

Ganiraju Manyam, Ph.D

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Research & Professional Appointments

- Research Bioanalyst, Department of Bioinformatics & Computational Biology, The University of Texas MD Anderson Cancer Center, Houston, Texas (2010-Present)
- Senior Bioinformatics Specialist, Enterprise Solutions and Consulting Inc.(NCI Cancer Bioinformatics Grid - caBIG contractor), Rockville, Maryland (2009-2010)
- Graduate Research Assistant, Department of Molecular and Microbiology, George Mason University, Fairfax, Virginia (2006-2009)
- Junior research fellow, Genomics Research Group, Centre for Cellular and Molecular Biology (CCMB), Hyderabad, India (2004-2006)

Education

- Doctorate in Biosciences (Jan. 2010), George Mason University, Fairfax, Virginia, USA (GPA: 3.96/4)
- Master of Science in Bioinformatics (July 2004), International Institute of Information Technology (IIIT), Hyderabad, Andhra Pradesh, India (GPA: 9.66/10)
- Bachelor of Engineering in Computer Science (June 2002), Bharatiar University, Coimbatore, Tamil Nadu, India (Aggregate: 79.5% - First class with distinction)

Affiliations & Honors

- ✓ International Society for Computational Biology (ISCB)
- ✓ *Eastern North American Region* (ENAR) International Biometric Society
- ✓ BIO IT Coalition scholarship in the student recognition program by Virginia's Center for Innovative Technology (2008)
- ✓ Graduate Assistantship, George Mason University, Fairfax, Virginia, USA (2006-2009)
- ✓ Junior Research Fellowship from Centre for Cellular and Molecular Biology (CCMB), Hyderabad, India (2004-2006)

Experience

Research Bioanalyst, UT MD Anderson Cancer Center, Houston, TX

Role: Bioinformatics Research & Development (April 2010 – present)

- ❖ Carrying out complex functional, structural and statistical analyses of biological data in collaboration with the faculty of Bioinformatics and clinicians.
- ❖ Provides skilled scientific programming for a variety of research projects in the areas of bioinformatics and perform functional analysis of the data.
- ❖ Assists faculty members in the development of new methodologies, for bio-analysis of the high-throughput genomic data.
- ❖ Prepares bioinformatics reports, manuscripts and bioinformatics sections of the grant applications for investigators.
- ❖ Presents research findings at meetings of biological and bioinformatics professional groups inside and outside of the institution.

Sr.Bioinformatics Specialist, E-SAC Inc., Rockville, MD

Role: Bioinformatics Development & Analysis (November 2009 – April 2010)

- ❖ As a subject matter expert for the National Cancer Institute's caBIG effort – provided Quality Assurance and Data Validation support for several bioinformatics applications which are integral part of the caBIG initiative.

- ❖ Provided data analysis and validation support for microarray, comparative genomic hybridization and next-gen sequencing data for various cancer related studies.
- ❖ Contributed towards bioinformatics and Subject Matter Expertise for company's product development activities in the translational research and data management.

PhD Student, George Mason University, Manassas, VA

Role: Bioinformatics Development & Analysis (August 2006 – October 2009)

- ❖ Performed analysis of the tumor-specific telomere elongation effects on the adjacent gene expression using cancer microarray datasets at the NCBI Gene expression Omnibus using R data analysis package.
- ❖ Developed a tool that extracts the molecular pathways associated with genes of interest and present their modulation pattern of gene expression using Perl-CGI and KEGG API.
- ❖ Carried out complex functional and statistical analyses of multiple microarray data sets associated with various types of cancer.
- ❖ Developed an analysis platform to find variation in the expression patterns between normal and tumor cells across all human tissues in the NCBI Unigene database using Perl with a MySQL database.
- ❖ Designed and developed a MySQL database of hyperlinks with a PHP interface, consisting of the Pubmed articles associated with online accessible data and tools.

Junior Research Fellow, Centre for Cellular & Molecular Biology (CCMB), Hyderabad, India

Role: Bioinformatics Development & Comparative Genomic Analysis (July 2004 – July 2006)

- ❖ Constructed the phylogeny of BTB and zinc-finger domain containing proteins and identified the Homologue(s) for Trl-GAGA (D.melanogaster) in vertebrates by automating the smith-waterman local alignment using Perl.
- ❖ Identified the conserved non-coding sequences (in vertebrates) flanking to the human oncogenes and tumor suppressors and developed a tool in Java to visualize these conserved genomic elements in the context of ESTs and transcription factors.
- ❖ Identified the conserved sequences over a wide range of vertebrate species in the upstream, downstream and intergenic regions of HOX clusters by comparative genomic studies using C++.

Research Intern, Genomics Research Group, CCMB, Hyderabad, India

Role: Software Development (October 2003 - June 2004)

- ❖ Developed a software package for extraction and visual analysis of the Non-coding DNA sequences in the genome using Java.
- ❖ Developed a tool to predict eukaryotic translation initiation sites based on the contextual DNA sequences using Hidden Markov Models with C.

Journal Publications

1. "Hierarchical Bayesian methods for integration of various types of genomics data", Elizabeth M Jennings, Jeffrey S Morris, Raymond J Carroll, **Ganiraju Manyam** and Veerabhadran Baladandayuthapani (**Submitted to EURASIP Journal on Bioinformatics and Systems Biology**)
2. "Bayesian hierarchical structured variable selection methods with application to MIP studies in breast cancer", Lin Zhang, Veerabhadran Baladandayuthapani, Bani K. Mallick, **Ganiraju Manyam**, Patricia A. Thompson, Melissa L. Bondy and Kim-Anh Do (**submitted to Journal of the Royal Statistical Society**)
3. "targetHub: a programmable interface for miRNA-gene interactions", **Ganiraju Manyam**, Cristina Ivan, George Calin and Kevin Coombes **In Revision: Bioinformatics, 2013**

4. "Phenotypic and genotypic profiling of MDM2 and p53 in diffuse large B-cell lymphoma patients treated with rituximab-CHOP: A Report from the International DLBCL Rituximab-CHOP Consortium Program", Zijun Y. Xu-Monette, Michael B. Møller, Alexander Tzankov, Santiago Montes-Moreno, Wenwei Hu, Ganiraju Manyam, Lei Fan, Carlo Visco, Karen Dybkær, April Chiu, Wayne Tam, Youli Zu, Govind Bhagat, Kristy L. Richards, Eric D. Hsi, William W.L. Choi, J. Han van Krieken, Qin Huang, Jooryung Huh, Weiyun Ai, Maurilio Ponzoni, Andrés J.M. Ferreri, Yong Li, Jane N. Winter, Lin Wu, Xiaoying Zhao, Ronald S. Go, Miguel A. Piris, L. Jeffrey Medeiros and Ken H. Young ***In Revision: Blood, 2013***
5. "Colonic Epithelial PPAR- δ Overexpression Strongly Alters Colon Cancer Susceptibility in Mice", Xiangsheng Zuo, Min Xu, Jiang Yu, Yuanqing Wu, Micheline J. Moussalli, **Ganiraju Manyam**, Sun Il Lee, Shoudan Liang, Jeffrey Morris, Russell Broaddus and Imad Shureiqi ***In Revision: Journal of the National Cancer Institute, 2013***
6. "Integrating Multi-Platform Genomic Data Using Hierarchical Bayesian Relevance Vector Machines", Sanvesh Srivastava, Wenyi Wang, **Ganiraju Manyam**, Carlos Ordonez and Veerabhadran Baladandayuthapani ***Accepted: EURASIP Journal on Bioinformatics and Systems Biology, 2013***
7. "ZKSCAN3 (ZNF306) is a Novel Master Transcription Repressor of Autophagy", Santosh Chauhan, Goodwin JG, Chauhan S, **Ganiraju Manyam**, Jing Wang, Kamat AM, and Douglas D. Boyd ***Molecular Cell, 2013***
8. "CD30 expression defines a novel subgroup of diffuse large B-cell lymphoma with superior clinical outcome: a report from International DLBCL Rituximab-CHOP Consortium Program Study", Shimin Hu, Zijun Y. Xu-Monette, Balasubramanyam A, **Ganiraju Manyam**, Carlo Visco, Li Zhang, Alexander Tzankov, Santiago Montes-Moreno, Karen Dybkær, April Chiu, Attilio Orazi, Youli Zu, Govind Bhagat, Kristy L. Richards, Eric D. Hsi, X. Frank Zhao, William W.L. Choi, Xiaoying Zhao, Xiaohong Zhang, J. Han van Krieken, Qing Huang, Jooryung Huh, Weiyun Ai, Maurilio A. Ponzoni, Andres JM. Ferreri, Fan Zhou, Jane N. Winter, Ronald S. Go, Yong Li, Miguel A. Piris, Michael B. Møller, Roberto N. Miranda, Lin Wu, L. Jeffrey Medeiros, and Ken H. Young ***Blood, 2013***
9. "Access to the nucleus and functional association with c-Myc is required for the full oncogenic potential of δ EGFR/EGFRvIII", Anupama Gururaj, Laura Gibson, Sonali Panchabai, Minghui Bai, **Ganiraju Manyam**, Yue Lu, Khatri Latha, Marta Rojas, Yeohyeon Hwang, Shoudan Liang and Oliver Bogler ***Journal of Biological Chemistry, 2013***
10. "iBAG: Integrative Bayesian Analysis of High-Dimensional Multi-platform Genomics Data", Wenting Wang, Veerabhadran Baladandayuthapani, Jeffrey Morris, Bradley Broom, **Ganiraju Manyam**, and Kim-Anh Do ***Bioinformatics, 2013***
11. "Temporal transcriptional response during infection of Type II alveolar epithelial cells with *Francisella tularensis* LVS supports a general host suppression and bacterial uptake by macropinocytosis", Christopher Bradburne, Anne Verhoeven, **Ganiraju Manyam**, Saira Chaudhry, Eddie Chang, Dzung Thach, Charles Bailey and Monique van Hoek ***Journal of Biological Chemistry, 2013***
12. "Relax with CouchDB - Into the non-relational DBMS era of Bioinformatics", **Ganiraju Manyam**, Michelle Payton, Jack Roth, Lynne Abruzzo and Kevin Coombes ***Genomics, 2012***
13. "An efficient algorithm for systematic analysis of nucleotide strings suitable for siRNA design", Ancha Baranova, Jonathan Bode, **Ganiraju Manyam** and Maria Emelianenko. ***BMC Research Notes, 2011***

14. "Proteomic characterization and functional analysis of outer membrane vesicles of *Francisella novicida* suggests possible role in virulence and use as a vaccine", Tony Pierson, Demetrios Matrakas, Yuka U. Taylor, **Ganiraju Manyam**, Victor N. Morozov, Weidong Zhou, and Monique L. van Hoek. *Journal of Proteome Research*, 2011
15. "Functional pathway analysis of genes associated with response to treatment for chronic Hepatitis C, Journal of Viral Hepatitis", Aybike Biredinc, Arian Afendy, Maria Stepanova, Issah Younossi, **Ganiraju Manyam**, Ancha Baranova and Zobair Younossi. *Journal of Viral Hepatitis*, 2010
16. "Pro-apoptotic and anti-proliferative activity of human KCNRG, a putative tumor suppressor for CLL and multiple myeloma", Aybike Biredinc, Elizabeth Nohelty, Andrey Marakhonov, **Ganiraju Manyam**, Ivan Panov, Stephanie Coon, Eugene Nikitin, Mikhail Skoblov, Vikas Chandhoke and Ancha Baranova. *Tumor Biology*, 2010
17. "SnS-Align: A graphic tool for alignment of distantly related proteins", **Ganiraju Manyam**, Ancha Baranova, Mikhail Skoblov and Rakesh Mishra. *International Journal of Bioinformatics Research and Applications*, 2009
18. "Early gene expression profiles of patients with chronic hepatitis C treated with pegylated interferon-alfa and ribavirin", Zobair Younossi, Ancha Baranova, Arian Afendy, Rochelle Collantes, Maria Stepanova, **Ganiraju Manyam**, Anita Bakshi, Christopher Sigua, Joanne Chan, Ayuko Iverson, Christopher Santini and Sheng-Yung Chang. *Hepatology*, 2009

Conference Publications & Posters

1. "Prediction of bone metastasis in primary breast cancer patients by reverse-phase protein array", Naoki Hayashi, **Ganiraju C. Manyam**, Ana M. Gonzalez-Angulo, Naoki Niikura, Hideko Yamauchi, Seigo Nakamura, Gabriel N. Hortobagyi, Keith A. Baggerly and Naoto T. Ueno. *American Society of Clinical Oncology* at Chicago, IL in May-June, 2013
2. "MET overexpression as a hallmark of the epithelial-mesenchymal transition (EMT) phenotype in colorectal cancer", Kanwal Pratap Singh Raghav, Hesham M. Amin, Wenting Wang, **Ganiraju Manyam**, Bradley Broom, Cathy Eng, Michael J. Overman and Scott Kopetz. *American Society of Clinical Oncology* at Chicago, IL in May-June, 2013
3. "Role of intracrine vascular endothelial growth factor (VEGF) signaling in colorectal cancer cell survival and metastasis", Rajat Bhattacharya, Shaija Samuel, Fan Fan, **Ganiraju Manyam**, Veera Baladandayuthapani and Lee Ellis. *AACR Annual Meeting* at Washington, DC in April, 2013
4. "MET overexpression as a hallmark of the epithelial-mesenchymal transition (EMT) phenotype in colorectal cancer", Kanwal Raghav, Wenting Wang, **Ganiraju Manyam**, Bradley M Broom, Cathy Eng, Michael J. Overman and Scott Kopetz. *Gastrointestinal Cancers Symposium* at San Francisco, CA in January, 2013
5. "Hierarchical Bayesian Methods for Integration of Various Types of Genomics Data", Elizabeth M. Jennings, Jeffrey S. Morris, Raymond J. Carroll, **Ganiraju Manyam** and Veerabhadran Baladandayuthapani. *GENSIPS* at Washington DC in December, 2012
6. "Integrative Bayesian Analysis of High-Dimensional Multi-Platform Genomics Data", Kim-Anh Do, Wenting Wang, Bradley M Broom, Jeffrey S Morris and **Ganiraju Manyam**. *Joint Statistical Meetings(JSM) - American Statistical Association* at San Diego, CA in July 2012

7. "Bayesian Hierarchical Structured Variable Selection Methods with Application to MIP Studies in Breast Cancer", Lin Zhang, Veera Baladandayuthapani, Bani K Mallick, **Ganiraju Manyam**, Patricia Thompson, Melissa Bondy and Kim-Anh Do. **Joint Statistical Meetings(JSM) - American Statistical Association** at San Diego, CA in July 2012
8. "GeneSmash: A RESTful web service for gene annotations", **Ganiraju Manyam**, Michelle Payton, Chris Wakefield, Jack Roth, Lynne Abruzzo and Kevin Coombes. **9th Annual Rocky Mountain Bioinformatics Conference** at Aspen, CO in December 2011
9. "Integrative Bayesian Analysis of Genomics with Application to Analyze Gene Expression and Methylation Data for TCGA Glioblastoma Study", Wenting Wang, Veera Baladandayuthapani, Jeffrey S. Morris, Bradley M. Broom, **Ganiraju Manyam**, Kenneth D Aldape and Kim-Anh Do. **Biotechnology and Bioinformatics Symposium (BIOT)** at Houston TX in October 2011
10. "Access to the nucleus is required for the full oncogenic potential of Δ EGFR/EGFRVIII", Anupama E. Gururaj, Laura Gibson, Sonali Panchabai, MingHui Bai, **Ganiraju Manyam**, Yue Lu, Khatri Latha, Marta L. Rojas, Yeohyeon Hwang, Shoudan Liang and Oliver Bogler. **Symposia on Cancer Research (New Roles for the EGFR Family in Cancer)**, at Houston, TX in September 2011.
11. "Gene expression profile of the tumor as a composite biomarker", Ancha Baranova, Wang Lei, Alessandro Giuliani and **Ganiraju Manyam**. **Moscow conference on computational molecular biology** at Moscow, Russia in July 2011
12. "Antigen processing and proteasome degradation pathways are involved in patients with chronic Hepatitis-C with negative predictors of response to pegylated interferon and ribavirin (PEG-IFN/RBV) " Aybike, Biredinc, Arian Afendy, Maria Stepanova, Issah Younossi, **Ganiraju Manyam**, Ancha Baranova and Zobair Younossi. **The International Liver Congress™** at Berlin, Germany in March 2011
13. "Up-Regulation of Matrix Metalloproteinase 9 (MMP-9) and Interleukin-8 (IL-8) in African American Patients with Chronic Hepatitis C", Aybike, Biredinc, Maria Stepanova, **Ganiraju Manyam**, Arian Afendy, T Gramlich, and Ancha Baranova. **Disease Digestive Week**, at New Orleans, LA in May 2010.
14. "Genome-wide expression pattern as a composite biomarker of cancer", **Ganiraju Manyam**, Giuliani Alessandro, and Ancha Baranova. **AACR 101st Annual Meeting**, at Washington DC in April 2010.
15. "Functional Pathway analysis of Gene Expression in Patients with Non-alcoholic Fatty Liver Disease (NAFLD) and Non-alcoholic Steatohepatitis (NASH)", Zobair Younossi, **Ganiraju Manyam**, Maria Stepanova, Ancha Baranova, Noreen Hossain, Zachary Goodman, and Vikas Chandhoke. **The International Liver Congress**, at Vienna, Austria in April 2010.
16. "Tumor as an attractor: Toward the use of global patterns of gene expression in the predictive diagnostics of tumorigenesis", **Ganiraju Manyam**, Giuliani Alessandro, and Ancha Baranova. **NCI Circulating Tumor Cells Meeting**, at Bethesda, MD in September 2009.
17. "Gene expression biomarkers predicting response to pegylated interferon alpha and ribavirin in the peripheral blood of patients with chronic hepatitis C, non-responder to previous treatment", Zobair Younossi, Rochelle Collantes, Ancha Baranova, Amy Kim, **Ganiraju Manyam**, Maria Stepanova, Chris Santini, Chris Sigua, Joanne Chan and Ayuko I. **Annual meeting of AASLD** at Boston, MA in November 2007
18. "Gene expression biomarkers predicting response to pegylated interferon alpha and ribavirin in Treatment-Naive patients with chronic hepatitis C", presented as poster by Zobair

Younossi, Rochelle Collantes, Ancha Baranova, Amy Kim, **Ganiraju Manyam**, Maria Stepanova, Chris Santini, Chris Sigua, Joanne Chan and Ayuko I. **Annual meeting of AASLD** at Boston, USA in November 2007

19. "Effects of the tumor-specific telomere elongation on the adjacent gene expression", **Ganiraju Manyam**, Bagrat Kapanadze, Galina Glazko, Maria Stepanova, Vikas Chandhoke and Ancha Baranova. **HUGO Annual Meeting** at Montreal, Canada in May 2007
20. "Comparative Genomics of the Vertebrate HOX Clusters", Venu Madhav, **Ganiraju Manyam**, S Krishnan, Navneet Mathur and Rakesh Mishra. **EMBO Workshop** at Hyderabad, India in December 2005.
21. "The Fab-7 boundary in the Bithorax Complex requires Trl-GAGA", **Ganiraju Manyam**, Ram P Kumar and Rakesh K Mishra. **ISDB conference** at Bangalore, India in December 2004.

Patents

"**Tumor Discriminator**", Ancha Baranova, **Ganiraju Manyam** and Giuliani Alessandro (US Patent Application No: 20110301853)

Books & Book Chapters

- i. "An introduction to next-generation biological platforms", Virginia Mohlere, Wenting Wang and **Ganiraju Manyam**. Book Chapter in "Advances in Statistical Bioinformatics: Models and Integrative Inference for High-Throughput Data", *Cambridge University Press, June 2013*
- ii. "Gene expression during carcinogenesis - A bioinformatics perspective: An analysis of the global patterns of changes in the gene expression associated with genesis of cancer", **Ganiraju Manyam** and Ancha Baranova. *Lambert Academic Publishing, May 2010*

Talks & workshops

1. "Bioinformatics Tools for Clinical Researchers: How to access, analyze, and interpret data from the Cancer Genome Atlas" Swog meeting", John Weinstein, **Ganiraju Manyam** and Rehan Akbani. *Hands-on workshop* held at **South Western Oncology Group Meeting** in San Francisco, CA (2013)
2. "GeneSmash: A RESTful web service for gene annotations", **Ganiraju Manyam**, Michelle Payton, Chris Wakefield, Jack Roth, Lynne Abruzzo and Kevin Coombes. **9th Annual Rocky Mountain Bioinformatics Conference** in Aspen, CO (2011)
3. "Whole-transcriptome pattern as a composite biomarker for cancer", **Ganiraju Manyam**, Giuliani Alessandro, and Ancha Baranova. **Bioinformatics Colloquium, George Mason University** in Manassas, VA (2010)
4. "KPP: KEGG pathway painter", **Ganiraju Manyam**, Vikas Chandhoke and Ancha Baranova. **Annual Meeting of the Virginia Academy of Science** in Richmond, VA (2009)
5. "Tumor as an attractor. Toward the use of the global patterns of gene expression in the predictive diagnostics of tumorigenesis", **Ganiraju Manyam**, Giuliani Alessandro, and Ancha Baranova. **2nd Systems Biology Research Panel, George Mason University** in Fairfax, VA (2009)