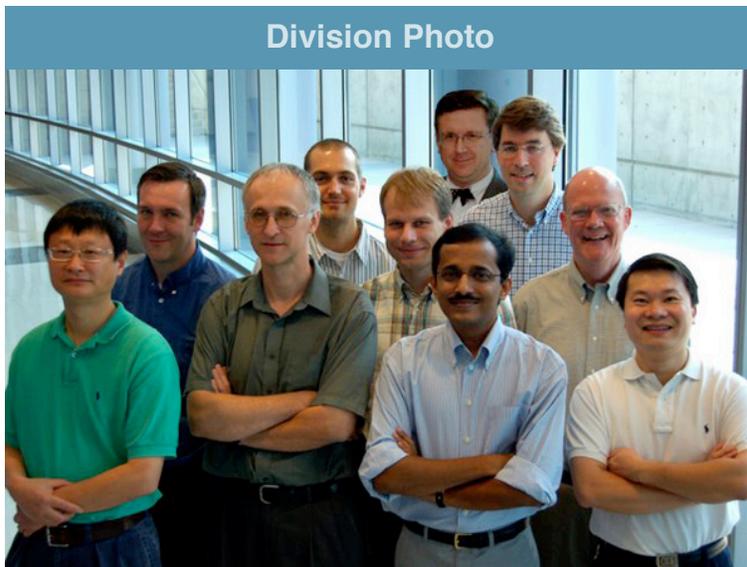


## Biomedical Informatics



*First Row: J. Ma, M. Medvedovic, A. Jegga, J. Lu; Second Row: E. Hall, M. Kouril, J. Hutton; Third Row: K. Marsolo, M. Wagner; Fourth Row: A. Spooner*

### Division Data Summary

Research and Training Details	
Number of Faculty	11
Number of Joint Appointment Faculty	7
Number of Research Fellows	3
Number of Research Students	26
Number of Support Personnel	28
Direct Annual Grant Support	\$773,182
Peer Reviewed Publications	45

## Faculty Members

**John Hutton, MD**, Professor ; *Director, Division Chief*

**Bruce Aronow, PhD**, Professor ; *Co-Director, Computational Medicine Center*

**Research Interests:** Gene Expression Analysis, Gene Regulation, Clinical Genomics, Functional Genomics of Development and Disease

**Anil Jegga, MS, DVM**, Research Assistant Professor

**Research Interests:** Gene Regulatory Networks, Biomedical Ontologies, Integrative Genomics

**Michal Kouril, PhD**, Research Instructor ; *Director, Research IT*

**Research Interests:** Computational Support, High-performance computing, Parallel Programming, High-end Data Storage

**Long Jason Lu, PhD**, Assistant Professor

**Research Interests:** Bioinformatics, Machine Learning, Integrative Genomics, Biological Networks, Computational Modeling, Software Development

**Jun Ma, PhD**, Associate Professor

**Research Interests:** Development, Transcription, Morphogen Gradient, Embryo, Robustness, Quantitative Studies

**Keith Marsolo, PhD**, Research Instructor ; *Director, Software Development and Data Warehouse*

**Research Interests:** i2b2, Data Integration, Data Warehousing and Data Management

**John Pestian, PhD, MBA**, Associate Professor ; *Director, Computational Medicine Center*

**Research Interests:** Natural Language Processing, Clinical Decision Support, Suicide Research, Pathology Research, Psychiatric Research

**Jerry Phillips, MS**, Field Service Assistant Professor

**Research Interests:** High-end SUN Solaris Computational Support

**S. Andrew Spooner, MD, FAAP**, Associate Professor Clinical ; *Chief Medical Information Officer*

**Research Interests:** Decision Support, Pharmacy Information Systems

**Michael Wagner, PhD**, Research Assistant Professor ; *Faculty Liaison*

**Research Interests:** Machine Learning, Proteomics, Genome-wide Association, Parallel Computing, Computational Infrastructure, Bioinformatics

## Joint Appointment Faculty Members

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**Karen Davis, PhD**, Associate Professor

UC ECECS

Electrical & Computer Engineering and Computer Science

**Eric Hall, PhD**, Research Instructor

Neonatology & Pulmonary Biology

Clinical Informatics, Knowledge Discovery Tools, Data Mining and Warehousing

**Mark Halsted, MD**, Associate Professor

Radiology

**Michael Jansen, PhD**, Research Instructor

Experimental Hematology

**Mario Medvedovic, PhD**, Associate Professor

UC Environmental Health

**Jarek Meller, PhD**, Associate Professor

UC Environmental Health

**Yan Xu, PhD**, Associate Professor

Pulmonary Medicine

## Trainees

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- **Jacek Biesiada, PhD**, University of Silesia, Poland
- **Walter Jessen, PhD**, Texas A&M University
- **Mirosław Kordos, PhD**, Silesian University of Technology, Poland

## Significant Accomplishments in FY08

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### Developing computational approaches to understand the regulatory networks of tumor suppressor protein p53 (Anil Jegga, MS, DVM)

Dr. Jegga's current research is focused on deciphering the micro and macro regulation of pathways and networks underlying cancer. Specifically, he is developing computational approaches to help understand the regulatory networks – transcriptional and posttranscriptional – of the tumor suppressor protein p53, the master regulator and the guardian of the genome. Mutations in p53 are implicated in over 50% of human cancers. Following toxic exposure, p53 binds to specific sites on our DNA sequence called p53 response elements and brings about numerous, coordinated changes in target genes. The way p53 binds to its target genes is governed by several rules, which Jegga and his team is identifying. Understanding these rules and the consequences of breaking them (because of DNA mutations) will provide a better understanding of what makes some of us more prone to cancer than others.

### Establishment of an i2b2 Research Data Warehouse (Keith Marsolo, PhD)

One of the biggest challenges faced by medical investigators today is determining whether a group of patients is available for a research study. Trying to identify patients based on criteria like their demographics or diagnostic history typically requires the analysis of individual medical records, which is a difficult, time consuming task constrained by

privacy concerns. To circumvent this process, Dr. Marsolo has implemented a research data warehouse that employs the i2b2 framework (Informatics for Integrating Biology and the Bedside, <https://www.i2b2.org/>). The i2b2 framework allows users to perform a CCHMC-wide search on a de-identified dataset to determine the existence of a patient cohort. Marsolo and his team have loaded information on almost 500,000 patients, including roughly 5 years worth of basic clinical information and patient data (demographics, diagnoses, laboratory, medications). The warehouse incorporates data from the hospital's new Epic electronic health record, as well as information from research groups, including genetic variations and associated biomarkers. At the same time, Marsolo's group is ensuring that the appropriate regulatory and security safeguards are in place to protect the privacy of patients. By bringing these disparate resources together, the group can present CCHMC investigators with a comprehensive view of patients who are potential subjects for clinical research. Marsolo believes that the research data warehouse and associated software applications will be a key resource for investigators addressing medicine's most complex puzzles.

## Division Highlights

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### Bruce Aronow, PhD

The overall goal for Bruce Aronow's group is to enable, through the emerging field of integrative genomics, the advancement of basic and translational research across many different areas of disease research that can lead to improved human health. His research is based on the application of modeling and data analysis techniques both to existing knowledge and to new data from high-throughput genomic and genetic analyses. His research group provides infrastructure and helps to develop models of how biological systems assemble, adapt, are genetically modified, and become impaired in disease.

Publications this year detail how integrative biological analyses can be accomplished in cardiac gene regulatory programs, brain injury, prostate cancer, septic shock, and colon cancer. In the case of colon cancer, the group showed that oncogenesis leads to the subversion of normal embryonic colon development.

### Eric Hall, PhD

Dr. Hall's research has focused on the development of knowledge discovery tools that enable the identification of clinical concepts and care practice patterns in clinical documentation. Specifically, he has focused on the extraction of associations between nursing care patterns and patient outcomes in hospital Labor and Delivery.

### Michal Kouril, PhD

Cincinnati Children's is implementing a new Research Data Storage (RDS) system. The goals of the RDS are: 1) to make centrally managed, secure data storage easily and transparently available to all researchers at Cincinnati Children's; 2) to manage growth of the storage system so that it is predictable for the institution, and 3) to provide basic amounts of storage for free and make larger allocations available for a very competitive and attractive price. This new system will accommodate data that are currently stored on external hard drives and will facilitate compliance with federal rules governing clinical research, as well as protect investigators from loss of data.

### Long (Jason) Lu, PhD

Dr. Lu is a computational biologist with several ongoing projects:

1. Integrating diverse genomic features (microarray data, GO function annotation, proteomics data, etc) to predict protein-protein interaction networks as well as transcription regulatory network in yeast and mouse, and further prioritize protein pairs or TF-TG pairs for experimental validation.
2. Using advanced machine-learning and statistical techniques to identify key therapeutic targets in human microbial pathogens.
3. Computational modeling of the dynamics of morphogen diffusion in the fly embryo using imaging data.
4. Development of software to facilitate multi-source data integration and visualization.

### Jun Ma, PhD

A remarkable feature of development is its reproducibility, the ability to correct embryo-to-embryo variations and instruct precise patterning. In *Drosophila*, embryonic patterning along the anterior-posterior axis is controlled by the morphogen gradient Bicoid, by mechanisms that remain controversial. Jun Ma recently performed quantitative studies to evaluate the behaviors of the native Bicoid gradient and its direct target Hunchback in early embryos. The results support a simple model of a robust Bicoid gradient sufficient to achieve scaled and precise activation of its target genes. These results will be published in the journal, *Developmental Cell*. Dr. Ma's group is now conducting

interdisciplinary studies to model the formation and action of the Bicoid gradient mathematically and to test the model directly by measurements in the developing embryo.

### Jarek Meller, PhD

Jarek Meller's recent efforts are primarily focused on developing methods and tools for functional and structural annotation of proteins and their complexes. Several web servers and portals, such as SABLE and POLYVIEW-3D, have been developed to enhance such annotations, and are being widely used (over 250,000 submissions from over 80 countries to this time). Meller is also actively participating in a number of collaborative projects that involve applications of computational approaches to map, characterize and predict protein interaction sites, and other functional hot spots, that can be subsequently targeted for therapeutics. In collaboration with basic research and clinical colleagues, Meller is currently using docking simulations (utilizing BMI computational cluster for these CPU intensive tasks) to identify compounds that could attenuate protein signaling and other crucial events in the context of gastroenteritis, leukemia, and prostate cancer.

### John Pestian, PhD, MBA

John Pestian's research group focuses on use of natural language processing (NLP) to analyze clinical free-text, with the goal of enhancing clinical processes and outcomes. This free-text can be discharge summaries, radiology reports or text books. While free-text is data, it is different from structured data, which have forced choices -- for example, zip codes, states, specific diagnostics or therapeutics. There are many methods for natural language processing, but Pestian's group is focusing on rule-based inference and neurocognitive computing. Together with collaborators, they are applying these methods to anonymize clinical free-text, cluster text into categories, develop corpora, develop visual languages and, most recently, develop artificial experts. The specific clinical problem they are addressing is the estimation of risk of recurrent suicide attempts based upon analyses of suicide notes using natural language processing.

### Andrew Spooner, MD

Dr. Spooner is engaged in a collaborative project with pediatric investigators at Vanderbilt University. The aim is to fill two gaps in drug-related decision support in child health care: automated rounding of oral liquid drug doses to convenient and safe quantities, and representing formulas for pediatric drugs which are commonly compounded by compounding pharmacies.

### Michael Wagner, PhD

Michael Wagner is a computational scientist who focuses on machine learning techniques to interpret proteomics data. With graduate student Rachana Jain he has been using large-scale linear programming techniques to improve database search engines commonly used for peptide mass fingerprinting. Dr. Wagner is also involved in collaborations to perform genome-wide association studies, where his work has concentrated on providing adequate, rapid data flow infrastructure, including the parallelization of genotype calling algorithms.

## Division Publications

1. Aronow BJ. [Dysfunctional genomics: toward an integrative biology of disease and health--application to IBDs](#). *J Pediatr Gastroenterol Nutr*. 2008; 46 Suppl 1: E3-4.
2. Banach-Petrosky W, Jessen WJ, Ouyang X, Gao H, Rao J, Quinn J, Aronow BJ, Abate-Shen C. [Prolonged exposure to reduced levels of androgen accelerates prostate cancer progression in Nkx3.1; Pten mutant mice](#). *Cancer Res*. 2007; 67: 9089-96.
3. Chen J, Xu H, Aronow BJ, Jegga AG. [Improved human disease candidate gene prioritization using mouse phenotype](#). *BMC Bioinformatics*. 2007; 8: 392.
4. Chen X, Ehrhardt WM, Halberg RB, Aronow BJ, Dove WF. [Cellular expression patterns of genes upregulated in murine and human colonic neoplasms](#). *J Histochem Cytochem*. 2008; 56: 433-41.
5. Heineke J, Auger-Messier M, Xu J, Oka T, Sargent MA, York A, Klevitsky R, Vaikunth S, Duncan SA, Aronow BJ, Robbins J, Crombleholme TM, Molkentin JD. [Cardiomyocyte GATA4 functions as a stress-responsive regulator of angiogenesis in the murine heart](#). *J Clin Invest*. 2007; 117: 3198-210.
6. Liu X, Jessen WJ, Sivaganesan S, Aronow BJ, Medvedovic M. [Bayesian hierarchical model for transcriptional module discovery by jointly modeling gene expression and ChIP-chip data](#). *BMC Bioinformatics*. 2007; 8: 283.
7. Mayhew CN, Carter SL, Fox SR, Sexton CR, Reed CA, Srinivasan SV, Liu X, Wikenheiser-Brokamp K, Boivin GP, Lee JS, Aronow BJ, Thorgeirsson SS, Knudsen ES. [RB loss abrogates cell cycle control and genome integrity to promote liver tumorigenesis](#). *Gastroenterology*. 2007; 133: 976-84.
8. McMahon AP, Aronow BJ, Davidson DR, Davies JA, Gaido KW, Grimmond S, Lessard JL, Little MH, Potter SS, Wilder

- EL, Zhang P. [GUDMAP: the genitourinary developmental molecular anatomy project](#). *J Am Soc Nephrol*. 2008; 19: 667-71.
9. Ouyang X, Jessen WJ, Al-Ahmadie H, Serio AM, Lin Y, Shih WJ, Reuter VE, Scardino PT, Shen MM, Aronow BJ, Vickers AJ, Gerald WL, Abate-Shen C. [Activator protein-1 transcription factors are associated with progression and recurrence of prostate cancer](#). *Cancer Res*. 2008; 68: 2132-44.
10. Shanley TP, Cvijanovich N, Lin R, Allen GL, Thomas NJ, Doctor A, Kalyanaraman M, Tofil NM, Penfil S, Monaco M, Odoms K, Barnes M, Sakthivel B, Aronow BJ, Wong HR. [Genome-level longitudinal expression of signaling pathways and gene networks in pediatric septic shock](#). *Mol Med*. 2007; 13: 495-508.
11. Hall ES, Thornton SN. [Extracting nursing practice patterns from structured labor and delivery data sets](#). *AMIA Annu Symp Proc*. 2007; : 309-13.
12. Jegga AG, Inga A, Menendez D, Aronow BJ, Resnick MA. [Functional evolution of the p53 regulatory network through its target response elements](#). *Proc Natl Acad Sci U S A*. 2008; 105: 944-9.
13. Kamath MB, Houston IB, Janovski AJ, Zhu X, Gowrisankar S, Jegga AG, DeKoter RP. [Dose-dependent repression of T-cell and natural killer cell genes by PU.1 enforces myeloid and B-cell identity](#). *Leukemia*. 2008; 22: 1214-25.
14. Markey MP, Bergseid J, Bosco EE, Stengel K, Xu H, Mayhew CN, Schwemberger SJ, Braden WA, Jiang Y, Babcock GF, Jegga AG, Aronow BJ, Reed MF, Wang JY, Knudsen ES. [Loss of the retinoblastoma tumor suppressor: differential action on transcriptional programs related to cell cycle control and immune function](#). *Oncogene*. 2007; 26: 6307-18.
15. Sinha AU, Kaimal V, Chen J, Jegga AG. [Dissecting microregulation of a master regulatory network](#). *BMC Genomics*. 2008; 9: 88.
16. Kouril M, Paul JL. [The Van der Waerden number \\$W\(2,6\)\\$ is 1132](#). *Exp Math*. 2008; 17: 53-61.
17. Huang Y, Anderson KE, Nagamani M, Grady JJ, Lu LJ. [Dietary intake of lactose as a strong predictor for secretor status of nipple aspirate fluid in healthy premenopausal nonlactating women](#). *Clin Cancer Res*. 2008; 14: 1386-92.
18. Liu YL, Nie ZY, Lu LJ, Hui YZ. [\[Peritoneal "melanosis": report of a case\]](#). *Zhonghua Bing Li Xue Za Zhi*. 2007; 36: 572-3.
19. Lu LJ, Nishino TK, Khamapirad T, Grady JJ, Leonard MH, Jr., Brunder DG. [Computing mammographic density from a multiple regression model constructed with image-acquisition parameters from a full-field digital mammographic unit](#). *Phys Med Biol*. 2007; 52: 4905-21.
20. Lu LJ, Sboner A, Huang YJ, Lu HX, Gianoulis TA, Yip KY, Kim PM, Montelione GT, Gerstein MB. [Comparing classical pathways and modern networks: towards the development of an edge ontology](#). *Trends Biochem Sci*. 2007; 32: 320-31.
21. Wu L, Hwang SI, Rezaul K, Lu LJ, Mayya V, Gerstein M, Eng JK, Lundgren DH, Han DK. [Global survey of human T leukemic cells by integrating proteomics and transcriptomics profiling](#). *Mol Cell Proteomics*. 2007; 6: 1343-53.
22. Zha DJ, Wang ZM, Lin Y, Liu T, Qiao L, Lu LJ, Li YQ, Qiu JH. [Effects of noradrenaline on the GABA response in rat isolated spiral ganglion neurons in culture](#). *J Neurochem*. 2007; 103: 57-66.
23. Zha DJ, Xue T, Qiao L, Lu LJ, Lin Y, Wang ZM, Li YQ, Qiu JH. [\[Inhibition of gamma-aminobutyric acid receptor-gated chloride currents by noradrenaline in rat spiral ganglion neuron\]](#). *Zhonghua Er Bi Yan Hou Tou Jing Wai Ke Za Zhi*. 2008; 43: 302-5.
24. Zhou MN, Xu AE, Lu LJ, Li YW, Zhao DK, Guan CP. [\[Association of single nucleotide polymorphisms of Nrf2 promoter region with susceptibility to vitiligo\]](#). *Zhonghua Yi Xue Za Zhi*. 2008; 88: 969-72.
25. Zou YQ, Lu LJ, Li SJ, Zeng T, Wang XD, Bao CD, Chen SL, Yang CD. [The levels of macrophage migration inhibitory factor as an indicator of disease activity and severity in adult-onset Still's disease](#). *Clin Biochem*. 2008; 41: 519-24.
26. Song Y, He F, Xie G, Guo X, Xu Y, Chen Y, Liang X, Stagljar I, Egli D, Ma J, Jiao R. [CAF-1 is essential for Drosophila development and involved in the maintenance of epigenetic memory](#). *Dev Biol*. 2007; 311: 213-22.
27. Wen H, Marsolo KA, Bennett EE, Kuttan KS, Lewis RP, Lipps DB, Epstein ND, Plehn JF, Croisille P. [Adaptive postprocessing techniques for myocardial tissue tracking with displacement-encoded MR imaging](#). *Radiology*. 2008; 246: 229-40.
28. Bakshi S, Zhang X, Godoy-Tundidor S, Cheng RY, Sartor MA, Medvedovic M, Ho SM. [Transcriptome analyses in normal prostate epithelial cells exposed to low-dose cadmium: oncogenic and immunomodulations involving the action of tumor necrosis factor](#). *Environ Health Perspect*. 2008; 116: 769-76.
29. Ganguly K, Stoeger T, Wesselkamper SC, Reinhard C, Sartor MA, Medvedovic M, Tomlinson CR, Bolle I, Mason JM, Leikauf GD, Schulz H. [Candidate genes controlling pulmonary function in mice: transcript profiling and](#)

- [predicted protein structure](#). *Physiol Genomics*. 2007; 31: 410-21.
30. Hardie WD, Korfhagen TR, Sartor MA, Prestridge A, Medvedovic M, Le Cras TD, Ikegami M, Wesselkamper SC, Davidson C, Dietsch M, Nichols W, Whitsett JA, Leikauf GD. [Genomic profile of matrix and vasculature remodeling in TGF-alpha induced pulmonary fibrosis](#). *Am J Respir Cell Mol Biol*. 2007; 37: 309-21.
  31. Popa I, Zubkova I, Medvedovic M, Romantseva T, Mostowski H, Boyd R, Zaitseva M. [Regeneration of the adult thymus is preceded by the expansion of K5+K8+ epithelial cell progenitors and by increased expression of Trp63, cMyc and Tcf3 transcription factors in the thymic stroma](#). *Int Immunol*. 2007; 19: 1249-60.
  32. Tam NN, Szeto CY, Sartor MA, Medvedovic M, Ho SM. [Gene expression profiling identifies lobe-specific and common disruptions of multiple gene networks in testosterone-supported, 17beta-estradiol- or diethylstilbestrol-induced prostate dysplasia in Noble rats](#). *Neoplasia*. 2008; 10: 20-40.
  33. Duch W, Swaminathan K, Meller J. [Artificial intelligence approaches for rational drug design and discovery](#). *Curr Pharm Des*. 2007; 13: 1497-508.
  34. Howarth JW, Meller J, Solaro RJ, Trehwella J, Rosevear PR. [Phosphorylation-dependent conformational transition of the cardiac specific N-extension of troponin I in cardiac troponin](#). *J Mol Biol*. 2007; 373: 706-22.
  35. Mikhaylova O, Ignacak ML, Barankiewicz TJ, Harbaugh SV, Yi Y, Maxwell PH, Schneider M, Van Geyte K, Carmeliet P, Revelo MP, Wyder M, Greis KD, Meller J, Czyzyk-Krzeska MF. [The von Hippel-Lindau tumor suppressor protein and Egl-9-Type proline hydroxylases regulate the large subunit of RNA polymerase II in response to oxidative stress](#). *Mol Cell Biol*. 2008; 28: 2701-17.
  36. Olshavsky NA, Groh EM, Comstock CE, Morey LM, Wang Y, Revelo MP, Burd C, Meller J, Knudsen KE. [Cyclin D3 action in androgen receptor regulation and prostate cancer](#). *Oncogene*. 2008; 27: 3111-21.
  37. Porollo A, Meller J. [Versatile annotation and publication quality visualization of protein complexes using POLYVIEW-3D](#). *BMC Bioinformatics*. 2007; 8: 316.
  38. Sinha AU, Meller J. [Sensitivity analysis for reversal distance and breakpoint reuse in genome rearrangements](#). *Pac Symp Biocomput*. 2008; : 37-48.
  39. Takatori A, Geh E, Chen L, Zhang L, Meller J, Xia Y. [Differential transmission of MEKK1 morphogenetic signals by JNK1 and JNK2](#). *Development*. 2008; 135: 23-32.
  40. Duch W, Matykiewicz P, Pestian JP. **Towards understanding of natural language: neurocognitive inspirations.** *Lect Notes Comput Sci*. 2007; : 953-962.
  41. Duch W, Matykiewicz P, Pestian JP. (2007) 2007 International Joint Conference on Neural Networks conference proceedings. Orlando, FL, IEEE Xplore.
  42. Pestian JP, Matykiewicz PM, Grupp-Phelan J, Lavanier SA, Combs J, Kowatch R. (2008) BioNLP 2008: current trends in biomedical natural language processing. Columbus, OH, Association for Computational Linguistics.
  43. Rajan J, Davis KC, Matykiewicz P, Duch W, Pestian J. (2007) International Conference on Enterprise Information Systems and Web Technologies. Orlando, FL,
  44. Kuhl J, Rosenbloom ST, Spooner SA. **Improving the functionality of electronic health record systems for children's healthcare..** *J Healthc Qual*. 2008; 30: W3-5.
  45. Jain A, Velayutham P, Wagner M, Butler DL. [Accessing the tissue engineering literature: a new paradigm](#). *Tissue Eng Part A*. 2008; 14: 459-60.

## Grants, Contracts, and Industry Agreements

### Grant and Contract Awards

### Annual Direct / Project Period Direct

#### Aronow, B

##### Mouse Models Of Gastrointestinal Cancer

National Institutes of Health (Ohio State University)

U01 CA 084291 04/01/04 - 03/31/09 \$100,812 / \$448,993

##### Murine Atlas of Genitourinary Smooth Muscle Development

National Institute of Diabetes and Digestive and Kidney Diseases

U01 DK070219 04/01/05 - 03/31/10 \$130,000 / \$266,480

##### Digestive Health Center - Bench to Bedside Research in Pediatric Digestive Disease - Gene Expression Core

National Institutes of Health

P30 DK 078391 08/01/07 - 05/31/12 \$105,395 / \$217,606

#### Jegga, A.

##### Murine Atlas of Genitourinary Smooth Muscle Development

National Institute of Diabetes and Digestive and Kidney Diseases  
U01 DK070219

04/01/05 - 03/31/10

\$20,783 / \$45,565

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**Lu, L**

**Breast Cancer Biomarker Discovery Using Protein Network**

American Cancer Society - National (University of Cincinnati)

01/01/08 - 12/31/08

\$20,000 / \$20,000

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**Ma, J**

**Activities Of The Bicoid Gradient In Drosophila Embryos**

National Institutes of Health

R01 GM 072812

07/01/05 - 06/30/09

\$180,154 / \$760,000

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**Pestian, J**

**Gene Expression in Pediatric Arthritis - Core B**

National Institutes of Health

P01 AR 048929

08/22/03 - 07/31/08

\$100,521 / \$304,734

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**Wagner, M.**

**Biomarkers for Amyotrophic Lateral Sclerosis in Active Duty Military**

Department of Defense - Army (University of Cincinnati)

W81XWH-06-2-0016

01/23/06 - 01/22/09

\$29,534 / \$85,238

**Bayesian Mixture Modeling of Functional Genomics Data**

National Institutes of Health (University of Cincinnati)

R01 HG 003749

07/01/06 - 06/30/10

\$13,536 / \$53,679

**Optimization of Structures and Networks of Proteins**

National Institutes of Health (The University of Texas at Austin)

R01 GH 067823

06/01/08 - 05/31/11

\$18,613 / \$57,535

**Cincinnati Rheumatic Disease Core Center - Core 4**

National Institutes of Health

P30 AR 047363

09/01/06 - 06/30/11

\$53,834 / \$264,829

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**Current Year Direct**

**\$773,182**

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**Total \$618,827**

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