, Paigen BJ, Svenson KL. 2007. The mouse as a model for human biology: a resource guide for complex trait analysis. *Nat Rev Genet* 8(1):58-69.

Bouma GJ, Affourtit JP, **Bult CJ**, Eicher EM. 2007. Transcriptional profile of mouse pre-granulosa and Sertoli cells isolated from early-differentiated fetal gonads. *Gene Expr Patterns.* 7(1-2):113-23.

Kim, S, Huang LW, Snow KJ, Ablamunits V, Hasham MG, Young TH, Paulk AC, Richardson JE, Affourtit JP, Barak TS, **Bult CJ**, Barak Y. 2007. A mouse model of conditional lipodystrophy. *PNAS* 104:16627-16632.

Collins F, Rossant J, Wurst W and the International Mouse Knockout Consortium. 2007. A mouse for all reasons. *Cell* 128:9-13.

Bogue MA, Grubb SC, Maddatu TP, **Bult CJ**. 2007. Mouse Phenome Database (MPD). *Nucleic Acids Res.* 35(Database):D643-9.

Eppig JT, Blake JA, **Bult CJ**, Kadin JA, Richardson JE, and the Mouse Genome Database Group. 2007. The Mouse Genome Database (MGD): new features facilitating a model system. *Nucleic Acids Res.* 35: D630-D637.

Eppig JT, Blake JA, **Bult CJ**, Richardson JE, Kadin JA, Ringwald M. 2007. Mouse genome informatics (MGI) resources for pathology and toxicology. *Toxicol Pathol* 35:456-7.

Begley DA, Krupke DM, Vincent MJ, Sundberg JP, **Bult CJ**, Eppig JT. 2007. Mouse Tumor Biology Database (MTB): status, update, and future directions. *Nucleic Acids Res.* 35:D638-42.

Blake JA and **Bult CJ**. 2006. Beyond the data deluge. *Biomedical Informatics* 39(3):314-320.

Frith MC, Bailey TL, Kasukawa T, Mignone F, Kummerfeld SK, Madera M, Sunkara S, Furuno M, **Bult CJ**, Quackenbush J, Kai C, Kawai J, Carninci P, Hayashizaki Y, Pesole G, Mattick JS. 2006. Discrimination of non-protein-coding transcripts from protein-coding mRNA. *RNA Biol.* 3(1):40-8.

Furuno M, Pang KC, Ninomiya N, Fukuda S, Firth MC, **Bult CJ**, Mattick JS and Suzuki H. 2006. Clustering of internally-primed transcripts reveals novel long non-coding RNAs. *PLOS Genetics* 2(4):e37.

Maeda N, Kasukawa T, Oyama R, Gough J, Frith M, Engström PG, Lenhard B, Aturaliya RN, Batalov S, Beisel KW, **Bult CJ**, et al. 2006. Transcript annotation in FANTOM3: mouse gene catalog based on physical cDNAs. *PLoS Genet.* 2(4):e62.

Shopland LS, Lynch CR, Peterson KA, Thornton K, Kepper N von Hase J, Stein S, Vincent S, Molloy KR, Kreth G, Cremer C, **Bult CJ** and O'Brien TP. 2006. Folding and organization of a contiguous chromosome region according to the gene distribution pattern in primary genomic sequence. *J Cell Biol* 174(1): 27-38.

Blake JA, Eppig JT, **Bult CJ**, Kadin JA, Richardson JE; Mouse Genome Database Group. 2006. The Mouse Genome Database (MGD): updates and enhancements. *Nucleic Acids Res.* 34(Database):D562-7.

Bult CJ. 2006. From information to understanding: The role of model organism databases in comparative and functional genomics. *Animal Genetics* 37(S1):28-48.

Dolan ME, Holden C, Beard MK and **Bult CJ**. 2006. Genomes as geography: using GIS technology to build interactive genome feature maps. *BMC Bioinformatics* 7:416.

Eppig JT, **Bult CJ**, Kadin, JA, Richardson JE, Blake JA and the Mouse Genome Database Group. 2005. The Mouse Genome Database (MGD): From Genes to Mice, A Comprehensive Resource for Mouse Biology. *Nucleic Acids Res* 33:D471-5

Krupke, DM, Naf D, Vincent MJ, Allio T, Mikaelian I, Sundberg JP, **Bult CJ**, Eppig JT. 2005. The Mouse Tumor Biology Database: integrated access to mouse cancer biology data. *Exp Lung Res* 31(2):259-270.

Richardson JE, Kadin JA, Blake JA, **Bult CJ**, Eppig JT, Ringwald M and the Mouse Genome Informatics Group. 2004. From sipping on a straw to drinking from a fire hose; data integration in a public genome database. Proceedings of the 20th *IEEE International Conference on Data Engineering*. March 04:795-798.

Bult CJ, JA Blake, JE Richardson, JA Kadin, JT Eppig, and the members of the Mouse Genome Database Group. 2004. The Mouse Genome Database (MGD): Integrating biology with the genome. *Nucleic Acids Res*. Jan1:32.

Gene Ontology Consortium. 2004. The Gene Ontology (GO) database and informatics resource. *Nucleic Acids Res*. Jan 1:32.

Baldarelli RM, DP Hill, JA Blake, J Adachi, M Furuno, D Bradt, LE Corbani, S Cousins, KS Frazer, D. Qi., L Yang, S Ramachandran, D Reed, Y Zhu, T Kasukawa, M Ringwald, BL King, LJ Maltais, LM McKenzie, L Schriml, D Maglott, D Church, K Pruitt, Y Okazaki, Y Hayashizaki, JT Eppig, JE Richardson, JA Kadin, **CJ Bult**. 2003. Connecting sequence and biology in the laboratory mouse. *Genome Research* 13:6B 1505-19.

Kasukawa T, M Furuno, I Nikaido, H Bono, DA Hume, **C Bult**, DP Hill, R Baldarelli, J Gough, A Kanapin, H Matsuda, LM Schriml, Y Hayashizaki, Y Okazaki, and J Quackenbush. 2003 Development and evaluation of an automated annotation pipeline and cDNA annotation system. *Genome Research* 13:6B 1542-51.

Zhu Y, BL King, B Parvizi, B Brunks, C Stoeckert, J Quackenbush, J Richardson, and **CJ Bult**. 2003. Integrating computationally assembled mouse transcript sequences with the Mouse Genome Informatics (MGI) database. *Genome Biology* 4(2):R16

Blake JA, JE Richardson, **CJ Bult**, JA Kadin, JT Eppig, and the members of the Mouse Genome Database Group. 2003. MGD: The Mouse Genome Database. *Nucleic Acids Res* 31(1):193-195.

The FANTOM Consortium and the RIKEN Genome Exploration Research Group. 2005. The Transcriptional Landscape of the Mammalian Genome. *Science* 309:1559-1563. (Core author)

Bult CJ, Kibbe WA, Snoddy J, Vitaterna M, Seanson D, Pretel S, Li Y, Hohman MM, Rinchik E, Takahashi JS, Frankel WN, Goldowitz D. 2004. A genome end-game: understanding gene function in the nervous system. *Nat Neurosci* 7: 484-5.

Goldowitz D, Frankel WN, Takahashi JS, Holtz-Vitaterna M, **Bult C**, Kibbe WA, Snoddy J, Li Y, Pretel S, Yates J, Swanson DJ. 2004. Large -scale mutagenesis of the mouse to understand the genetic bases of nervous system structure and function. *Molec Brain Res* 132:105-115.

Evsikov A, de Vries WN, Peaston AE, Radford EE, Fancher KS, Chen FH, Blake JA, **Bult CJ**, Latham KE, Solter D, Knowles BB. 2004. Systems biology of the 2-cell mouse embryo. *Cytogenet Genome Res* 105:240-250.

Mikaelian I, Nanney LB, Parman KS, Kusewitt DF, Ward JM, Naf D, Krupke DM, Eppig JT, **Bult CJ**, Seymour R, Ickiki T, Sundberg JP. 2004. Antibodies that label paraffin-embedded mouse tissues: a collaborative endeavor. *Toxicol Pathol* 32(2):181-91.

Bult CJ. 2003. Mice and More. *Genome Biol.* 4(10):340.

O'Brien TP, **CJ Bult**, C Cremer, M Grunze, BB Knowles, J Langowski, J McNally, T. Pederson, J Politz, A Pombo, G Schmahl, JP Spatz and R van Driel. 2003. Genome function and nuclear architecture: gene expression as nanoscience. *Genome Research* 13:1029-1041.

Bult CJ 2002. Data integration standards in model organisms: from genotype to phenotype in the laboratory mouse. *Targets/Drug Discovery Today* 1:163-168.

Bradt D, **CJ Bult**, JA Blake, JA Kadin, JE Richardson, JT Eppig. 2002. Mouse genome informatics: mapping/homology data. *Scientific World Journal*. Jan2:2(1 Suppl 2):11-2.

Dolan M, C Holden, MK Beard, and **CJ Bult**. 2002. GenoSIS: Genome Data Interpretation Using GIS. 2002 Proceedings of the Environmental Systems Research Institute, <http://gis.esri.com/library/userconf/proc02/pap0719/p0719.htm>.

Näf D, DM Krupke, JP Sundberg, JT Eppig, **CJ Bult**. 2002. The mouse tumor biology database: a public resource for cancer genetics and pathology of the mouse. *Cancer Res* 62:1235-1240.

Blake JA, JE Richardson, **CJ Bult**, JA Kadin, and JT Eppig. 2002. The Mouse Genome Database (MGD): the model organism database for the laboratory mouse. *Nucleic Acids Res* 30(1):113-115.

Mouse Genome Sequencing Consortium and Mouse Genome Analysis Group. 2002. Initial sequencing and comparative analysis of the mouse genome. *Nature* 420: 520-562.

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. 2002. Analysis of the mouse transcriptome based upon functional annotation of 60,770 full length cDNAs. *Nature* 420: 563-573. (Core author)

Peterson KA, BL King, A Hagge-Greenberg, JJ Roix, **CJ Bult**, and TP O'Brien. 2002. Functional and comparative genomic analysis of the piebald deletion region of mouse chromosome 14. *Genomics* 80:172-184.

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. 2001. Functional annotation of a full-length mouse cDNA collection. *Nature* 409:685-690.

Bult CJ, DM Krupke, D Näf, JP Sundberg, JT Eppig. 2001. Web-based access to mouse models of human cancers: the Mouse Tumor Biology (MTB) Database. *Nucleic Acids Res* 29(1):95-97.

Blake JA, JT Eppig, JE Richardson, **CJ Bult**, and JA Kadin. 2001. The Mouse Genome Database (MGD): integration nexus for the laboratory mouse. *Nucleic Acids Res* 29(1):91-94.

Maltais LJ, JA Blake, JE Richardson, JA Kadin, CJ Bult and JT Eppig. 2001. The Mouse Genome Database (MGD): A Comprehensive Biological Information System for the 21st Century. *Eur J Hum Genet* 9:319.

Bult CJ, JE Richardson, JA Blake, JA Kadin, M Ringwald, JT Eppig, et al. 2000. Mouse genome informatics in a new age of biological inquiry. *Proceedings of the IEEE International Symposium on Bio-Informatics and Biomedical Engineering*, Washington, D.C., November 8-10, pp 29-32.

Bult CJ, DM Krupke, JP Sundberg, and JT Eppig. 2000. Mouse tumor biology database (MTB): enhancements and current status. *Nucleic Acids Research* 28:(1) 112-114.

Bult CJ, DM Krupke, BJ Tennent, and JT Eppig. 1999. A survey of web resources for basic cancer genetics research. *Genome Research* 9:(5)397-408.

Bult CJ, DM Krupke, and JT Eppig. 1999. Electronic access to mouse tumor data: the mouse tumor biology database (MTB) project. *Nucleic Acids Research* 27: (1) 99-105.

Blake JA, JT Eppig, JE Richardson, and MT Davisson and the Mouse Genome Informatics Group. 1998. The Mouse Genome Database (MGD): a community resource. Status and enhancements. *Nucleic Acids Res*. 26:130-137.

Bult CJ 1998. Making sense of sequences. *Science* 282:635-636.

- Bult CJ.** 1998. Current issues in molecular systematics. *Monographs in Systematic Biology from the Missouri Botanical Garden* (N. Bacigalupo and R. Fortunato, eds.) 68:445-459.
- Harasewych MG, SL Adamkewicz, JA Blake, D Saudek, T Spriggs, and **CJ Bult.** 1997. Neogastropod phylogeny: a molecular perspective. *Journal of Molluscan Studies* 63:32-351.
- Adamkewicz SL, MG Harasewych, J Blake, D Saudek, T Spriggs, and **CJ Bult.** 1997. A molecular phylogeny of the bivalve mollusks. *Molecular Biology and Evolution* 14(6):619-629.
- Harasewych MG, SL Adamkewicz, JA Blake, D Saudek, T Spriggs, and **CJ Bult.** 1997. Phylogeny and relationships of pleurotomariid gastropods (Mollusca:Gastropoda): an assessment based on partial 18S rDNA and cytochrome c oxidase I sequences. *Mol. Marine Biol. and Biotech.* 6(1):1-20.
- Bult CJ** et al. (40 authors). 1996. Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*. *Science* 273:1058-1073.
- Fraser CM, JD Gocayne, O White, MD Adams, RA Clayton, RD Fleischmann, **CJ Bult,** et al. (29 authors). 1995. The minimal gene complement of *Mycoplasma genitalium*. *Science* 270:397-403.
- Adams MD, AR Kerlavage, RD Fleischmann, RA Fuldner, **CJ Bult,** et al. (80 authors). 1995. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence. *Nature* 377(6547 Supplement): 3-174.
- Fleischmann RD, MD Adams, O White, RA Clayton, E F Kirkness, AR Kerlavage, **CJ Bult,** et al. (40 authors). 1995. Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd. *Science* 269:496-512.
- Bult CJ,** JA Sweere, and EA Zimmer. 1995. Cryptic sequence simplicity, nucleotide composition bias, and molecular coevolution in the large subunit of ribosomal rDNA in plants: Implications for phylogenetic analyses. *Ann. Mo. Bot. Gard.* 82:235-246.
- Farris JS, M Kallersjo, A Kluge, and **C Bult.** 1995. Constructing a significance test for incongruence. *Systematic Biology* 44:572-575.
- Clayton RA, G Sutton, PS Hinkle, **C Bult,** and C Fields. 1995. Intraspecific variation in small subunit ribosomal RNA sequences in GenBank: Why single sequences may not adequately represent prokaryotic taxa. *Int. J. Syst. Bact.* 45(3):595-599.
- Blake JA, **CJ Bult,** MJ Donoghue, J Humphries, and C. Fields. 1994. Interoperability of biological databases: A meeting report. *Systematic. Biol.* 43:585-589.
- Farris JS, M Kallersjo, AG Kluge, and **CJ Bult.** 1994. Testing significance of incongruence. *Cladistics* 10:315-320.
- Farris JS, M Kallersjo, A Kluge, and **CJ Bult.** 1994. Permutations. *Cladistics* 10:65-76.
- Kallersjo M, JS Farris, A Kluge and **CJ Bult.** 1993. Skewness and permutation. *Cladistics* 8:275-287.
- Bult CJ** and EA Zimmer. 1993. Nuclear ribosomal gene sequences for inferring tribal relationships within Onagraceae. *Systematic Botany* 18:48-64.
- Bult CJ,** M Kallersjo, and Y Suh. 1992. Amplification and sequencing of 16/18S rDNA from total plant DNA. *Plant Molecular Biology Reporter* 10:273-284.
- Bult CJ** and YT Kiang. 1992. Electrophoretic and morphological variation within and among natural populations of the wild soybean, *Glycine soja* (Sieb. & Zucc.) *Botanical Bulletin of Academia Sinica* 33:111-122.
- Devine TE, JJ O'Neill, YT Kiang and **CJ Bult.** 1991. Genetic linkage of the *rj2* gene in soybean. *Crop Science* 31:665-668.

Kiang YT and **CJ Bult**. 1991. Genetic and linkage analysis of aconitate hydratase variants in soybean. *Crop Science* 31:322-325.

Bult CJ, YT Kiang, TE Devine and JJ O'Neill. 1989. Testing for genetic linkage of morphological and electrophoretic loci in the cultivated soybean. *Soybean Genetics Newsletter* 16:168-174.

Bult CJ, YT Kiang, YC Chiang, HJY. Doong and MB Gorman. 1989. Electrophoretic methods for soybean genetics studies. *Soybean Genetics Newsletter* 16:175-187.

Bult CJ, KE Rasmussen and YT Kiang. 1989. A compilation of genetic linkage groups in the cultivated soybean, *Glycine max*. *Isozyme Bulletin* 22:24-32.

Bult CJ and YT Kiang. 1989. Inheritance and linkage analysis of an esterase locus in the cultivated soybean, *Glycine max*. *J. Heredity* 80:82-85.

Kiang YT, YC Chiang and **CJ Bult**. 1987. Genetic study of glutamate oxaloacetic transaminase in soybean. *Genome* 29:370-373.

Bult CJ and AN Murphy. 1984. Allozyme variation in low versus high salinity populations of the hard-shell clam, *Mercenaria mercenaria*. *Virginia Journal of Science* 35(20):78. (abstract)

Book Chapters

Bult CJ, Krupke DM, Vincent MJ, Allio T, Sundberg JP, Mikaelian I, and Eppig JT. 2006. The Mouse Tumor Biology Database: An online resource for mouse models of human cancer. In: Cancer Bioinformatics: From Therapy Design to Treatment (S. Nagl, ed.). John Wiley and Sons. pp. 143-153.

Goldsmith CW, Ringwald M, Sundberg JP, **Bult CJ**, and Eppig JT. 2006. Mouse genome informatics: database access to integrated phenotype data for mutant and genetically engineered mice. In: Handbook on Genetically Engineered Mice. J.P. Sundberg and T. Ichiki (eds). CRC Press Taylor and Francis Group, pp. 39-55.

Sundberg JP and **Bult CJ**. 2006. Professional use of mutant laboratory mice in research. In: Handbook on Genetically Engineered Mice. J.P. Sundberg and T. Ichiki (eds). CRC Press Taylor and Francis Group, pp. 185-209.

Woychik, R and **Bult CJ**. Functional analysis of genes. In: Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics. L.B. Jorde, P.F. R. Little, M. J. Dunn and S. Subramaniam (eds.). John Wiley and Sons. *In press*.

Blake J, Eppig JT, and **Bult CJ**. 2003. Mouse and Rat Genome Informatics. In: Bioinformatics for Geneticists. M.R. Barnes and I.C. Gray (ed.). Wiley Press, London.

Bult CJ. 1998. Archaea. In: McGraw Hill Yearbook of Science and Technology 1999. McGraw Hill Publisher (New York) pp. 29-31.

Bult CJ. 1998. Current issues in molecular systematics. In: Monographs in Systematic Biology from the Missouri Botanical Garden. N. Bacigalupo and R. Fortunato (eds.) 68:445-459.

Bult CJ, J. Blake, M. Adams, O. White, G. Sutton, R. Clayton, A. Kerlavage, C. Fields, and J.C. Venter. 1997. The impact of rapid gene discovery technology on studies of evolution and biodiversity. In: Biodiversity II: Understanding and protecting our natural resources, (E.O. Wilson, D. Wilson, and M. Reaka-Kudla, eds). Joseph Henry Press (Washington, D.C.) pp. 289-299.

Blake JA and **CJ Bult**. 1996. Biological databases in an electronic age: Access to and use of biological databases. In: Molecular zoology: Advances, strategies, protocols, (J.D. Ferraris and S.R. Palumbi, eds.), John Wiley & Sons, Inc. (New York) pp. 3-18.

Bult CJ and C. Fields. 1996. Informatics and Genomic Research. In: The Impact of Plant Molecular Genetics, (B.W. Sobral, ed.), Birkhauser Publishers (Boston) pp. 221-238.

Bult CJ and Y.T. Kiang. 1993. One dimensional electrophoretic comparisons of plant proteins. In: Methods in Enzymology vol. 224, (E. Zimmer, T. White, R. Cann and A. Wilson, eds.). Academic Press pp:81-97.

Funded Research

| | | |
|--|---|-----------------------|
| 5 R25 HG007053-08 | Role: Principal Investigator/Program Director | 4/26/2016 - 3/31/2021 |
| Diversity Action Plan for Mouse Genome Database <i>Extended one year due to pandemic</i> | | |
| 5 R01 CA089713-18 | Role: Principal Investigator/Program Director | 5/1/2016 - 4/30/2021 |
| Electronic Access to Mouse Tumor Data <i>Will be renewed</i> | | |
| 5 U41 HG000330-32 | Role: Principal Investigator/Program Director | 4/19/2016 - 3/31/2021 |
| Mouse Genome Database <i>Will be renewed</i> | | |
| 5 P01 HD068250-09 | Role: Principal Investigator | 8/29/2017 - 4/30/2022 |
| Gene Mutation and Rescue in Human Diaphragmatic Hernia | | |
| 5 U24 HG010859-02 | Role: Principal Investigator | 9/1/2019 - 8/31/2024 |
| Alliance Central: A Platform for Sustainable Development of Next Generation Genome Knowledgebases | | |
| 5 U24 CA220341-03 | Role: Consortium PI | 5/1/2018 - 4/30/2023 |
| Supporting and Evolving Gene Set Enrichment Analysis and the Molecular Signatures Database for Cancer Research | | |
| 5 U24 CA224067-03 | Role: Co-Investigator (with Jeff Chuang) | 9/25/2017 - 8/31/2022 |
| Data Coordination Center for PDX Net | | |
| Cancer Center Pilot | Role: co-PI (with Gary Ren, Mingyang Lu) | 6/01/19 -3/31/21 |
| Dynamics of the immune microenvironment during lung tumorigenesis | | |
| Directors Innovation Fund | Role: PI | 6/01/18- 3/31/21 |
| Mouse Genome Variation Registry | | |

Advisory/Editorial Boards

- Steering Committee Member, NIH Common Fund Stimulating Peripheral Activity to Relieve Conditions (SPARC) Data Resource Center (2019 - present)
- External Consultant Committee (ECC) member, NHGRI Genomic Data Science Analysis, Visualization, Informatics, Lab-space (AnVIL) Program (2019 - present)
- Scientific Advisory Board, GenCode (2017- present)
- Scientific Advisory Board, Baylor PDX Program (2017- present)
- Scientific Advisory Board, ZFIN (Zebrafish Model Organism Database) (2016 – present)
- Member, NHGRI Genomic Medicine Working Group (2015 - present)
- Scientific Advisory Board, On Line Mendelian Inheritance in Man (OMIM) (2013 – present)
- Scientific Advisory Board, UniProt (2016 – 2020)
- NHGRI 2020 Strategic Planning Education and Training Task Force (2019)
- Member, NHGRI Research Training Advisory Committee (2015 – 2020)
- Scientific Advisory Board, Genome Space (2013 – 2018)
- Scientific Advisory Board, Galaxy Bioinformatics Platform (2012 – 2019)
- Member, National Human Genome Research Institute (NHGRI) Advisory Council (2014 – 2018)
- Scientific Advisory Board, Joint Genome Institute (2016 – 2018)
- Advisory Board Member, Free ME from Lung Cancer (2013- 2014)
- Member, NIH Multi Council Working Group on Big Data To Knowledge (BD2K) (2014 – 2017)
- Scientific Advisory Board, The Genome Reference Consortium (2010 - 2016)
- Scientific Advisory Board, The BioCyc Database Project (2010 - 2013)
- Scientific Advisory Board, Protein Structural Genomics Knowledgebase (2008 -2013)
- Associate Editor, Database: The Journal of Biological Databases and Curation (2008 - 2014)
- Associate Editor, Genomics (2007 – 2012)
- Advisory Board Member, PathoSystems Resource Integration Center (PATRIC), Virginia Biotechnology Institute (2005 - 2012)

- Advisory Board Member, Genome Biology (2005 - 2011)
- NSF Plant Genome Advisory Panel (2005)
- Advisor, "NSF Workshop on Phylogenetic Informatics." University of California, Davis (2000)
- Advisory Board Member, Bigelow Laboratory for Ocean Sciences, Provasoli-Guillard Center for the Culture of Marine Phytoplankton, Boothbay Harbor, Maine (2000)
- Biomedical Engineering Advisory Group, University of Maine (1999 - 2001)

Grant Review Panels/Study Sections

- National Institutes of Health: Genome Research Review Committee (2010-2014; Chair 2013-2014)
- National Institutes of Health: Centers of Cancer Nanotechnology Excellence Study Section (2010)
- National Science Foundation: Plant Genomics Program Study Section (2009)
- Wellcome Trust Sanger Institute Mouse Informatics Review (2008)
- National Institutes of Health: BioData and Management Study Section (2004 - 2008)
- Chair, National Institutes of Health Special Bioinformatics Study Section (SBIR and BISTI) (2003)
- Department of Energy: Genomes To Life Program
- National Science Foundation: Biological Databases and Informatics (1999 - 2002)
- Department of Energy: Chemical and Biological Nonproliferation Program
- National Institutes of Health: SBIR Study Section (Genetics/Bioinformatics; 1998- 2004)
- National Science Foundation: Science and Technology Center Program Site Visit Team (1999)
- Department of Energy: Ethical, Legal, and Social Implications (ELSI) of the Human Genome Project Program
- Department of Energy: Microbial Genome Program
- Department of Energy: Genome Database (GDB) site visit team (1997)
- Department of Energy: Alexander Hollaender Postdoctoral Fellowship
- National Science Foundation: Advanced Technology Education Program
- National Science Foundation: Research Collections in Systematics and Ecology (1993 - 1996)
- United States Department of Agriculture: Plant Genome Program

Honors and Awards

- Thomson Reuters/Clarivate Highly Cited Researcher (2015, 2016)
- Knowlton Family Chair (December 2015)
- Jackson Laboratory National Council Award for Scientific Achievement (August 2013)
- Jackson Laboratory Community Award (May 2013)
- Roy H. Behnke Distinguished Lecturer, University of South Florida (March 2011)
- Bult et al., 1996. Science 273:1058 cited as a "Hot Paper in Genetics" by The Scientist (June 1998)
- "Hottest Research of 1996" (based on numbers of literature citations), The Institute for Scientific Information (ISI) (1997)
- Carl Von Linneaus Lecturer, Uppsala University, Uppsala, Sweden (1997)
- Discover magazine top 100 science stories for 1996
- National Science Foundation Travel Grant recipient to attend the 6th Congreso Latino Americano de Botanica, Mar del Plata, Argentina (1994)
- Appointed an honorary Research Associate at the Smithsonian Institution, Laboratory of Molecular Systematics, Washington, D.C. (1993-1996)
- Elected full member of the Sigma Xi Research Honor Society (1989)
- Awarded full tuition to attend the Sloan Foundation sponsored "Workshop on Molecular Evolution" (1989)
- UNH Women's Commission Award for "significant contributions to the advancement of women in the sciences at UNH" (1989)
- UNH Dissertation Fellowship Award (1988)
- Faculty Award for "Outstanding Senior in Biology," GMU (1984)
- Elected to the Beta Beta Beta Biological Honor Society (1984)

Institutional Committee Service

- The Jackson Laboratory Scientific Advisory Committee (SAC) (2001-2006; 2008-2013; 2016-2017; 2021-2022)
- JAX Emergency Response Committee (2020 -)
- JAX Type 2 Diabetes CUBE initiative Data Standards Working Group Leader (2018 -)
- Genetic Diversity Initiative (GDI) Steering Committee (2018 -)
- JAX Laboratory Informatics Domain Portfolio Group (2016 -)

- JAX Patient Derived Xenograft Governance Committee (2016 -)
- JAX Chief Information Officer Search Committee (2019)
- JAX Diversity and Inclusion Director Search Committee (2018)
- The Jackson Laboratory Cancer Center Scientific Executive Committee (2014 - 2019)
- The Jackson Laboratory Cancer Center Operations Group (chair; 2012 - 2019)
- The Jackson Laboratory Internal Cancer Center Advisory Committee (2006 - 2016)
- eLIMS Steering Committee (2012 – 2015)
- The Jackson Laboratory High Throughput Sequencing Advisory Board (2010 - 2014)
- Graduate School of Biomedical Sciences (GSBS) Admissions Committee (2007 - 2013)
- The Jackson Laboratory Faculty Recruiting Committee (2006 - 2012)
- The Jackson Laboratory Information Technology Advisory Committee (2004 - 2014)
- The Jackson Laboratory Training and Education Committee (2000 - 2013)
- The Jackson Laboratory Cancer Center Deputy Director Recruiting Committee (2008 - 2009)
- The Jackson Laboratory Bioinformatics Recruiting Committee (2004 - 2006)
- The Jackson Laboratory Aging Center Internal Advisory Committee (2007 - 2010)
- International Mouse Genome Society Nominations Committee (2007- 2009)
- The Jackson Laboratory Graduate Student Advisory Committee (Chair, 2008)
- The Jackson Laboratory BioData Coordination Committee (2001)
- The Jackson Laboratory Research Grants Council (2001)
- The Jackson Laboratory Compensation and Benefits Program Review/ Science Advisory Committee (2000 – 2002)
- Bioinformatics Subcommittee Chair, Programs in Genomic Applications, National Heart, Lung, and Blood Institute (2000 - 2002)
- The Jackson Laboratory Staff Computing Committee (1999 - 2000)

Other Activities

- Reviewer, EuroPDX Research Infrastructure Trans-national Access Programme (2019,2020)
- Reviewer, ELIXIR Core Data Resources (2018, 2020)
- Lecturer, Advances in Patient Derived Xenograft Modeling in Cancer Workshop, AACR (April 2018)
- Lecturer, Patient Derived Xenografts (PDXs): A Platform for Precision Oncology, HUGO Workshop series (Taiwan and Japan) (March 2017)
- Organizer, Genomic Medicine IX “Bedside to Bench – Mind the Gaps” (April 2016)
- Organizer, NHGRI Computational Genomics and Data Science Workshop (Sept 2016)
- Organizer, NHGRI Large Genome Resource Meeting (May 2016)
- Guest editor, Special issue of Cancer Genetics on Cancer Genomics
- Organizing Committee, Maine Biomedical and Biological Sciences Symposium (2006 - 2016)
- Faculty Supervisor, Jackson Laboratory Computational Sciences Service (2005 - 2015)
- Organizer, JAX-MDIBL Joint Scientific Symposium (2010, 2011)
- Organizer, Mouse Genome International Annotation Summit Meeting (2008, 2010)
- Organizer, Bioinformatics Workshops for the International Mammalian Genome Conference (2004 - 2012)
- Coordinator, Jackson Laboratory Bioinformatics Interest Group (2003 -2007)
- Organizer, Short Course on Genome Sequence Analysis (2002 - 2006)
- Organizer, Annual Conference on Computational Genomics (2002-2006)
- Member of the Mouse Genome Sequencing Consortium’s Mouse Genome Analysis Group (2002)
- Member of the RIKEN Functional Annotation of the Mouse (FANTOM) Consortium (2001 - 2006)
- Participant in the RIKEN Genome Network Project Consortium (2006-2009)
- Member of the Mouse Genome Informatics Database Consortium (with JT Eppig, M Ringwald, J Blake, J Richardson, and J Kadin) (1999 - present)
- Participant, Biomedical Research Infrastructure Network of Maine (BRIN; <http://www.brinme.net/>)
- Curriculum development, Interdisciplinary Graduate Program in Functional Genomics
- Symposium organizer, “Genomics and Genome Informatics.” University of Maine Annual EPSCOR conference on Molecular Biology in Maine (1999)
- Board of Technical Advisors, Visual Genomics, Inc. (1999-2000)
- Statewide Cooperative Ph.D. Program Planning Committee, University of Maine (1998 - 1999)
- Society of Systematic Biologists ,WWW Home Page Design and Use committee (1995-1996)
- Comparative Genomics Section Leader, NIH-DOE Human Genome Program Informatics Workshop (1998)
- Research Community Panel, Next Generation Internet Conference, University of Maine (1998)

- Organizer, Workshop on Spatial Genomics, University of Maine (1998)
- Organizer, Workshop on Database Interoperability, The Institute for Genomic Research (1994)
- Editorial Board, Systematic Biology (1992-1995)
- Co-founder and Executive Board Member, UNH Chapter of the Association for Women in Science (AWIS) (1988-1989)
- Reviewer: Journal of Heredity, Cladistics, Molecular Biology and Evolution, Systematic Biology, Science, Journal of Molecular Evolution, Genomics, Genome Research, Genome Biology, Nucleic Acids Research, Nature, Science, IEEE, BMC Bioinformatics

Educational Outreach

- Faculty /Instructor, Humanized Mice in Biomedicine, Challenges and Innovations Course, EMBO/EMBL (2019)
- Faculty, Tufts University School of Graduate Biomedical Sciences program in Mammalian Genetics
- Faculty, Graduate School of Biomedical Sciences and Engineering (GSBSE), University of Maine
- Mentor, Jackson Laboratory High School Intern Program
- Mentor, Jackson Laboratory Summer Student Program
- Mentor, Olympia Snowe Women's Leadership Institute (2017-2020)
- Organizer and Instructor, Bioinformatics Workshops at the Annual International Mammalian Genome Conference (2003 -2012)
- Organizer and Faculty member, Annual Genome Sequence Analysis Short Course (2002 - 2006)
- Faculty member, Jackson Laboratory Annual Short Course in Experimental Mammalian Genetics
- Faculty member, Jackson Laboratory Experimental Genetics of the Laboratory Mouse in Cancer Research
- Faculty member, Jackson Laboratory Mathematics Approaches to Complex Traits
- Faculty member, Jackson Laboratory Genomic and Proteomic Approaches to Complex Heart, Lung, and Sleep Disorders
- Lecturer/Coordinator, graduate course in Functional Genomics (University of Maine)
- Lecturer, Graduate course in Computational Methods in Genomics (University of Maine)
- Lecturer, Jackson Laboratory Phenotyping Workshop
- Lecturer, Jackson Laboratory Workshop on the Pathology of Mouse Models for Human Disease
- Lecturer, Jackson Laboratory Modeling Human Mammary Cancer in Mice
- "What the genome means," Jackson Laboratory Summer Visitor Program lecture
- "The Wonderful World of Cells and DNA", Mount Desert Island Elementary School (1998)
- Instructor, "Keys to Science" summer enrichment program for high school science teachers, Keystone, Colorado. (1994 - 1995)
- Developed "Understanding Genome Science" tutorial for student and general public tours of The Institute for Genomic Research. (1994)
- Preparator for Smithsonian Young Resident Associates "Museums and Molecules" educational program. (1992)
- Participant in science careers mentoring program for students at Thomas Jefferson High School, Fairfax, Virginia. (1991-1992)
- Science Fair Judge, State Science Fair, Baton Rouge, Louisiana. (1990 - 1991)
- Participant, University of New Hampshire Department of Plant Science annual "Greenhouse Open House" public outreach program. (1984 - 1989)

Advisees/Interns

Postdoctoral Fellows

Dr. Masaaki Furuno, Jackson Laboratory Postdoctoral Fellow (2003- 2005)

Dr. Lixin Zhou, TIGR Postdoctoral Fellow (1995 - 1996)

Graduate Students

Dr. Joan Malcolm, Graduate School of Biomedical Sciences and Engineering, University Maine (2015 - 2018)

Dr. Kyle Beauchemin, Graduate School of Biomedical Sciences and Engineering, University of Maine (2010 - 2016)

Dr. Jill Recla, Graduate School of Biomedical Sciences and Engineering, University of Maine (2008 - 2012)

Ms. Stacy Doore, Department of Spatial Information and Engineering, University of Maine (2009 -2010)

Dr. Kevin Peterson, Interdisciplinary Graduate Program in Functional Genomics (2002-2005)

Ms. Penny Russell, Interdisciplinary Graduate Program in Functional Genomics (2003-2004)

Ms. Sarah Matthews, DOE Predoctoral Intern (1993)

Post-Baccalaureate

Ms. Teresa McGee, Gail Gutrad Cancer Research Fellow (2019-2021)
Ms. Wendy Memishian, Gail Gutrad Cancer Research Fellow (2019-2021)
Ms. Ashley Tucker, The Jackson Laboratory Post-Baccalaureate Fellow (2021-)

Undergraduate and High School Students

Ms. Sirohi Kumar, Mount Desert Island High School Academic Year Intern (2020)
Mr. Joshua Quigley, College of the Atlantic Academic Year Intern (2019-)
Ms. Angelina Guerra, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2019)
Mr. Antonio Mendoza, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2018)
Ms. Taylor Mouton, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2017)
Ms. Bailey West, Searsport High School (2017)
Mr. Raphael Espinoza, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2016)
Mr. Jacob Lubert, Jackson Laboratory Summer Student Program (2015)
Mr. Adam Lavertu, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2015)
Ms. Vania Lopez, Colby College Summer Coop Program (2015)
Ms. Vania Lopez, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2014)
Ms. Janaya Shelly, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2013)
Ms. Megan Taylor, Jackson Laboratory Summer Student Program (2012)
Ms. Elizabeth Adesanya, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2012)
Ms. Emma Albee, University of New England (2010-2011)
Ms. Tess Lameyer, George Stevens Academy (2011)
Ms. Haley Maiden, George Stevens Academy (2011)
Ms. Jennifer Rodriguez, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2010)
Mr. Isaac St. John, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2009)
Mr. Kevin Hawkins, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2008)
Mr. Patrick Breen, Mount Desert Island High School Intern (2007-2008)
Ms. Cecily Swinburne, Jackson Laboratory Summer Student Program and College of the Atlantic Senior Project (2007-2008)
Mr. Dorian Britt, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2006)
Mr. Brad Witham, Mount Desert Island High School Intern (2006)
Mr. Troy Shapiro, Jackson Laboratory Summer Student Program (2005)
Mr. Curtis Thorman, Mount Desert Island High School Intern (2005)
Ms. Rebecca Barter, Jackson Laboratory Summer Student Program (2004)
Mr. Ayodele Adesanya, Jackson Laboratory Summer Student Program; MGD Diversity Action Plan (2004)
Mr. Brad Witham, Mount Desert Island High School Intern and Jackson Laboratory Summer Student Program (2002–2004)
Mr. Ben Hewlett, Mount Desert Island High School Intern (2000-2002)
Mr. Pierre Vanden Borre, Jackson Laboratory Summer Student Program (2000)
Mr. Robin Fernald, Mount Desert Island High School Intern (1999 - 2000)
Ms. Amber Bethell, NCGIA (University of Maine) Undergraduate Assistant (1999)
Mr. Robert “Beto” Peliks, Jackson Laboratory Summer Student Program (1999)
Ms. Winnie Liang, Jackson Laboratory Summer Student Program (1999)
Ms. Tracy Spriggs, TIGR Special Projects Intern (1995 - 1996)
Mr. Bryan Fitzpatrick, TIGR Summer High School Intern (1995)
Ms. Debbie Saudek, TIGR special projects intern (1993 - 1995)
Mr. Tae Hoon Kim, Smithsonian Summer Intern (1992)

Teacher Interns

Ms. Sarah Dunbar, Maine Science Teacher Intern (2014)
Ms. Savannah Lodge-Scharff, Maine Science Teacher Intern (2012)
Ms. Margaret Southworth, Maine Science Teacher Intern (2006)
Mr. Adam Zukowski, Maine Science Teacher Intern (2005)

Invited Presentations

- “The changing landscape of human disease gene discovery using the laboratory mouse”, Massachusetts General Hospital Seminar Program (April 2021)
- “PDXs as preclinical cancer models: 2 case studies”, Humanized mice in Biomedicine, European Molecular Biology Organization (EMBO), Heidelberg, Germany (November 2019)

- “Alliance of Genome Resources and MGI”, Sustainability of Mouse Informatics Resources, Infrafrontier Workshop, Strasbourg, France (September 2019)
- “The Alliance of Genome Resources: Transforming comparative genomics for human and model organisms”, 33 Annual International Mammalian Genome Conference, Strasbourg, France (September 2019)
- “Comparative genetics and genomics of mouse strains at MGI”, 32nd Annual International Mammalian Genome Conference, Puerto Rico (November 2018)
- “Maine Cancer Genomics Initiative”, Primary Source Speaker Series, Jesup Library, Bar Harbor, Maine (July 2018)
- “New Therapies for Triple Negative Breast Cancer (TNBC)”, Maine Breast and Cervical Health Mammography Conference, Augusta, Maine (May 2018)
- “Alliance of Genome Resources (AGR): An experiment in community genome resource sustainability”, Mammalian Genetics and Genomics: From Molecular Mechanisms to Translational Applications, EMBL Heidelberg, Germany (October 2017)
- “Functional and Phenotype Data from Model Organisms as Evidence for Disease Relevance of Human Genes and Variants”, Curating the Clinical Genome, Washington, DC (June 2017)
- “Precision Oncology”, Downeast Colloquy, Blue Hill, Maine (May 2017)
- “From Data to Knowledge: Why it Matters to be FAIR”, NHGRI Trainees Meeting, St. Louis, MO (April 2017)
- “Patient Derived Xenografts (PDX): A Platform for Precision Oncology”, Human Genome Organization workshop on Patient Derived Xenografts, Taipei, Taiwan and Yokohama, Japan (March 2017)
- “Patient Derived Xenografts (PDX) for Precision Oncology”, University of Connecticut Grand Rounds, Farmington, CT (May 2016)
- “Hyperbole and hope in cancer research”, Acadia Senior College, Bar Harbor, Maine (2015)
- “Patient Derived Xenografts (PDX): A Platform for Precision Oncology”, 29th Annual International Mouse Genome Conference, Yokohama, Japan (November 2015)
- “The Maine Triple Negative Breast Cancer Study: An Update”, Partridge Foundation 6th Annual Breast Cancer Symposium (October 2015)
- “The Tunable Mouse”, Maine Science Festival, Bangor, Maine (May 2015)
- “Patient Derived Xenografts (PDX): A Platform for *in vivo* Modeling for Precision Oncology”, Symposium on Optimizing Cooperative Group Specimen-based Sarcoma Biology Investigation for Future Discovery, Philadelphia, PA (April 2015)
- “Cancer Avatars and Individualized Cancer Therapy”, RNA Matters Lecture Series, Thomas Jefferson University (November 2014)
- “Biomarker Basics”, The Jeri and Noboru Oishi Symposium, Southwest Oncology Group (SWOG) (October 2014)
- “The Maine Triple Negative Breast Cancer Study: An Update”, Partridge Foundation 5th Annual Breast Cancer Symposium (October 2014)
- “Cancer Avatars and Individualized Cancer Therapy”, Annual Maine Biological and Biomedical Sciences Symposium keynote (April 2014)
- “Cancer Avatars and Individualized Cancer Therapy”, University of Maine at Presque Isle Distinguished Lecturer (February 2014)
- “A unified gene catalog for the reference mouse genome”, Genome Informatics, Cold Spring Harbor, NY. (October 2013)
- “Cancer Avatars”, Partridge Foundation Fourth Annual Breast Cancer Symposium, Bangor, Maine (October 2013)
- “Computational prediction of knockout phenotypes and gene function”, International Mammalian Genome Conference, Salamanca, Spain (September 2013)
- “Cancer Avatars and Genome Guided Cancer Therapy”, Maine Chapter of the College of Surgeons, Bar Harbor, Maine (May 2013)
- “Normal development as a framework for understanding disease processes”, Maine-Dartmouth Family Medicine Distinguished Lecturer in Medicine Series (May 2012)
- “Data integration strategies for the Mouse Genome Informatics Database”, Functional Genomics Data Society, Boston, MA (February 2012)
- “Good Genes Gone Bad: what our genome is telling us about cancer”, Little Forum, Bronxville, NY (October 2011)
- “Genomics of lung development and cancer”, Maine Medical Center, Portland, Maine (May 2011)
- “Mouse models of human disease: Where we are and where we are going”, Roy H. Behnke Distinguished Lecture, University of South Florida (February 2011)
- “What normal development can tell us about cancer”, The Jackson Laboratory-Dartmouth Regional Symposium for Cancer Biology, The Jackson Laboratory, Bar Harbor, ME (September 2010)
- “Development and Cancer”, Eastern Maine Medical Center, Brewer, ME (August 2010)

- "MouseNET: predicting gene function in the laboratory mouse," Massachusetts General Hospital, Center for Human Genetic Research, Boston, MA (April 2010)
- "Lung development and disease," Boston University Genome Sciences Institute, Boston, MA (April 2010)
- "Genes, Cancer, and the Future of Personalized Medicine," Annual Women's Health Luncheon, Portland, Maine (February 2010)
- "Can Your DNA Help Doctors Choose Your Prescription?" Bank of New York Mellon (September 2009)
- "Integrating MouseCyc with the Protein Ontology Resource project," 2nd Annual Protein Ontology Meeting, Georgetown University, Washington, D.C. (2008)
- "Virchow revisited: Can understanding normal development of the mouse lung provide insights into the genetics of human lung cancer?," Medical College of South Carolina, Charleston, South Carolina (February 2008)
- "MouseCyc: a curated database of biochemical pathways database for the laboratory mouse," Cambridge HealthTech Tri-Medicine Conference, San Francisco, California (February 2008)
- "Good genes gone bad: Understanding the genetic basis of lung cancer," 2nd Annual Women's Health Luncheon, Portland, Maine (November 2007)
- "Accelerating the functional characterization of the mouse genome," 21st Annual International Mouse Genome Conference, Kyoto, Japan (November 2007)
- "Towards a unified gene catalog for the mouse," 20th Annual International Mouse Genome Conference Charleston, South Carolina (November 2006)
- "Bio-ontologies for neuroscience," 45th Annual Meeting of the American College of Neuropsychopharmacology, Hollywood, Florida (December 2006)
- International Gene Trap Consortium Meeting: Mouse Genome Informatics, San Francisco, California, April (2005)
- "From Information to Understanding: Data integration for functional and comparative genomics," Integration of Structural and Functional Genomics Symposium, Iowa State University (2005)
- "Science In Silico," BioQuest Curriculum Consortium (2004)
- "The mouse genome sequence as a framework for complex trait analysis," 3rd Annual Complex Trait Analysis Conference, The Jackson Laboratory, Bar Harbor, Maine, (July 2004).
- "Connecting sequences and biology in the laboratory mouse," Mount Desert Island Biological Laboratory Symposium (2004)
- "Mouse Genome Informatics and Gene Ontology: Progress and Promises", 27th Annual Scientific Meeting of the Research Society on Alcoholism (2004)
- "Beyond Sequence Comparison: Why Data Integration is Important for Comparative Genomics," Novartis Workshop on Comparative Genomics (2003)
- "Beyond the genome", University of Iowa Center for Bioinformatics Lecturer Series (2003)
- "Bridging the Digital Biology Divide", Maine Medical Center Research Institute (2003)
- "Mapping biology to the mouse genome," 15th International Mouse Genome Conference (2002)
- "After the genome: Back to biology," University of New Hampshire Genetics Program (2002)
- "Genome sequence analysis," Advances in Nanostructural Genomics II (2002)
- "Mapping biology to the mouse genome," Genome Informatics (2002)
- "Bioinformatics resources for mouse models of cancer," National Cancer Institute retreat (2002)
- "Informatics infrastructure for the mouse: the view from JAX", Samuel Lunenfeld Research Institute, Toronto, Canada (2002)
- "Making sense of sequence: The need for integrating computational and human-curated genome annotation processes," Advances in Genome Biology and Technology, Marco Island, FL (2002).
- "Integrating computational and human-curated annotations for the mouse genome," International Mouse Genome Conference, Edinburgh, Scotland (2001).
- "Connecting sequence and biology: From catalog to context," Genomics Meets Nanoscience Conference, The Jackson Laboratory, Bar Harbor, ME (2001)
- "Developing a genome spatial information system," Applications of GIS to Bioinformatics Symposium, Virginia Tech University, Blacksburg, VA (2001).
- "Closing the phenotype gap: large-scale mutagenesis at The Jackson Laboratory, Celltech, Seattle, WA (2001).
- "Why the mouse genome?," National Association of Science Writers, UC Berkeley, Berkeley, CA (2001).
- "Mouse Genome Informatics (MGI): The power of an integrated view of mouse biology," UPenn Bioinformatics Forum, (2001).
- "The power of an integrated view of the mouse genome," Proteome, Inc., Beverly, MA(2000).
- "Mouse genome informatics in a new age of biological inquiry," IEEE International Symposium on Bio-Informatics and Biomedical Engineering, Washington, D.C. (2000).

- "Bioinformatics: Critical tools for mouse and human genetic research," Third Animal Models as Biomedical Tools: Skin and Hair Mutations Workshop, The Jackson Laboratory, Bar Harbor, ME (2000).
- "Mouse Genome Informatics (MGI): An integrated view of mouse biology." 12th Annual International Genome Sequencing and Analysis Conference, Miami, FL (2000).
- "Connecting sequence and biology: Informatics resources for mouse genomics," UC Davis/The Jackson Laboratory Symposium on Advances in Biomedical Research through Mouse Biology, UC Davis, Davis, CA (2000).
- "Connecting sequence and biology: Informatics resources for mouse genomics," Meet your New Neighbor: The Jackson Laboratory, Roche Biosciences, Palo Alto, CA (2000).
- "Integrating sequence and biology: The Mouse Genome Sequence database project," 8th Annual DOE Contractors Meeting, Santa Fe, N.M. (2000).
- "To the genome and beyond: Bioinformatics in a new age of biological inquiry", University of Buffalo, Buffalo, NY (2000)
- "The Mouse Tumor Biology Database (MTB) Project," Mouse Molecular Genetics Conference, Heidelberg, Germany (1999)
- "Bioinformatics in a new age of biological inquiry," University of Maine Annual EPSCOR Conference on Molecular Biology in Maine, Orono, ME (October 1999)
- "Genome Informatics: A Status Report," IDEXX Laboratories, Inc. Westbrook, ME (1999)
- "Developing a Genome Spatial Information System," Maine GIS Users Group Annual Meeting, Bangor, ME (1999)
- "Genome Informatics: Where we've been, Where we're going," BioEngineering Resource Group, University of Maine, Orono, ME (1999)
- "Genomes as Geographic Landscapes," Dept. of Biochemistry, Microbiology and Molecular Biology, University of Maine, Orono, ME (1999)
- "Whole Genome Sequencing of Microbes and Plants: Status and Implications," Centro Internacional de Agricultura Tropical (CIAT), Cali, Colombia (1997).
- "From Information to Understanding: The Present and Future of Comparative Genomics" Carl Von Linneaus Lecture, Uppsala University, Uppsala, Sweden (1997).
- "From Sequence to Biology: Data mining and complete genomes. Frontiers in Genetic Research, University of Connecticut, Storrs, CT. (1997)
- "The complete genome of *Methanococcus jannaschii*," New England Molecular Evolutionary Biologists annual meeting, Durham, N.H. (1996)
- "The genome of *Methanococcus jannaschii* and the origins of life," University of New Hampshire, Durham, N.H. (1996)
- "Complete genome sequencing and characterization of the thermophilic methanogen, *Methanococcus jannaschii*," DOE Annual Contractor-Grantee Workshop, Santa Fe, NM. (1996)
- "Fire-breathing dragons, archaebacteria and the future of genomic medicine," Conference on Genomic Medicine, Rockville, MD. (1995)
- "The genomes of *Haemophilus influenzae* Rd and *Mycoplasma genitalium*," European Molecular Biology Organization (EMBO) Workshop on Microbial Genome Evolution, Balsta, Sweden (1995).
- "Rapid gene discovery and the human genome project," Maine Medical Center, Portland, ME (1995).
- "From information to understanding: The role of informatics in genome biology," Bates College, Lewiston, ME (1995).
- "The development and implementation of the Sequences, Sources, Taxa (SST) database," Society for the Study of Evolution, McGill University, Montreal, Canada (1995).
- Round table discussion on careers in science, Women's Center, California Institute of Technology, Pasadena, CA (1995).
- "Human gene discovery and comparative genomics," California Institute of Technology, Pasadena, CA. (1995)
- "The Expressed Gene Anatomy and Sequences, Sources, Taxa Databases: models for interoperability among biological databases," Plant Genome III, San Diego, CA (1995).
- "Metodos modernos de reconstruccion filogenetica utilizando datos moleculares," Centro de Investigacion y Desarrollo en Criotecnologia de Alimentos, La Plata, Argentina (1994).
- "La filogenia y los caracteres moleculares," VI Congreso Latinoamericano de Botanica, Mar del Plata, Argentina. (1994)
- "Genomics, systematics, and the metazoa," 6th Annual Genome Sequencing and Analysis Conference, Hilton Head, SC (1994).
- "Integrated biological databases to support research in gene discovery, expression, and evolution," International Society of Plant Molecular Biologists, Amsterdam, The Netherlands. (1994)
- "Sequences, Sources, Taxa: Linking diverse database resources on the Internet for research in biodiversity and evolution," Smithsonian Institution Biodiversity Seminar Series, Washington, D.C. (1994)

- "Cladistic analysis of protein evolution," Willi Hennig Society, Fullerton, CA. (1993)
- "The impact of rapid gene discovery technology on studies of biodiversity and evolution," Inaugural Symposium of the Biodiversity Consortium. Washington, D.C. (Plenary speaker, 1993)
- "The utility of the large subunit (LSU, 28S) of rDNA for phylogenetic reconstruction in plants," American Institute for Biological Sciences, Ames, Iowa. (1993)
- "Tribal relationships within Onagraceae: morphological and molecular data," Society for the Study of Evolution Annual Meeting, Berkeley, CA. (1992)
- "Differential amplification of nuclear and organellar rDNA from total plant DNA," International Society of Plant Molecular Biologists, Tucson, AZ. (1991)
- "Using organellar and nuclear ribosomal gene sequences in studies of plant evolution," George Mason University, VA (1991).
- "Integrating molecular and non-molecular data in systematic analyses," Willi Hennig Society, Royal Ontario Museum, Toronto, Canada (1991).
- "Tribal relationships within Onagraceae: Insights from nuclear ribosomal RNA sequences," George Washington University, Washington, D.C. (1990).
- "Genetic structure within and among natural populations of the wild soybean," Louisiana State University, LA (1990).
- "Is there life after graduate school? Job hunting skills for new graduates and postdocs," Panel member. American Association for the Advancement of Science Annual Meeting, New Orleans, LA (1990).
- "Women's voices in science," New Hampshire Women in Higher Education Association, Dartmouth College, N.H. (1988).
- "Genetic differentiation among seven natural populations of wild soybean: Implications for germplasm conservation," University of New Hampshire, N.H. (1988).
- "Where have all the flowers gone?: Reproductive efficiency in the wild soybean, *Glycine soja*," Society for the Study of Evolution, Montana State University, Bozeman, MT (1987).
- "Isozyme variation in low versus high salinity populations of hard-shell clams, *Mercenaria mercenaria*," Annual meeting of the Virginia Academy of Sciences, George Mason University, Fairfax, VA (1984).