

CURRICULUM VITAE

Chao Cheng

Ph.D. in Computational Biology

M.S. in Molecular Genetics

M.S. in Statistics

Title

Assistant Professor
Department of Biomedical Data Science,
Department of Molecular and Systems Biology,
Institute for Quantitative Biomedical Sciences,
Norris Cotton Cancer Center,
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PubMed Bibliography:

<http://www.ncbi.nlm.nih.gov/sites/myncbi/10G4ptVhS0ykg/bibliography/47197895/public/?sort=date&direction=descending>

Google Scholar: <https://scholar.google.com/citations?user=ny1FMnsAAAAJ&hl=en>

Academic Appointments

2016	Assistant Professor	Department of Biomedical Data Science, Department of Molecular and Systems Biology, Geisel School of Medicine at Dartmouth College
2013	Investigator	Norris Cotton Cancer Center, Geisel School of Medicine at Dartmouth College
2012	Investigator	Institute for Quantitative Biomedical Science, Geisel School of Medicine at Dartmouth College
2012	Assistant Professor	Department of Genetics, Geisel School of Medicine at Dartmouth College

Education

- University of Southern California: Aug. 2002 – Dec. 2006
Ph.D. in Computational Biology and Bioinformatics
Dissertation: *Detecting and understanding differentiation of microarray expression data.*
- University of Southern California: Aug. 2005 – Dec. 2006
M.S. in Statistics
Dissertation: *Algorithms and application of least trimmed squares taking into account errors in both predictor and response variables.*
- Fudan University: Sep. 1999 – July 2002
M.S. in Molecular Genetics

Dissertation: *Cloning and function studies of human dual specificity phosphatases.*

- East China University of Sci. and Tech.: Sep. 1995 – July 1999
B.S. Degree in Biochemistry
Minor: Applied Mathematics and Software

Postdoctoral Training

- Yale University: Mar. 2008 – July 2012
Post-Doc Associate in Bioinformatics
Supervisor: Mark Gerstein
- University of Southern California: Jan. 2007 – Feb. 2008
Post-Doc Associate in Bioinformatics
Supervisor: Lei Li

Research Interests

- Precision Medicine
- Cancer Systems Biology
- Translational Cancer Research and Precision Medicine
- Cancer Immunology and Immunotherapy
- Drug Repurposing
- Cancer Epidemiology and Pharmacoepidemiology
- Biomarkers for diagnosis, prognosis and predicting treatment efficacy
- Functional Genomics
- Microarray and Next Generation Sequencing
- Gene Regulatory Network and Systems Biology

Honor and Awards

- Award for Excellence in Research (2016), Norris Cotton Cancer Center at Dartmouth
- Final Summer Dissertation Fellowship (2006), USC
- Graduate Student Xie Xide Award (2001), Fudan University
- Outstanding Student Award (1999), East China University of Sci. & Tech.
- Outstanding Student Award (1998), East China University of Sci. & Tech.
- Outstanding Student Award (1997), East China University of Sci. & Tech.
- Outstanding Student Award (1996), East China University of Sci. & Tech.
- Freshman Fellowship (1995), East China University of Sci. & Tech.

Professional Services

Editorial board (4):

Frontiers in Genetics
Journal of Genetics and Genome Research
Scientific Report
Tumor and Microenvironment

Ad hoc Reviewer for the following journals (26):

African Health Sciences
Bioinformatics
Bioinformatics and Biology Insights
BioScience

BMC Bioinformatics
 BMC Cell Biology
 BMC Chinese Medicine
 BMC Medical Genomics
 BMC System Biology
 Cell Report
 Clinical Cancer Research
 Evolutionary Bioinformatics
 Frontiers in Genetics
 Gastroenterology
 Genome Biology and Evolution
 Genome Research
 Human Genetics
 Lung Cancer
 Methods
 Nature Communications
 Nucleic Acids Research
 PLoS Genetics
 PLoS One
 PLoS Computational Biology
 Scientific Report
 Tumor Biology

Conference program committee:

February 20-22, 2017 Program committee
 CPH 2017, DahShu Data Science Symposium: Computational Precision Health
 2017
 San Francisco Bay Area, USA
 September 3-4, 2016 Program committee
 MLSB 2016, The 10th International Workshop on Machine Learning in Systems
 Biology
 Hague, Netherlands
 June 08-12, 2016 Poster prize committee
 Intelligent Systems for Molecular Biology (ISMB 2016)
 Orlando, FL, USA
 January 11-13, 2016 Program committee
 APBC 2016, The Fourteenth Asia Pacific Bioinformatics Conference
 San Francisco, CA, USA
 December 12, 2015 Program committee
 Workshop in Machine Learning in Computational Biology (MLCB)
 Annual Conference on Neural Information Processing Systems (NIPS 2015)
 Montreal, Canada
 January 21-23, 2015 Program committee
 APBC 2015, The Thirteenth Asia Pacific Bioinformatics Conference
 HsinChu, Taiwan
 January 13, 2014 Program committee
 Workshop in Machine Learning in Computational Biology (MLCB)
 Annual Conference on Neural Information Processing Systems (NIPS 2014)
 Montreal, Canada
 January 3-7, 2014 Workshop organizer
 Noncoding RNA workshop,
 Pacific Symposium on Biocomputing (PSB 2014)

The Big Island of Hawaii, USA

October 14-17, 2007 Program committee,
Institute of Electrical and Electronics Engineers (IEEE), 7th International
Symposium on Bioinformatics and Bioengineering (BIBE 2007)
Boston, USA

Publications

* Co-first author

§ Corresponding author

Journals

110. Wang Y, Ung HM, Xia T, Cheng W[§], **Cheng C[§]**. Comparative analyses of FOXM1 cistromes in diverse human cell lines reveals substantial impact of co-factors on genomic occupation. 2016 (Under review)
109. Beattie RS, Mark K, **Cheng C**, Dhingra S, Ries L, Goldman G, Caffrey A, Obar J, Cramer R. Carbon Catabolite Repression is Essential for Fungal Bioenergetics, Virulence and Drug Resistance. *PLoS Pathog.* 2017 (Under revision)
108. Ung HM, MacKenzie AT, Onega T, **Cheng C[§]**. Hydrochlorothiazide prescription and survival after diagnosis in Medicare breast cancer patients: A retrospective cohort study. 2017 (Under review)
107. Varn F, Wang Y, Mullin D, Fiering S, **Cheng C[§]**. Systematic pan-cancer analysis reveals immune cell interactions in the tumor microenvironment. *Cancer Research.* 2017 Jan 26. pii: canres.2490.2016. doi: 10.1158/0008-5472.CAN-16-2490.
106. Almiron AD, Ran C, Havrda CM, Liu H, Hitoshi Y, Zhang Z, Ung HM, **Cheng C**, Israel AM. Insulin-mediated signaling facilitates resistance to PDGFR inhibition in proneural hPDGFB-driven gliomas. *Molecular Cancer Therapeutics.* 2017 Jan 30. pii: molcanther.0616.2016. doi: 10.1158/1535-7163.MCT-16-0616.
105. Nowak CE, Louise JL, FrVarn SF, Deng J, Sarde A, Mabaera R, Kuta A, Le Mercier I, **Cheng C**, Noelle JR. Immunoregulatory Functions of VISTA. *Immunological Reviews.* 2017 Mar;276(1):66-79. doi: 10.1111/imr.12525. Review.
104. Andrews E, Wang Y, Xia T, Cheng W, **Cheng C[§]**. Regulator target contextual refinement reveals effects on breast cancer prognosis of the regulome. *PLoS Comput. Biol.* 2017 Jan 19;13(1):e1005340.
103. Mark K, Qian F, **Cheng C[§]**. The E2F4 prognostic signature predicts 1 pathological response to neoadjuvant chemotherapy in breast cancer patients. *BMC Cancer.* 2016 (Accepted)
102. Deng J, Lines JL, Lee Y, Pechenick AD, Qian D, Manivanh R, Sarde A, LeMercier I, Lowrey HC, Varn F, **Cheng C**, Amos IC, Leib AD, Noelle JR, Mabaera R. Hypoxia-induced VISTA promotes the suppressive function of myeloid-derived suppressor cells in the tumor microenvironment. *Cancer Research.* 2016 (Under revision)
101. Tian A, Wang Z, **Cheng C**, Ahmed Y. Reprogramming of transcription cofactors mediates the hyperactivation of Wingless/Wnt signal transduction. 2016 (Under review)
100. Posternak V, Ung HM, **Cheng C**. MYC mediates mRNA cap methylation of canonical Wnt/ β -catenin signaling transcripts by recruiting cyclin-dependent kinase 7 and RNA methyltransferase. *Molecular Cancer Res.* 2016 Nov 29. doi: 10.1158/1541-7786.MCR-16-0247.
99. Wang Y, Mark K, Ung M, Kettenbach A, Miller T, Xu W, Cheng W, Xia T[§], **Cheng C[§]**. Application of RNAi-induced gene expression profiles for prognostic prediction in breast cancer. *Genome Medicine.* 2016 Oct 27. doi: 10.1186/s13073-016-0363-3.

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98. Ung M, Varn SF, **Cheng C**[§]. In silico frameworks for systematic pre-clinical screening of potential anti-leukemia therapeutics. *Expert Opin Drug Discov*. 2016 Dec;11(12):1213-1222. Epub 2016 Oct 11.
 97. Yang C, Andrews E, Chen M, Wang W, Chen J, Gerstein M, Liu C[§], **Cheng C**[§]. TIP: a web server for identifying target genes of transcription factors from ChIP-seq or ChIP-chip data. *BMC Genomics*. 2016 Aug 12;17(1):632.
 96. Chesmore K, Bartlett J, **Cheng C**, Williams S. Pleiotropic Constraints on the Evolution of the Human Transcription Factor Network. *Genome Biol Evol*. 2016 Sep 15. pii: evw228.
 95. Liu X, Yu P, **Cheng C**, Potash JB, Han S. GLITTER: a web-based application for gene link inspection through tissue-specific coexpression. *Sci Rep*. 2016 Sep 14;6:33460. doi: 10.1038/srep33460.
 94. Varn SF, Mullins D, Arias-Pulido H, Fiering S, Cheng C. Adaptive immunity programs in breast cancer. *Immunology*. 2016 Aug 26. doi: 10.1111/imm.12664.
 93. Kato M, Kashem A, **Cheng C**. MicroRNA-mediated endocytotic and innate immune pathways modulate an adaptive response against chronic oxidative stress in *C. elegans*. 2016 Sep 12. doi: 10.18632/aging.101029.
 92. Ung M, Wang G, Varn SF, **Cheng C**[§]. Application of pharmacologically induced transcriptomic profiles to interrogate PI3K-Akt-mTOR pathway activity associated with cancer patient prognosis. *Oncotarget*. 2016 Aug 31. doi: 10.18632/oncotarget.11776.
 91. Canfield K, Wells W, Geradts J, Kinlaw WB, Kornbluth S, **Cheng C**, Kurokawa M. Inverse association between MDM2 and HUWE1 protein expression levels in human breast cancer and liposarcoma. *Int J Clin Exp Pathol*. 2016;9(6):6342-6349.
 90. Petrone A, Adamo ME, **Cheng C**, Kettenbach AN. Identification of candidate CDK1 substrates in mitosis by quantitative phosphoproteomics. *Mol Cell Proteomics*. 2016 May 1. pii: mcp.M116.059394.
 89. Yan KK, Wang D, Sethi A, Muir P, Kitchen R, **Cheng C**, Gerstein M. Cross-Disciplinary Network Comparison: Matchmaking Between Hairballs. *Cell Syst*. 2016. 2: 147-157.
 88. Ung M, Liu C, **Cheng C**[§]. Integrative analysis of cancer genes in a functional interactome. *Scientific Report*. 2016 Jun 30;6:29228. doi: 10.1038/srep29228.
 87. Yang H, Yin J, Ficarrota K, Hsu SH, Zhang W[§], **Cheng C**[§]. Aberrant expression and hormonal regulation of Galectin-3 in endometriosis women with infertility. *J Endocrinol Invest*. 2016 Feb 17.
 86. Ung M, Sun C, Weng C, Huang C, Lin C[§], Liu C[§], **Cheng C**[§]. Integrated Drug Expression Analysis for Leukemia -- An integrated in silico and in vivo approach to drug discovery. *Pharmacogenomics*. 2016 Mar 15. doi: 10.1038/tpj.2016.18.
 85. Rahmea G, Zhang Z, Young A, Hitoshi Y, **Cheng C**, Bivona E, Fiering S, Israel M. PDGF Signaling Maintains Survival of Proneural Glioma. *Cancer Research*. 2016 Mar 7. pii: canres.2157.2015.
 84. Varn SF, Andrews EH, Mullins DW, **Cheng C**[§]. Integrative analysis of breast cancer reveals prognostic haematopoietic activity and patient-specific immune response profiles. *Nat Commun*. 2016 Jan 4;7:10248. doi: 10.1038/ncomms10248.
 83. **Cheng C**[§], Lou S, Andrews HE, Ung M, Varn SF. Integrative Genomic Analyses Yields Cell Cycle Regulatory Programs with Prognostic Value. *Molecular Cancer Res*. 2016. Feb 8. pii: molcanres.0368.
 82. Varn F, Andrews E, **Cheng C**[§]. Systematic identification of hematopoietic cell type-specific profiles for prognostic prediction in acute myeloid leukemia. *Scientific Report*. 2015 Nov 24;5:16987. doi: 10.1038/srep16987.

81. Zhang S, Zhou J, Hu H, Gong H, Chen L, **Cheng C**[§], Zeng J[§]. A deep learning framework for modeling structural features of RNA-binding protein targets. *Nucleic Acids Research*. 2015. Oct 13. pii: gkv1025.
80. Liu Y, Li J, Sun C, Andrews E, Chao R, Lin F, Weng S, Hsu S, Huang C, **Cheng C**, Chun-Chi Liu C, Huang H. CircNet: A database of circular RNAs derived from transcriptome sequencing data. *Nucleic Acids Research*. 2016 Jan 4;44(D1):D209-15. doi: 10.1093/nar/gkv940.
79. Integrative analysis reveals regulatory programs in endometriosis. Yang H, Kang K, **Cheng C**, Mamillapalli R, Hugh T. *Reproductive Sciences*. 2015 Sep;22(9):1060-72. doi: 10.1177/1933719115592709.
78. **Cheng C**[§], Varn F, Marsit, C. E2F4 Program is Predictive of Progression and Intravesical Immunotherapy Efficacy in Bladder Cancer. *Mol Cancer Res*. 2015 Jun 1. pii: molcanres.0120.2015.
77. Ung M, Varn F, **Cheng C**[§]. IDEA: Integrated Drug Expression Analysis – Integration of gene expression and clinical data for the identification of therapeutic candidates. *CPT: Pharmacometrics & Systems Pharmacology*. 2015 Jul;4(7):415-25. doi: 10.1002/psp4.51.
76. **Cheng C**[§], Andrews E, Yan K, Ung M, Wang D, Gerstein M[§]. An Approach for Determining and Measuring Network Hierarchy: Application to Comparing the Phosphorylome and the Regulome. *Genome Biol*. 2015 March 31; 16:63 doi:10.1186/s13059-015-0624-2.
75. Ung M, Lou S, Varn F, **Cheng C**[§]. Regulators associated with clinical outcomes revealed by DNA methylation data in breast cancer. *PLoS Comput Biol*. 2015 May 21;11(5):e1004269.
74. Wang D, Yan K, Sisu C, **Cheng C**, Rozowsky J, Meyerson W, Gerstein M. Loregic: A method to characterize the cooperative logic of regulatory factors. *PLoS Comput Biol*. 2015 Apr 17; 11(4):e1004132.
73. Varn F, Ung M, Lou S, **Cheng C**[§]. Integrative analysis of survival-associated gene sets in breast cancer. *BMC Medical Genomics*. 2015, 8:11 doi:10.1186/s12920-015-0086-0.
72. Balboni AL, Cherukuri P, Ung M, DeCastro AJ, **Cheng C**, DiRenzo J. p53 and DeltaNp63alpha Co-regulate the Transcriptional and Cellular Response to TGFbeta and BMP Signals. *Mol Cancer Res*. 2015 Feb 19. pii: molcanres.0152.2014.
71. Tan J, Ung M, **Cheng C**, Greene CS. Unsupervised feature construction and knowledge extraction from genome-wide assays of breast cancer with denoising autoencoders. *Pac Symp Biocomput*. 2015;20:132-43.
70. Fan Y, Wu J, Ung M, De Lay, N, **Cheng C**, Ling J. Protein mistranslation protects bacteria against oxidative stress. *Nucleic Acids Research*. 2015; doi: 10.1093/nar/gku1404.
69. Chung D, Barker BM, Carey CC, Merriman B, Werner ER, Lechner BE, Dhingra S, **Cheng C**, Xu W, Blosser SJ, Morohashi K, Mazurie A, Mitchell TK, Haas H, Mitchell AP, Cramer RA. ChIP-seq and in vivo gene expression analyses of the pathogenic fungus *Aspergillus fumigatus* SREBP SrbA reveals new insights into hypoxia adaptation and fungal virulence. *PLoS Pathog*. 2014 Nov 6;10(11):e1004487.
68. Hurley JM, Dasgupta A, Emerson JM, Zhou X, Ringelberg CS, Knabe N, Lipzen AM, Lindquist EA, Daum CG, Barry KW, Grigoriev IV, Smith KM, Galagan JE, Bell-Pedersen D, Freitag M, **Cheng C**, Loros JJ, Dunlap JC. Analysis of clock-regulated genes in *Neurospora* reveals widespread posttranscriptional control of metabolic potential. *Proc Natl Acad Sci U S A*. 2014 Oct 31.
67. Khaleel S, Andrews E, Yan K, Ung M, Dorenzo J, and **Cheng C**[§]. E2F4 regulatory program predicts patient survival prognosis in multiple cancer types. *Breast Cancer Res*. 2014 Dec 2;16(6):486.

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66. Yan K, Wang D, Rozowsky J, Zheng H, **Cheng C**, Gerstein M. OrthoClust: An orthology-based network framework for clustering data across multiple species. *Genome Biology*. 2014 August 28;15:R100.
 65. Boyle A, Araya C, Brdlik C, Cayting P, **Cheng C**, Cheng Y, Gardner K, Hillier L, Janette J, Jiang L, et al. Comparative analysis of regulatory information and circuits across diverse species. *Nature*. 2014 August 28;512: 453–456.
 64. Yang H, Li D, **Cheng C**[§]. Relating gene expression evolution with CpG content changes. 2014 Aug 20;15(1):693.
 63. Gerstein M*, Rozowsky J*, Yan K*, Wang D*, **Cheng C***, Brown B*, Davis C, Hillier L, Sisu C, Li J, et al. Comparative analysis of the transcriptome across distant species. *Nature*. 2014 August 28; 512: 445–448.
 62. Greene C, Tan J, Ung M, Moore J[§], **Cheng C**[§]. Big data bioinformatics. *J. Cell. Physiol.* 2014 May 6. doi: 10.1002/jcp.24662.
 61. Mishra B, Zaffuto K, Artinger E, Org T, Mikkola H, **Cheng C**, Djabali M, Ernst P. The histone methyltransferase activity of MLL1 is dispensable for hematopoiesis and leukemogenesis. *Cell Rep*. 2014 May 22;7(4):1239-47.
 60. Min R, Ning X, **Cheng C**, Gerstein M. Interpretable Sparse High-Order Boltzmann Machines. *Journal of Machine Learning Research*. JMLR W&CP 33:614-622, 2014.
 59. Ung M, Ma X, Johnson K, Christensen B, **Cheng C**[§]. Effect of estrogen receptor alpha binding on functional DNA methylation in breast cancer. *Epigenetics*. 2014 Jan 16;9(4).
 58. Tzeng DT, Tseng YT, Ung M, Liao IE, Liu CC, **Cheng C**[§]. DPRP: a database of phenotype-specific regulatory programs derived from transcription factor binding data. *Nucleic Acids Res*. 2014 Jan 1;42(1):D178-83.
 57. **Cheng C**, Moore J, Greene C. Applications of bioinformatics to non-coding rnas in the era of next-generation sequencing. *Pac Symp Biocomput*. 2014;19:412-6.
 56. Johnson KC, Koestler DC, **Cheng C**, Christensen BC. Age-related DNA methylation in normal breast tissue and its relationship with invasive breast tumor methylation. *Epigenetics*. 2013 Nov 6;9(2).
 55. Li D, Sulovari A, **Cheng C**, Zhao H, and Gelernter J. Association of Gamma-Aminobutyric Acid A Receptor α 2 Gene (GABRA2) with Alcohol Use Disorder. *Neuropsychopharmacology*. 2013 Oct 18. doi: 10.1038/npp.2013.291.
 54. Grant G, Martyanov V, Brooks L, Mahoney M, Wood T, Sherlock G, **Cheng C**, Whitfield M. Identification of cell cycle-regulated genes periodically expressed in U2OS cells and their regulation by Forkhead and E2F transcription factors. *Molecular Biology of the Cell*. 2013 Dec;24(23):3634-50.
 53. Artinger EL, Mishra BP, Zaffuto KM, Li BE, Chung EK, Moore AW, Chen Y, **Cheng C**, Ernst P. MLL1 coordinates proliferation with self-renewal in hematopoietic stem cells. *Proc Natl Acad Sci U S A*. 2013 Jul 16;110(29):12000-5.
 52. Zhu M, Liu CC, **Cheng C**[§]. REACTIN: Regulatory activity inference of transcription factors underlying human diseases with application to breast cancer. 2013 Jul 26;14:504.
 51. Yang C, Buck J.M, Chen M, Chen Y, Lan H, **Cheng C**, Chen J, Liu C. Discovering chromatin motifs using FAIRE sequencing and the human diploid genome. *BMC Genomics*. 2013 May 8;14:310.
 50. **Cheng C**[§], Fu Y, Gerstein M[§]. Predict yeast cell cycle regulated genes based on genomic features. *BMC Systems Biology*. 2013 Jul 29;7:70.

49. **Cheng C[§]**, Ung M, Grant G, Whitfield M. Transcription factor binding profiles reveal cyclic expression of human protein-coding genes and non-coding RNAs. *PLoS Computational Biology*. 2013 Jul;9(7):e1003132.
48. Yin J, Wu N, Zeng F, **Cheng C**, Kang K, Yang H. Paeonol induces apoptosis in human ovarian cancer cells. *Acta Histochemica*. 2013. Jun 12. pii: S0065-1281(13)00076-7.
47. Kevin Y, **Cheng C**, Gerstein, M. Machine learning and genome annotation: A match meant to be? *Genome Biology*. 2013 May 29;14(5):205.
46. Kittler R, Zhou J, Hua S, Ma L, Liu Y, Pendleton E, **Cheng C**, Gerstein M, White KP. A Comprehensive Nuclear Receptor Network for Breast Cancer Cells. *Cell Rep*. 2013 Jan 30.
45. Dong X, Greven M, Kundaje A, Djebali S, Brown BJ, **Cheng C**, Gerstein M, Guigó Serra R, Birney E, Weng Z. Modeling gene expression using chromatin features in various cellular contexts. *Genome Biology*. 2012 Sep 5;13(9):R53.
44. Yang H, Lei C, **Cheng C**, Feng Y, Zhang W, Petracco RG, Sak S. The Anti-Apoptotic Effect of Galectin-3 in Human Endometrial Cells under the Regulation of Estrogen and Progesterone. *Biol Reprod*. 2012 Jun 6.
43. Gerstein MB*, Kundaje A*, Hariharan M*, Landt SG*, Yan KK*, **Cheng C***, Mu XJ*, Khurana E*, Rozowsky J*, Alexander R*, Min R*, Alves P, Abyzov A, Addleman N, Bhardwaj N, Boyle AP, Cayting P, Charos A, Chen DZ, Cheng Y, Clarke D, Eastman C, Euskirchen G, Fietze S, Fu Y, Gertz J, Grubert F, Harmanci A, Jain P, Kasowski M, Lacroute P, Leng J, Lian J, Monahan H, O'Geen H, Ouyang Z, Partridge EC, Patacsil D, Pauli F, Raha D, Ramirez L, Reddy TE, Reed B, Shi M, Slifer T, Wang J, Wu L, Yang X, Yip KY, Zilberman-Schapira G, Batzoglou S, Sidow A, Farnham PJ, Myers RM, Weissman SM, Snyder M. Analysis of the human regulatory network using ENCODE Data. *Nature*. 2012 Sep 6;489(7414):91-100.
42. The ENCODE Project Consortium. An integrated encyclopedia of DNA elements in the human genome. *Nature*. 2012 Sep 6;489(7414):57-74.
41. Yip YK, **Cheng C**, Bhardwaj N, Brown BJ, Leng J, Kundaje A, Rozowsky J, Birney E, Bickel JP, Snyder M and Gerstein M. Genome-wide analysis of the binding sites of more than 100 transcription factors defines different types of genomic regions with distinct biological properties. *Genome Biology*. 2012 Sep 5;13(9):R48.
40. **Cheng C**, Alexander R, Min R, Leng J, Yip KY, Rozowsky J, Yan KK, Dong X, Djebali S, Ruan Y, Davis CA, Carninci P, Lassman T, Gingeras TR, Guigó R, Birney E, Weng Z, Snyder M, Gerstein M. Understanding transcriptional regulation by integrative analysis of transcription factor binding data. *Genome Res*. 2012 Sep;22(9):1658-67.
39. Yang H*, **Cheng C^{*,§}**, Zhang W[§]. Average rank-based score to measure deregulation of molecular pathway gene sets. *PLoS ONE*. 2011;6(11):e27579.
38. **Cheng C**, Gerstein M. Modeling the relative relationship of transcription factor binding and histone modifications to gene expression levels in mouse embryonic stem cells. *Nucleic Acids Research*. 2011 Sep 16.
37. **Cheng C***, Shou C*, Yip Y, Gerstein M. Genome-wide analysis of chromatin features identifies chromatin-sensitive and chromatin-insensitive classes of yeast transcription factors. *Genome Biology*. 2011 Nov 7;12(11):R111.
36. **Cheng C**, Min R, Gerstein M. A Probabilistic Method for identifying Transcription Factor Target Genes from CHIP-Seq Binding Profiles. *Bioinformatics*. 2011 Dec 1;27(23):3221-7.
35. **Cheng C**, Yan, K, Hwang W, Qian J, Bhardwaj N, Rozowsky J, Lu Z, Niu W, Alves P, Kato M, Snyder M, Gerstein M. Construction and Analysis of an Integrated Regulatory Network Derived from High-throughput Sequencing Data. *PLoS Computational Biology*. 2011 Nov;7(11):e1002190.

34. The ENCODE Project Consortium. A User's Guide to the Encyclopedia of DNA Elements (ENCODE). *PLoS Biol.* 2011 Apr;9(4):e1001046.
33. Yang H, Taylor HS, Lei C, **Cheng C**, Zhang W. Hormonal Regulation of Galectin 3 in Trophoblasts and Its Effects on Endometrium. *Reprod Sci.* 2011 May 9.
32. Nègre N, Brown CD, Ma L, Bristow CA, Miller SW, Wagner U, Kheradpour P, Eaton ML, Loriaux P, Sealfon R, Li Z, Ishii H, Spokony RF, Chen J, Hwang L, **Cheng C**, Auburn RP, Davis MB, Domanus M, Shah PK, Morrison CA, Zieba J, Suchy S, Senderowicz L, Victorsen A, Bild NA, Grundstad AJ, Hanley D, MacAlpine DM, Mannervik M, Venken K, Bellen H, White R, Gerstein M, Russell S, Grossman RL, Ren B, Posakony JW, Kellis M, White KP. A cis-regulatory map of the *Drosophila* genome. *Nature.* 2011 Mar 24;471(7339):527-31.
31. **Cheng C**, Yan KK, Yip KY, Rozowsky J, Alexander R, Shou C, Gerstein M. A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. *Genome Biol.* 2011 Feb 16;12(2):R15.
30. Lu ZJ, Yip KY, Wang G, Shou C, Hillier LW, Khurana E, Agarwal A, Auerbach R, Rozowsky J, **Cheng C**, Kato M, Miller DM, Slack F, Snyder M, Waterston RH, Reinke V, Gerstein MB. Prediction and characterization of noncoding RNAs in *C. elegans* by integrating conservation, secondary structure, and high-throughput sequencing and array data. *Genome Res.* 2011 Feb;21(2):276-85.
29. Niu W, Lu ZJ, Zhong M, Sarov M, Murray JI, Brdlik CM, Janette J, **Cheng C**, Alves P, Preston E, Slightham C, Jiang L, Hyman AA, Kim SK, Waterston RH, Gerstein M, Snyder M, Reinke V. Diverse transcription factor binding features revealed by genome-wide ChIP-seq in *C. elegans*. *Genome Res.* 2011 Feb;21(2):245-54.
28. Gerstein MB*, Lu ZJ*, Van Nostrand EL*, **Cheng C***, Arshinoff BI*, Liu T*, Yip KY*, Robilotto R*, Rechtsteiner A*, Ikegami K, Alves P, Chateigner A, (et al. 132 authors). Integrative analysis of the *Caenorhabditis elegans* genome by the modENCODE project. *Science.* 2010 Dec 24;330(6012):1775-87.
27. **Cheng C**, Bhardwaj N, Gerstein M: The relationship between the evolution of microRNA targets and the length of their UTRs. *BMC Genomics.* 2009, 10:431.
26. **Cheng C***, Fu X*, Alves P, Gerstein M: mRNA expression profiles show differential regulatory effects of microRNAs between estrogen receptor-positive and estrogen receptor-negative breast cancer. *Genome Biol.* 2009, 10(9):R90.
25. Ge H, Wei M, Fabrizio P, Hu J, **Cheng C**, Longo VD, Li LM: Comparative analyses of time-course gene expression profiles of the long-lived sch9Delta mutant. *Nucleic Acids Res.* 2009, 38(1):143-158.
24. Lee Y, Yang X, Huang Y, Fan H, Zhang Q, Wu Y, Li J, Hasina R, **Cheng C**, Linggen MW et al: Network modeling identifies molecular functions targeted by miR-204 to suppress head and neck tumor metastasis. *PLoS Comput Biol.* 2010, 6(4):e1000730.
23. **Cheng C**, Li L, Alves P, Gerstein M: Systematic identification of transcription factors associated with patient survival in cancers. *BMC Genomics.* 2009, 10:225.
22. Mishima Y, Abreu-Goodger C, Staton AA, Stahlhut C, Shou C, **Cheng C**, Gerstein M, Enright AJ, Giraldez AJ: Zebrafish miR-1 and miR-133 shape muscle gene expression and regulate sarcomeric actin organization. *Genes Dev.* 2009, 23(5):619-32.
21. Wei M, Fabrizio P, Hu J, Ge H, **Cheng C**, Li L, Longo VD: Life span extension by calorie restriction depends on Rim15 and transcription factors downstream of Ras/PKA, Tor, and Sch9. *PLoS Genet.* 2008, 4(1):e13.
20. Ge H, **Cheng C**, Li LM: A probe-treatment-reference (PTR) model for the analysis of oligonucleotide expression microarrays. *BMC Bioinformatics.* 2008, 9:194.

19. **Cheng C**, Li LM: Systematic identification of cell cycle regulated transcription factors from microarray time series data. *BMC Genomics*. 2008, 9:116.
18. **Cheng C**, Li LM: Inferring microRNA activities by combining gene expression with microRNA target prediction. *PLoS ONE*. 2008, 3(4):e1989.
17. **Cheng C**, Yan X, Sun F, Li LM: Inferring activity changes of transcription factors by binding association with sorted expression profiles. *BMC Bioinformatics*. 2007, 8:452.
16. **Cheng C**, Fabrizio P, Ge H, Wei M, Longo VD, Li LM: Significant and systematic expression differentiation in long-lived yeast strains. *PLoS ONE*. 2007, 2(10):e1095.
15. **Cheng C**, Fabrizio P, Ge H, Longo VD, Li LM: Inference of transcription modification in long-live yeast strains from their expression profiles. *BMC Genomics*. 2007, 8:219.
14. **Cheng C**, Ma X, Yan X, Sun F, Li LM: MARD: a new method to detect differential gene expression in treatment-control time courses. *Bioinformatics*. 2006, 22(21):2650-2657.
13. Fabrizio P, Gattazzo C, Battistella L, Wei M, **Cheng C**, McGrew K, Longo VD: Sir2 blocks extreme life-span extension. *Cell*. 2005, 123(4):655-667.
12. **Cheng C**, Li LM: Sub-array normalization subject to differentiation. *Nucleic Acids Res*. 2005, 33(17):5565-5573.
11. Ye X, Xu J, **Cheng C**, Yin G, Zeng L, Ji C, Gu S, Xie Y, Mao Y: Isolation and characterization of a novel human putative anemia-related gene homologous to mouse sideroflexin. *Biochem Genet*. 2003, 41(3-4):119-125.
10. Ye X, Ji C, Huang Q, Cheng C, Tang R, Xu J, Zeng L, Dai J, Wu Q, Gu S et al: Isolation and characterization of a human putative receptor protein kinase cDNA STYK1. *Mol Biol Rep*. 2003, 30(2):91-96.
9. Wang W, Huang Y, Zhou Z, Tang R, Zhao W, Zeng L, Xu M, **Cheng C**, Gu S, Ying K et al: Identification and characterization of AGTRAP, a human homolog of murine Angiotensin II Receptor-Associated Protein (Agtrap). *Int J Biochem Cell Biol*. 2002, 34(1):93-102.
8. **Cheng C**, Zhou ZX, Xu M, Zhao W, Xu J, Zeng L, Huang Y, Wu QH, Dai JF, Ying K et al: [Tumor relevance analysis of a highly conserved gene by using gene microarray hybridization]. *Yi Chuan*. 2002, 24(3):227-231.
7. **Cheng C**, Ying K, Xu M, Zhao W, Zhou Z, Huang Y, Wang W, Xu J, Zeng L, Xie Y et al: Cloning and characterization of a novel human transcription factor AP-2 beta like gene (TFAP2BL1). *Int J Biochem Cell Biol*. 2002, 34(1):78-86.
6. **Cheng C**, Xu J, Ye X, Dai J, Wu Q, Zeng L, Wang L, Zhao W, Ji C, Gu S et al: Cloning, expression and characterization of a novel human VMP gene. *Mol Biol Rep* 2002, 29(3):281-286.
5. Zeng L, Zhou Z, Xu J, Zhao W, Wang W, Huang Y, **Cheng C**, Xu M, Xie Y, Mao Y: Molecular cloning, structure and expression of a novel nuclear RNA-binding cyclophilin-like gene (PPIL4) from human fetal brain. *Cytogenet Cell Genet*. 2001, 95(1-2):43-47.
4. Xu M, Zhou Z, **Cheng C**, Zhao W, Tang R, Huang Y, Wang W, Xu J, Zeng L, Xie Y et al: Cloning and characterization of a novel human TEKTIN1 gene. *Int J Biochem Cell Biol*. 2001, 33(12):1172-1182.
3. Xu J, Zhou Z, Zeng L, Huang Y, Zhao W, **Cheng C**, Xu M, Xie Y, Mao Y: Cloning, expression and characterization of a novel human REPS1 gene. *Biochim Biophys Acta*. 2001, 1522(2):118-121.
2. Wu Q, Xu M, **Cheng C**, Zhou Z, Huang Y, Zhao W, Zeng L, Xu J, Fu X, Ying K et al: Molecular cloning and characterization of a novel Dehydrogenase/reductase (SDR family) member 1 genea from human fetal brain. *Mol Biol Rep*. 2001, 28(4):193-198.

1. Huang Y, Tang R, Dai J, Gu S, Zhao W, **Cheng C**, Xu M, Zhou Z, Ying K, Xi Y et al: A novel human hydroxysteroid dehydrogenase like 1 gene (HSDL1) is highly expressed in reproductive tissues. *Mol Biol Rep.* 2001, 28(4):185-191.

Book chapters

4. **Cheng C** and Worzel W. Chapter: Application of machine-learning methods to understand gene expression regulation. Book: *Genetic Programming Theory and Practice XII*. Springer, 2014. Edited by Rick Riolo, William Worzel and Mark Kotenchek.
3. Ung M, Lou S, Varn F and **Cheng C**. Chapter: Integrative analysis identifies transcription factor-DNA methylation relationships and introduces new avenues for translating cancer epigenetics into the clinic. Book: *Next Generation Sequencing in Cancer Research (Volume 2)*. Springer, 2014. Edited by Wei Wu and Hani Choudhry.
2. **Cheng C**. Chapter: From transcription factor binding and histone modification to gene expression: integrative quantitative models. Book: *Integrating omics data: statistical and computational methods*. Cambridge University Press, 2014. Edited by George C. Tseng, Xianghong Jasmine Zhou and Debashis Ghosh.
1. Li L and **Cheng C**. Chapter: Differentiation detection in microarray normalization. Book: *DNA microarray normalization (drug discovery series)*. CRC Press, 2007. Edited by Phillip Stafford.

Patents

2. **Cheng C**. Application of an E2F4 Signature for the Prognosis Prediction of Breast Cancer. (Pending).
1. Li L, **Cheng C**, Ge H. Systems and Methods for Analyzing Microarrays.

Teaching

Fall 2016	QBS 110: Integrative Biomedical Sciences I Graduate students at Dartmouth College with Mike Whitefield <i>et al.</i>
Spring 2016	Genetics 146: Foundation of Bioinformatics I: Molecular and Computational Genomics, Graduate students at Dartmouth College with Mike Whitefield <i>et al.</i>
Fall 2015	BIOC 110: Biochemical and Genetic Basis of Medicine (FA15), MD students at Dartmouth Medical School with Lawrence Meyer <i>et al.</i>
Spring 2015	QBS 194: Biostat Journal Club and Seminar, Graduate students of Quantitative Biomedical Science Program with Jiang Gui <i>et al.</i>
Spring 2015	Genetics 146: Foundation of Bioinformatics I: Molecular and Computational Genomics, Graduate students at Dartmouth College with Mike Whitefield and Casey Greene <i>et al.</i>
Fall 2014	QBS 110: Integrative Biomedical Sciences I Graduate students at Dartmouth College with Jason Moore <i>et al.</i>
Spring 2014	Genetics 146: Molecular and Computational Genomics, Graduate students at Dartmouth College with Mike Whitefield and Jason Moore <i>et al.</i>
Spring 2014	Biology 39-139: Computational Molecular Biology Graduate and Undergraduate students at Dartmouth College with Robert Gross <i>et al.</i>

- Spring 2013 Genetics 146: Molecular and Computational Genomics,
Undergraduate students at Dartmouth College
with Mike Whitefield and Jason Moore et al.
- Spring 2013 Biology 39-139: Computational Molecular Biology
Graduate and Undergraduate students at Dartmouth College
with Robert Gross *et al.*

Qualify Committee

- 2016 Microenvironmental FGF2 and FGF10-mediated resistance to targeted therapies in ER+ breast cancer
Kevin Shee. (MD/PhD Candidate)
MD/PhD program
Department of Molecular and Systems Biology, Dartmouth College.
- 2015 Functional connectedness of highly pleiotropic genes in the human disease network
Kevin Chesmore. (PhD Candidate)
MCB program
Department of Genetics, Dartmouth College.
- 2014 Investigating the function of lncRNA MALAT1 in non-small cell lung cancer
Weiwei Yang. (PhD Candidate)
MCB program
Department of Genetics, Dartmouth College.
- 2014 Investigating the mechanism of GRK2's regulation on Smo in the Hedgehog signaling pathway via interacting with CK1 α and Gas8
Jie Tan. (PhD Candidate)
MCB program
Department of Genetics, Dartmouth College.
- 2013 Prediction and Investigation the Mechanism of miR-126 in Breast Cancer
Kevin Johnson. (PhD Candidate)
PEMM program
Department of Pharmacology and Toxicology, Dartmouth College.
- 2013 Prediction and Investigation the Mechanism of miR-126 in Breast Cancer
Jing Li. (PhD Candidate)
MCB program
Department of Genetics, Dartmouth College.

Thesis Committee (Advisor)

- 2016-? TBD
Bhaven Mehta. PhD Thesis.
MCB program
Department of Genetics, Dartmouth College.
- 2015-? TBD
Kevin Chesmore. PhD Thesis.
MCB program
Department of Genetics, Dartmouth College.
- 2015-? TBD
Kenneth Mark. PhD Thesis. (Advisor)
MCB program
Department of Genetics, Dartmouth College.
- 2014-2015 Molecular characterization of Immunoglobulin G allotypes
Nana Yaw Osei-Owusu. M.S. Thesis
MCB program

2014-?	Thayer School of Engineering, Dartmouth College. TBD Frederick Varn. PhD Thesis. (Advisor) MCB program Department of Genetics, Dartmouth College.
2014-2017	TBD Jie Tan. PhD Thesis. MCB program Department of Genetics, Dartmouth College.
2013-?	TBD Matthew Ung. PhD Thesis. (Advisor) MCB program Department of Genetics, Dartmouth College.
2013-2016	Integration and Development of Machine Learning Methodologies to Improve the Power of Genome-Wide Association Studies Jing Li. PhD Thesis. MCB program Department of Genetics, Dartmouth College.
2013-2016	On the Origins of Cancer Cell Identity - Epigenetic Deregulation of Cellular States Kevin Johnson. PhD Thesis. PEMM program Department of Pharmacology and Toxicology, Dartmouth College.
2015-2016	Integrative Multi-tissue Genomic Analyses Identify Mechanisms of Pathogenesis in Systemic Sclerosis Jaclyn N. Taroni. PhD Thesis. MCB program Department of Genetics, Dartmouth College.
2015-2016	Characterizing the Impact of Single Nucleotide Variation in Breast Cancer Kinjal Desai. PhD Thesis. MCB program Department of Genetics, Dartmouth College.
2015-2016	Gut Microbiome Composition in At-Risk Infants: Relationships Between Environment, Host Microbiota, and Health Diana Chernikova. PhD Thesis. MD/PhD program Department of Genetics, Dartmouth College.
2012-2015	Detecting, Characterizing and Interpreting Gene-Gene Interactions Associated with Metabolic Traits Rishika De. PhD Thesis. MCB program Department of Genetics, Dartmouth College.
2012-2014	The RNA Binding Landscape of the Histone Stem-Loop Binding Protein Lionel Brooks 3rd. PhD Thesis. MCB program Department of Genetics, Dartmouth College.
2012-2012	Systematic characterization of trait-associated variants Richard Cowper. PhD Thesis. MCB program Department of Genetics, Dartmouth College.

Rotation Students

Fall, 2016 Daniel Mattox, Quantitative Biomedical Sciences

Fall, 2016	Xingyu Zheng, Quantitative Biomedical Sciences
Spring, 2016	Aleksey Molodtsov, Molecular and Cellular Biology
Spring, 2016	Dillon Popovich, Molecular and Cellular Biology
Fall, 2015	Yanding Zhao, Molecular and Cellular Biology
Winter, 2014	Kenneth Mark, Molecular and Cellular Biology
Fall, 2014	Xue Xia, Molecular and Cellular Biology
Spring, 2014	Frederick Varn, Molecular and Cellular Biology
Spring, 2014	Balint Kacsoh, Molecular and Cellular Biology
Spring, 2013	Julianna Bozler, Molecular and Cellular Biology
Spring, 2013	Jie Tan, Molecular and Cellular Biology
Spring, 2013	Wei Yang, Program in Experimental and Molecular Medicine
Fall, 2012	Shan Cheng, Molecular and Cellular Biology
Fall, 2012	Mathew Ung, Molecular and Cellular Biology

Summer Students

Summer, 2013	Sari Khaleel, First year MD student
Summer, 2013	Erik Andrews, First year MD student

Undergraduate Students

2015-?	Ethan M Klein, Mathematics
2014-2015	Yachen Sun, Biology and Engineering (Double Major)
2014-?	Alexandra E. Dalton, Biochemistry with a Minor in Computer Science
2014-?	George L. Wang, Biology

Invited Presentations and Conference Talks

May 09, 2016	Computational Inference of Homologous Recombination Pathway Activity for Predicting Cancer Prognosis The Genome Instability Meeting Burlington, VM, USA
March 03, 2016	Development and Application of Integrative Computational Methods to Translational Cancer Research Cornell Medical School New York City, NY, USA
February 18, 2016	The Utilization of Gene Knockdown Expression Profiles to Predict Cancer Prognosis The Cancer Mechanism Program, Norris Cotton Cancer Center Lebanon, NH, USA
February 04, 2016	Drug Repositioning: Predict New Candidate Drugs for Cancer Treatment The Molecular Therapy Program, Norris Cotton Cancer Center Lebanon, NH, USA
February 03, 2016	The Utilization of Gene Knockdown Expression Profiles to Predict Cancer Prognosis The Breast Tumor Board, Dartmouth–Hitchcock Medical Center Lebanon, NH, USA
January 25, 2016	Development and Application of Integrative Computational Methods to Translational Cancer Research The Jackson Laboratory Farmington, CT, USA

- July 27, 2015 E2F4 Signature for Predicting Clinical Outcomes in Breast Cancer and Bladder Cancer
Benchmark to Bed (B2B), Dartmouth–Hitchcock Medical Center
Lebanon, NH, USA
- May 20, 2015 Application of E2F4 Signature to Prognostic prediction in Breast Cancer
Breast Cancer Board, Dartmouth–Hitchcock Medical Center
Lebanon, NH, USA
- November 5, 2014 From Genomics to Biomedical Studies: Application of Integrative Data Analysis
Microbiology and Molecular Genetics, University of Vermont
Burlington, VT, USA
- October 30, 2014 From Genomics to Biomedical Studies: Analysis and Application of ChIP-seq data
Bioinformatics Graduate Program, Boston University
Boston, MA, USA
- August 18, 2014 Inference of Regulatory Programs Associated with Cancer Clinical Outcomes
Genomics and Immuno-Oncology Retreat
Hanover, NH, USA
- May 8, 2014 Application of machine-learning methods to transcriptional regulation by histone modifications and transcription factors
Genetic Programming Theory and Practice (GPTP) Workshops 2014
Ann Arbor, MI, USA
- April 16, 2014 From ChIP-seq Data to Transcriptional Regulation
Center for Computational Molecular Biology (CCMB), Brown University
Providence, RI, USA
- June 11, 2013 Computational Identification of Regulatory Programs underlying Breast Cancer
Norris Cotton Cancer Center Grand Rounds, Dartmouth College
Lebanon, NH, USA
- April 26, 2013 Inferring Activity of Key Cancer Regulators via Systems Analysis
Norris Cotton Cancer Center Retreat, Dartmouth College
Hanover, NH, USA
- April 24, 2013 Transcriptional Regulation Inferred from ENCODE ChIP-seq Data
Academy of Mathematics and Systems Sciences, Chinese Academy of Sciences
Beijing, China
- February 13, 2012 Understanding Transcriptional Regulation by ChIP-seq Data Analysis
Department of Oncological Sciences, Huntsman Cancer Institute
Salt Lake City, UT, USA
- February 6, 2012 Understanding Transcriptional Regulation by ChIP-seq Data Analysis
Department of Genetics, Dartmouth College
Hanover, NH, USA
- November 8, 2011 Understanding Transcriptional Regulation by ChIP-seq Data Analysis
Department of Pathology, University of California at Los Angeles
Los Angeles, CA, USA
- May 22, 2011 An integrative framework for correlating gene expression with chromatin data
modENCODE fly/worm joint AWG meeting.
Rockville, MD, USA
- March 8, 2010 A Supervised Chromatin Model for Predicting Transcription Factor Binding
ENCODE Integrative Analysis Workshop. Rockville, Maryland
Rockville, MD, USA
- March 6, 2009 Inferring Transcription Factor Activities from Gene Expression Profiles
Center for Quantitative Biology, Beijing University
Beijing, China

Competitive Research Support

1R01CA547195 (Noelle) 1.2 Calendar 04/01/2017-03/31/2022
NIH/NCI \$435,000
Title: Targeting VISTA eradicates large, established PD-1/CTLA-4 resistant tumors
Role: co-Investigator

1R01CA2000994 (Miller) 0.6 Calendar 04/01/2017-03/31/2022
NIH/NCI \$245,000
Title: A precision medicine basis for estrogen therapy for advanced breast Cancer
Role: co-Investigator

Cancer Center Developmental Funds (Cheng) 12/01/2016-11/30/2017
NIH/NCI \$25,000
Title: A retrospective cohort study to investigate the association of statins, metformin, and hydrochlorothiazide exposure with lung cancer mortality
Role: PI

SYNERGY Scholars Award (Cheng) 10/01/2015-09/30/2017
NIH/NCATS \$100,000
Title: Integration of Computational and Epidemiological Approaches for Drug Repositioning in Breast Cancer
Role: PI

R56 HL122585 (Enelow PI) 1.20 Calendar 09/01/2015-08/31/2016
NIH/NHLBI \$405,000
Title: Early Events Regulating Post-viral Immunopathology
Role: co-Investigator

SYNERGY Pilot 2015 (Cheng) 06/01/2015-05/31/2016
The SYNERGY Translational Pilot Program \$31,000
Title: Regulatory Program Based Signature for Prognostic Prediction in Bladder Cancer
Role: PI

CCR15330848 (Miller) 0.36 Calendar 07/01/15-06/30/18
Susan G. Komen \$450,000
Title: Estrogen receptor re-activation for treatment of advanced ER+/HER2-Breast Cancer

IRG-82-003-30 (Cheng) 12/17/2014-12/16/2015
American Cancer Society \$30,000
Title: Application of E2F4 Signature for Prognosis Prediction in Breast Cancer
Role: PI

R01 AI081838 06A1 (Cramer PI) 0.6 Calendar 07/01/2014-06/30/2018
NIAID \$405,000
Title: Hypoxia Adaptation and Fungal Virulence of *Aspergillus fumigatus*
Role: co-Investigator

iQBS-NCCC funding for collaborative research (Cheng & DiRenzo) 09/01/2013-08/31/2014
iQBS and NCCC
Title: Mechanisms underlying Epithelial to Mesenchymal Transition
Role: co-PI

IRG-82-003-27 (Cheng PI) 04/01/2013-03/31/2014
American Cancer Society (ACS) Research Grant \$30,000
Title: Computational Analysis of Regulatory Programs in Breast Cancer
Role: PI

R01 LM010098 (Moore PI) 0.60 Calendar 09/30/2009-09/29/2018
NIH/NLM \$226,034
Title: Bioinformatics Strategies for Genome Wide Association Studies
Role: co-Investigator