RAMANA V. DAVULURI

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Academic Appointments

2001-present	Assistant Professor, Bioinformatics & Computational Biology, Human Cancer Genetics Program, Comprehensive Cancer Center, Department of Mol. Virology, Immunology and Medical Genetics, The Ohio State University, Columbus, OH 43210, USA
2001-present	Graduate Faculty Member, Integrated Biomedical Graduate Program (IBGP), The Ohio State University, Columbus, OH 43210, USA
2002-present	Adjunct Assistant Professor, Dept. of Biomedical Informatics, Dept. of Statistics, The Ohio State University, Columbus, OH 43210, USA
2003-present	Mentor in Biosciences, Mathematical Biosciences Institute, OSU, Columbus, OH 43210.
2001	Research Investigator, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 11724, USA.
1999–2001	Computational Post Doctoral Fellow, Zhang Lab, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 11724, USA.
1998-1999	Special Project Scientist (Bioinformatics), International Crops Research Institute for the Semi Arid Tropics, (ICRISAT), Patancheru, AP, INDIA and Visiting Scientist, Avesthagengraine Technologies, Bangalore, INDIA.
1998	Short term Post Doctoral Fellow (Bioinformatics), Dept. of Plant Genetics, VIB, University of Ghent, Gent, BELGIUM.
1993-1998	Asst. Professor of Statistics, ANGR Agricultural University, Hyderabad, INDIA.

Honors and Awards

2005-10	Member of the Information Technology & Computational Modeling Committee, Integrative Cancer Biology Program, National Cancer Institute, NIH.
2003-05	V Foundation Scholar (Awarded by The V Foundation for Cancer Research)
1997	Young Scientist Award (Statistics) merit certificate- 1996-97 by *Indian Science Congress Association* (ISCA), during the 84th annual session at Delhi, India.
1991-93	IASRI (Indian Council of Agricultural Research) Senior research fellowship
1989-91	IASRI (Indian Council of Agricultural Research) Junior research fellowship
1993	One of the three finalists for ISAS Young Scientist Award - Indian Society of Agricultural Statistics (ISAS) for the year 1993.
1991-93	VVR Murthy award for the best student of MS (Ag.Stat.) 1989-91 batch
1989	Sri CVS Narasimha Rao endowment scholarship awarded by SRR & CVR Government College, Vijayawada (India)
1983-85	State special merit scholarship awarded by AP state government, India
1983	Honorary medal awarded by Board of Secondary Education, AP, India, for securing state 7th rank in Secondary School Certificate examination.

Education

February 1996	PhD, Indian Agricultural Statistics Research Institute, IARI, New Delhi, India • Major: Statistics and Minor: Computer Applications
1991	MSc, Indian Agricultural Statistics Research Institute, IARI, New Delhi, India • Major: Statistics and Minor: Computer Applications
1988	BSc (Mathematics), Nagarjuna University, Guntur, India • Major: Mathematics; Minors: Physics and Chemistry

Peer Reviewed Publications

1. Jin, V., Leu, Y.W., Liyanarachchi, S., Sun, H., Fan, M., Nephew, K.P., Huang, T.H. and **Davuluri, R.V.** (2004). Identifying Estrogen Receptor α Target Genes Using Integrated Computational Genomics and Chromatin Immunoprecipitation Microarray. ***Nucleic Acids Res.*** **32**: 6627-6635.
2. Palaniswamy S.K., Jin, V., Sun, H., and **Davuluri, R.V.** (2004). OMGProm: A Database of Orthologous Mammalian Gene Promoters. ***Bioinformatics***. Nov 5; [Epub ahead of print].
3. Leu, Y.W., Yan P.S., Fan, M., Jin, V.X., Liu, J.C., Edward, M.C., Welshons, W.V., Wei, S.H., **Davuluri, R.V.** Plass, C., Nephew, K.P., and Huang, T.H. (2004). Loss of estrogen signaling triggers epigenetic silencing of its downstream targets in breast cancer. ***Cancer Res.*** **64**:8184-8192.
4. Nakagawa, H., Liyanarachchi, S., **Davuluri, R.V.**, Auer, H., Martin Jr., ED., and de la Chapelle, A., Frankel, W.L. (2004). The Role of Cancer-associated Stromal Fibroblasts in Metastatic Colon Cancer to the Liver and Their Expression Profiles. ***Oncogene***. **23**:7366-7377.
5. Yu, L., Liu, C., Bennett, K., Wu, YZ, Dai, Z, Vandeusen, J., Opavsky, R. Raval, A., Trikha, P., Rodriguez, B., Brian Becknell, B., Mao, C., Lee, S., **Davuluri, R.V.**, Leone, G., den Veyver, IBV, Caligiuri, MA. and Plass, C. (2004). A *Not*I-*Eco*RV promoter library for studies of genetic and epigenetic alterations in mouse models of human malignancies. ***Genomics***. **84**:647-660.
6. Aldred, M.A., Huang, Y., Liyanarachchi, S., Pellegata, N.S., Gimm, O., Jhiang, S., **Davuluri, R.V.**, de la Chapelle, A., and Eng, C. (2004). Papillary and follicular thyroid carcinomas show distinctly different microarray expression profiles and can be distinguished by a minimum of five genes. ***J. Clinical Oncology,*** **22**:3540–3548.
7. Stanchina, E.D., Querido, E., Narita, M., **Davuluri, R.V.**, Pandolfi, P.P., Ferbeyre, G. and Lowe, S.W. (2004) PML as a direct p53 target that modulates p53 effector functions. ***Molecular Cell.*** **13**: 523-535.
8. Besco, J.A., Popesco, M.C., **Davuluri, R.V.**, Frostholm, A.M. and Rotter, A. (2004) Genomic structure and alternative splicing of murine R2B receptor protein tyrosine phosphatases (PTP kappa, mu, rho and PCP-2). ***BMC Genomics,*** **5:** 14.
9. Baldus, C.D., Liyanarchchi, S., Mrózek, K., Auer, H., Tanner, S.M., Guimond, M. Ruppert, A.S., Mohamed, N., **Davuluri, R.V.**, Caligiuri, M.A., Bloomfield, C.D. and de la Chapelle, A. (2004) Acute myeloid leukemia with complex karyotype: amplification of two chromosome 21 regions discloses overexpression of *app, ets2* and *erg* genes. ***Proc Natl Acad Sci USA*** **101**:3915-3920.
10. Rush, L.J., Raval A., Funchain P., Johnson, A.J., Smith, L., Lucas, D., Bembea, M., Liu, T., Heerema, N.A., Rassenti, L., Liyanarachchi, S., **Davuluri, R.V.**, Byrd, J.C., and Plass, C. (2004) Epigenetic profiling in chronic lymphocytic leukemia reveals novel methylation targets. ***Cancer Res***. **64**:2424-33.
11. Sun, H. and **Davuluri, R.V.** (2004) Java-based Application Framework for Visualization of Gene Regulatory Region Annotations. ***Bioinformatics.*** **20**:727-734.
12. Pohar, T.T., Sun, H. and **Davuluri, R.V.** (2004) HemoPDB: Hematopoiesis promoter database, an information resource of transcriptional regulation in blood cell development. ***Nucleic Acids Res***. **32**:D86-90. (Note: This database was featured in ***Science,*** **303**: 291 (in NetWatch, *Database: Bad Blood*), January 16, 2004).
13. **Davuluri, R.V.** and Zhang, M.Q. (2003). Computer software to find genes in plant genomic DNA. ***Methods Mol Biol.***, **236**:87-108.
14. **Davuluri, R.V.** Sun, H. Palaniswamy, S.K. Matthews, N. Molina, C. Kurtz, M. and Grotewold, E.

AGRIS: (2003) Arabidopsis Gene Regulatory Information Server, an information resource of Arabidopsis cis-regulatory elements and transcription factors. ***BMC Bioinformatics,*** **4**:25.

15. Borrego, S., Wright, F.A., Fernández, R.M, Williams, N., López-Alonso, M., **Davuluri, R.V.**, Antiñolo, G., and Eng, C. (2003) A founding locus within the *RET* proto-oncogene may account for a large proportion of apparently sporadic Hirschsprung disease and a subset of sporadic medullary thyroid carcinoma cases. ***Am J Hum Genet*** **72**:88-100.
16. Nahle, Z., Polyakoff, J., **Davuluri, R.V.**, Jacobson, M.D., McCurrach, M.E., Narita, M., Zhang, M.Q., Lazebnik, Y., Bar-Sagi, D. and Lowe, S.W. (2002). Direct coupling of the cell cycle and cell death machinery by E2F. ***Nat Cell Biology***, **4**:859-64.
17. Yoon, H., Liyanarchchi, S., Wright, F.A., **Davuluri, R.V.**, Lockman, J., de la Chapelle, A., and Pellegata, N.S. (2002) Gene expression profiling of isogenic cells with different *TP53* gene dosage reveals that many genes are affected by *TP53* dosage and identifies *CSPG2 (Versican)* as a novel direct target of p53. ***Proc Natl Acad Sci. USA***, **99**:15632-15637.
18. Dai, Z., Weichenhan, D., Wu, Y.Z., Hall, J.L., Rush, L.J., Smith, L.T., Raval, A., Yu, L. Kroll, D., Muehlisch, J. Frühwald, F.C., de Jong, P., Catanese, J., **Davuluri, R.V.**, Smiraglia, J.D. and Plass, C. (2002) An *Asc*I boundary library for the studies of genetic and epigenetic alterations in CpG islands. ***Genome Res.,*** **12**:1591-1598.
19. Gupta, V.K., **Ramana, D.V.V.** and Parsad, R. (2002). Weighted A-optimal block designs for comparing test treatments with controls with unequal precision. ***J. of Statistical Planning and Inference,*** **106:**159-175.
20. **Davuluri R.V.**, Grosse, I. and Zhang, M.Q. (2001). Computational identification of first exons and promoters in the human genome. ***Nature Genetics,*** **29:** 412-417. (Note: This work was featured in *Nature Reviews Genetics,* **3**: 3-9; in Bioinformatics section of Highlights as "*Filling the gap in gene prediction"* January, 2002).
21. Tabaska, E. Jack, **Davuluri, R.V.,** and Michael Q. Zhang (2001). A novel 3'-Terminal exon recognition program for Human DNA Sequences. ***Bioinformatics*** **17:** 602-607.
22. **Davuluri, R.V.**, Suzuki, Y., Sugano, S. and Zhang, M.Q. (2000). CART classification of human 5'UTR sequences, ***Genome Research*** **10**: 1817-1827.
23. Pavy, N., Rombauts, S., Dehais, P., Mathe, C., **Davuluri R.V.**, Leroy, P. and Rouze, P. (1999). Evaluation of gene prediction software using a genomic dataset: Application to Arabidopsis Thaliana sequences. ***Bioinformatics*** 15: 887-899.
24. Gupta, V.K., **Ramana, D.V.V.** and Parsad, R. (1999). Weighted A-efficiency of block designs for making treatment-control and treatment-treatment comparisons. ***J. of Statistical Planning and Inference,*** **77:**301-319.
25. Gupta, V.K., **Ramana, D.V.V.** and Agarwal, S.K. (1998) Weighted A-optimal row-column designs for making treatment-control and treatment-treatment comparisons. ***J. Combinatorics, Information and System Sciences,*** **23(1-4***),* 333-344.

Papers Under Review/Submitted

1. **Davuluri, R.V.**, Grosse, I. and Zhang, M.Q. (2004) Computational annotation of promoters and first exons in the human genome. (Submitted).
2. Sun, H. Palaniswamy, S. Pohar, T.T. and **Davuluri, R.V.** (2004) Mammalian Promoter Database: Database for Annotation, Integration, and Visualization of Mammalian Gene Regulatory Regions (Submitted).
3. Sun, H. & **Davuluri, R.V.** (2004). Promoter Annotation Markup Language (PAML): A Specification for Promoter Annotation Data Integration, Representation and Exchange (Submitted).

Reviews and Book Chapters

1. **Davuluri V.R**. Application of FirstEF to find promoters and first exons in the human genome. Unit 4.7 in *Current Protocols in Bioinformatics*, edited by Andy Baxevanis, John Wiley & Sons, Inc. New York, NY, 2003.

Published Abstracts

1. **Davuluri, R.V.,** and Zhang, M.Q. Statistical characterization of human 5'UTR sequences. *Genome Sequencing & Biology Meeting*, Cold Spring Harbor, NY, May 10-14, 2000.
2. **Davuluri, R.V.**, Suzuki, Y. Sugano, S. and Zhang, M.Q. CART classification of human 5'UTR sequences. *Computational Genomics Conference* organized by The Institute of Genomic Research at Baltimore, MD, November 16-19, 2000.
3. **Davuluri, R.V.**, Grosse, I. and Zhang, M.Q. Computational Identification of Promoters and First Exons in the Human Genome. *Fifth Annual Conference On Computational Genomics*, November 28 - December 1, 2001 at Baltimore, MD.
4. Colella, S. **Davuluri, R.V.**, Lozano, G. and Krahe, R. Combination of expression profiling of *p53* knock-out MEFs and *in silico* data mining for *p53* responsive elements to identify novel putative *p53* transcriptional targets. *Oncogenomics* conference. May 1-5, 2002, Dublin, Ireland.
5. **Davuluri, R.V.**, Grosse, I. and Zhang, M.Q. Annotation of promoters and first exons in the human genome. *Genome Sequencing & Biology Meeting*, May 5-9, 2002, Cold Spring Harbor, NY, USA.
6. **Davuluri, R.V.** Genome based gene structure determination: Application of discriminant analysis. (Presented in the "Advances in Bioinformatics" session) Fourth Biennial International Conference on Statistics, Probability and Related Areas, held at Northern Illinois University in DeKalb, Illinois, June 14-16, 2002.
7. **Davuluri, R.V.**, Sun, H., and Palaniswamy, S.K. Initial annotation of experimentally supported promoters and cis-regulatory elements in mammalian genomes. *Systems Biology: Genome Approaches to Transcriptional Regulation*, March 6-9, 2003, Cold Spring Harbor, NY, USA.
8. **Davuluri, R.V.**, Grosse, I. and Zhang, M.Q. Annotation of promoters and first exons in the human genome. *Systems Biology: Genome Approaches to Transcriptional Regulation*, March 6-9, 2003, Cold Spring Harbor, NY, USA.
9. Sun, H., Palaniswamy, S.K. and **Davuluri, R.V.** MPromDb – A database of experimentally supported cis-regulatory elements in mammalian genomes. *Systems Biology: Genome Approaches to Transcriptional Regulation*, March 6-9, 2003, Cold Spring Harbor, NY, USA.
10. Tiongson, T. Sun, H., Palaniswamy, S.K. and **Davuluri, R.V.** HemoPDb – Initial annotation of experimentally defined promoters and cis-regulatory elements involved in hematopoietic regulation. *Systems Biology: Genome Approaches to Transcriptional Regulation*, March 6-9, 2003, Cold Spring Harbor, NY, USA
11. Sun, H., Palaniswamy, S.K., Nicole Matthews, Carlos Molina, Mike Kurtz, Erich Grotewold and **Davuluri, R.V.** Development of a genomewide map of *cis*-regulatory elements in *Arabidopsis. Systems Biology: Genome Approaches to Transcriptional Regulation*, March 6-9, 2003, Cold Spring Harbor, NY, USA.

Lectures, seminars and presentations

Invited Talks (out side OSU):

1. Computational identification of first exons and promoters in human genome. *Genome Sequencing & Biology Meeting*, May 9-13, 2001, Cold Spring Harbor, NY, USA.
2. Computational identification of first exons and promoters in human genome. *Computational Genomics Conference* organized by The Institute of Genomic Research, November 28-December 1, 2001, Baltimore, MD, USA.
3. Computational Identification and Characterization of Gene Regulatory Regions in Mammalian Genomes, Gerontology Research Center, National Institute on Aging, National Institutes of Health, Baltimore, MD, April 29, 2002.
4. Annotation of promoters and first exons in the human genome. *Genome Sequencing & Biology Meeting*, May 5-9, 2002, Cold Spring Harbor, NY, USA.
5. Genome based gene structure determination: Application of discriminant analysis. *Fourth Biennial International Conference on Statistics, Probability and Related Areas*, June 14-16, 2002, Dekalb, Illinois, USA.

6. Computational approaches to identify promoters and cis-regulatory logic in mammalian genomes. *NCI sponsored Cancer Cell Biology Branch Workshop - Genomic Microarrays for the study of Transcription Factors in Neoplasia*. June 5-6, 2003, Bethesda, MD.

Invited Talks (within OSU):

1. Seminar in Statistics & Biostatics Seminar Series, Department of Statistics, The Ohio State University, Columbus. Date: November 15, 2001. Topic: Identification of promoters and first exons in the human genome by discriminant Analysis.
2. Seminar in Hamilton in-house series talks. Department of Physiology and Cell Biology. Date: March 4, 2002. Topic: Computational identification of gene regulatory regions in the human genome.
3. Seminar in Guest Speaker Seminar Series, Department of Computer and Information Science, The Ohio State University, Columbus. Date: May 30, 2002. Topic: Computational identification and characterization of gene regulatory regions.
4. Seminar in Journal Club of Department of Plant Biology, The Ohio State University, Columbus. Date: September 25, 2002. Topic: Promoter Analysis: Application to the interpretation of gene expression data.
5. Seminar in Postdoctoral Research Forum, Mathematical Biosciences Institute, The Ohio State University, Columbus. Date: September 22, 2003. Topic: Deciphering the cis-regulatory logic in mammalian genomes by bioinformatics approaches.

Synergistic Activities

Bioinformatics software developed by Davuluri and his laboratory team

1. **FirstEF**©(2001): Software for Finding Promoters and First Exons in Human Genome (Technology license available from Cold Spring Harbor Laboratory, Cold Spring Harbor, NY) http://rulai.cshl.org/tools/FirstEF.

   (Davuluri V.R, Grosse, I. and Zhang, M.Q. 2001. *Nature Genetics,* **29:** 412-417. FirstEF was also featured in *Nature Reviews Genetics,* **3**: 3-9; in Bioinformatics section of Highlights as "*Filling the gap in gene prediction"*, January 2002). FirstEF is most widely used software for predicting promoter and non-coding first exons in the human genome. A special track to display the predictions of FirstEF is made available at UCSC genome browser – http://genome.ucsc.edu. FirstEF is freely available to academic and not-for profit institutes. Despite its free availability to academic community, it was successful commercially as well. Cold Spring Harbor Laboratory sold six commercial licenses so far to different biotech and pharmaceutical companies, which generated a reasonable amount of scientific fund to the institute and royalty money to the authors)

2. **JTEF** (2000): Software for finding 3'terminal exons in human DNA (Available by ftp at website http://rulai.cshl.org/software/index1.htm).

   (Jack, T.E., Davuluri, V.R. and Zhang, M.Q. 2001. *Bioinformatics* **17:** 602-607).

3. **MPromDb** (2003): Mammalian Promoter Database - A database of mammalian promoters, with mapping of experimentally known *cis*-regulatory elements and CpG islands. http://bioinformatics.med.ohio-state.edu/MPromDb.

   (Sun, H. Palaniswamy, S. Pohar, T.T. and Davuluri, R.V. 2004. *Submitted*).

4. **GDVTK** (2003): Genome Data Visualization Tool Kit - GDVTK provides a framework with an extensive set of data structures and classes for genome data visualization. We designed this framework to be robust, easy to use, and open for extension. The extensibility and portability of GDVTK that result from an object-oriented, generic programming approach and J2EE (Java™) technology distinguishes it from other software packages of this kind. http://bioinformatics.med.ohio-state.edu/GDVTK.

   (Sun, H. and Davuluri, R.V. 2004. *Bioinformatics.* (In Press).

5. **HemoPDb:** (2003) Hematopoiesis Promoter Database – HemoPDb is a comprehensive resource for the scientific research community focusing on hematopoiesis, the regulation thereof, and hematopoietic malignancies. http://bioinformatics.med.ohio-state.edu/HemoPDB.

   (Pohar, T.T., Sun, H. and Davuluri, R.V. 2004. *Nucleic Acids Res*. **32**:D86-90. This database was featured in *Science*, **303**: 291, in NetWatch, *Database: Bad Blood*, January 16, 2004).

6. **P53Scan:** (2003) P53Scan predicts p53 response elements in an input DNA sequence based on pattern recognition and comparative genomics approaches. http://bioinformatics.med.ohio-state.edu/P53Scan.

Head of the Bioinformatics Unit, HCG, Comprehensive Cancer Center, OSU.

Currently Funded Projects

10/01/03-09/30/05
V Foundation for Cancer Research
Title: Computational Approaches to Explore Transcriptional Regulation in Hematopoiesis and Leukemia
PI: Ramana V. Davuluri, Ph.D.

The major goal of this project is to build an information resource that helps in understanding how hematopoietic specific transcription factors and modules regulate their target genes resulting either in proper blood cell development or leukemia.

10/1/04 – 9/30/09
NIH/NCI (1P50CA113001-01; ***Center for Integrative Cancer Biology***)
Title: Interrogating Epigenetic Changes in Cancer Genomes
PI: Tim Huang, Ph.D.
PI (Core B – Data Management & Computational Modeling),
Co-PI (Project # 3),
Co-I (Project # 2)

Bringing together computational, experimental and cancer biologists, the major goal of this project is to increase our understanding of complex epigenetic interactions in neoplasms and to use high-end information for improved prognosis, intervention, and treatment of human female cancers. ***Project # 3****: Chromatin Landscaping of TGF-β/SMAD Signaling Targets;* ***Project # 1****: Dissecting hierarchies of epigenetic control in gene silencing.*

01/01/03-12/30/06
Ohio Biomed Research & Technology BRTT02-0003
Title: Biomedical Research Technology Transfer Application
PI: Joel Saltz, M.D., Ph.D.
Co-PI: Ramana V. Davuluri, Ph.D.

This project will develop software to allow the integration and communication of scientific and clinical data create local and grid-enabled virtual data warehouse.

09/01/04-08/31/07
NSF (NSF-01-162: The 2010 project)
Title: Establishing regulatory networks in Arabidopsis: Integrating AGRIS with the identification of direct targets for transcription factors
PI: Erich Grotewold, Ph.D.
Co-PI: Ramana V. Davuluri, Ph.D.

The goal of this project is to identify the direct target genes for a group of 31 selected transcription factors involved in regulatory networks associated with flower development and epidermal functions, using chromatin immunoprecipitation followed by analysis of microarrays of promoter sequences (ChIP-CHIP). Identified direct target genes will be validated by in vitro DNA-binding experiments, and the TF binding sites will be determined using in vitro footprinting. The information obtained will be integrated into the established AGRIS databases, resulting in public *resources that integrate TFs, their binding sites and the corresponding regulatory motifs. Results derived from this project will be made available at http://arabidopsis.med.ohio-state.edu. Dr. Davuluri is leading the Bioinformatics part of the project as a Co-PI.*

10/01/04-09/30/06 NIH/NCI 1 R21 CA110475-01
Title: Epigenetic Biomarkers for Ovarian Cancer Progression
PI: Tim H-M Huang, Ph.D.
Co-I: Ramana V. Davuluri, Ph.D.

The goal of this project is to identify a panel of DNA methylation biomarkers that have high levels of clinical sensitivity and specificity for predicting prognosis and disease relapse of ovarian cancer patients in a multi-center cohort.

10/01/02-09/30/07 NCI/NIH 1 P01 CA95426-01A1
Title: Innate Immunity: Elucidation and Modulation for Cancer Therapy
PI: Michael A. Caligiuri, M.D.
Co-I: Ramana V. Davuluri, Ph.D.

The P01 explores natural killer cell and macrophage biology and strives to translate basic findings into therapeutic paradigms for patients with lymphoma and leukemia. Dr. Caligiuri is the P01 Program Director and leader of the Administrative Core and Project 3, characterizing human NK cell subsets and their antibody-mediated cellular cytotoxicity.

09/01/03-07/31/06 NCI/NIH 2 R01 CA69065-07
Title: DNA hypermethylation in breast cancer
PI: Tim Huang, Ph.D.
Co-I: Ramana V. Davuluri, Ph.D.

The goal of the project is to identify DNA hypermethylation that is progressively accumulated in CpG island loci during breast tumorigenesis. Functional characterization of methylation-controlled genes will be performed using combination of experimental and bioinformatics approaches.

09/26/03-05/31/06 NCI/NIH 1 R33 CA94441-02
Title: Novel Tool for Analysis of Promoter Hypermethylation
PI: Tim Huang, Ph.D.
Co-I: Ramana V. Davuluri, Ph.D.

The goal of this project is to develop a novel microarray panel of short oligonucleotides, i.e., methylation-specific oligonucleotide microarray, for analysis of aberrant DNA methylation in breast cancer.

10/01/03-05/31/06 NHGRI/NIH 1R01HG03129-01
Title: Discovery of Binding Sites for Transcription Factors
PI: Roland Green, Ph.D.
Collaborator (Subcontract): Ramana Davuluri, Ph.D.

The major goal of this project is to discover the functional binding sites of transcription factors in the human genome, using NimbleGen promoter array synthesis technology. Dr. Davuluri is responsible for developing the bioinformatics programs to detect first exons and promoter sequences, binding sites of transcription factors with improved prediction accuracy.

10/1/04 – 9/30/06 NIH/NCI 1R21 CA110475-01
Title: Epigenetic Biomarkers for ovarian cancer progression
PI: Tim Huang, Ph.D.
Co-I: Ramana V. Davuluri, Ph.D.

The goal of this project is to identify a panel of 5-20 DNA methylation biomarkers that have high levels of clinical sensitivity and specificity for predicting prognosis and disease relapse of ovarian cancer patients in a multi-center cohort.

Pending/Submitted

04/01/05-03/31/09 NIH/NHGRI (1R01HG 003362-01)
Title: Genomewide discovery & analysis of alternative promoters
PI: Ramana V. Davuluri, Ph.D.

The major goal of this project is to develop computational methods to discover alternative promoters in human and mouse genomes, and experimentally verify by conducting Chip-on-chip assays.

Status: Pending

Completed Research Support

01/01/03-12/31/03 American Cancer Society Seed Grant
Title: Hematopoiesis Specific Promoter and Transcription Factor Database
PI: Ramana V. Davuluri, Ph.D.

The major goal of this project is to set up a database of transcription factors and promoters of genes involved in hematopoietic development.

10/01/01-09/30/04 Human Cancer Genetics, OSU Comprehensive Cancer Center Start-up Funds
Lab Head: Ramana V. Davuluri, Ph.D.

The major goal of this grant is to set up the Bioinformatics Laboratory for the OSU Comprehensive Cancer Center and conduct research in the field of Bioinformatics and Computational Biology.

Teaching and Advising

Courses

1. Course Director, MVIMG-734 “Cancer Genetics: Highthroughput Technologies”, Spring quarter, 2003-04. (Offered once in two years)
2. Participated in MVIMG 734 “Human Cancer Genetics” course and presented one lecture (60 minutes duration) on the topic *Human Genome and Bioinformatics*.
3. Participated in Module 2: “Genes and Genome Organization” and presented one lecture (120 minutes duration) on the topic “Computational Biology”.
4. One of the four faculty for course *Bioinformatics Applied to Human Disease (IBGP-705)*

Lab members

Present

1. Hao Sun, Ph.D. Bioinformatics Programmer (02/01/02 – till date)
2. Sandya Liyanarchchi, M.A.S. Statistician (3/19/01 – till date)
3. Saranyan K. Palaniswamy, Ph.D. Bioinformatics Programmer. (04/01/02 – till date)
4. Twyla Tiongson, M.S., Bioinformatics Programmer (10/01/02 – till date)
5. Victor Jin, Ph.D., Post Doctoral Fellow (04/01/03 – till date)
6. Gregory Singer, Ph.D. Post Doctoral Fellow (05/01/04 – till date)
7. Irene Joseph, M.S. Graduate Student, OSU Biophysics Program (Registered for Lab rotation, Spring & Summer 2004)
8. Francisco J. Agosto-Pérez Graduate Student, OSU Biophysics Program (Registered for Lab rotation, Spring & Summer 2004)

Past

1. Chittithalli Dharmanolla, M.S., GRA (01/01/02 – 05/15/02)

2. Song Xin, Ph.D. Research Assistant (08/26/02 – 09/13/02)
3. Anurag Jain, M.S.(EE) Graduate Research Associate ((07-01-2002 – 05/31/03)
4. Zhaohui Zhau, M.S. (CIS), Research Assistant (12/01/02 – 05/31/03)
5. James Stapleton, Undergraduate Student, Molecular Biology (Summer, 2003)
6. Kalyan Kumar Arava, Research Fellow (07/15/03 – 06/30/04)
9. Edward Chang, MD PhD student (Lab rotation, Summer 2004)

Collaborations:

Michael Caligiuri (OSU); Albert de la Chapelle (OSU); Charis Eng (OSU); Peggy Farhham (U. Wisconsin, Madison); Kevin Gardner (NCI, Bethesda); Roland Green (NimbleGen Systems, Madison); Eric Grotewold (OSU); Tim Huang (OSU); Ralf Krahe (MD Anderson Cancer Center, Houston); Scott Lowe (Cold Spring Harbor Laboratory, NY); Christoph Plass (OSU); Raphael Wenger (OSU), Michael Zhang (Cold Spring Harbor Laboratory, NY).

Graduate and Postdoctoral Advisors

M.S. & Ph.D. Advisor: Dr. V.K. Gupta, Indian Agricultural Statistics Research Institute, New Delhi, India.

Postdoctoral Advisor: Dr. Michael Q. Zhang, Cold Spring Harbor Lab., Cold Spring Harbor, NY.