Stephen C. J. Parker

100 Washtenaw Avenue
Ann Arbor, MI 48109
734-647-3144
scjp@umich.edu

EDUCATION

2014 – present **Assistant Professor**
University of Michigan
Department of Computational Medicine & Bioinformatics
Department of Human Genetics
Ann Arbor, MI

2009 – 2014 **Postdoctoral Fellow**
National Human Genome Research Institute
National Institutes of Health, Bethesda, MD
Advisors: Francis S. Collins, M.D., Ph.D. (2011-2014)
Elliott H. Margulies, Ph.D. (2009-2011)

2004 – 2009 **Ph.D. in Bioinformatics and Systems Biology**
Boston University, Boston, MA
Advisor: Thomas D. Tullius, Ph.D.

1998 – 2000 **M.S. in Molecular Biology and Biotechnology**
Advisor: Edmund J. Stellwag, Ph.D.

1994 – 1998 **B.S. in Biology, concentration in Molecular Biology**
East Carolina University, Greenville, NC

RESEARCH EXPERIENCE

Assistant Professor September 2014-present
University of Michigan, Department of Computational Medicine & Bioinformatics
The major goal of the lab is to generate mechanistic knowledge about how disease susceptibility is encoded in the non-coding portion of the genome, with a focus on type 2 diabetes. We accomplish this through an interdisciplinary combination of molecular/cellular and computational approaches. Specifically, we generate multiple high-throughput data sets on the genome, epigenome, transcriptome, and proteome across species and in disease-relevant tissues/cells and use computational approaches to integrate and analyze this data.

Postdoctoral Fellow August 2009-August 2014
National Human Genome Research Institute, National Institutes of Health, Bethesda, MD
Utilize high-performance computing platforms and high-throughput DNA sequencing technologies to address health-related biological problems.

Bioinformatics Consultant March 2009-August 2009
BD TriPath, RTP, NC
Performed various computational gene expression microarray analyses to help establish new cancer biomarker research projects.

Research Assistant August 2004-May 2009

Boston University, Boston, MA

Initiated various analyses to explore the relationship between DNA structure, evolutionary constraint, and genome function. Developed various computational algorithms and statistical approaches to investigate these relationships.

Genome Closure Data Analyst July 2002-August 2004

The Broad Institute & MIT Center for Genome Research, Cambridge, MA

Measured and monitored the quality and accuracy of human genome closure data using various computational tools. Designed and implemented new computational tools using Unix and Perl programming knowledge.

Associate Scientist January 2001-June 2002

Cogent Neuroscience Inc., Durham, NC

Responsible for all duties associated with operating the core sequencing facility. Simultaneously managed several side projects involving hit characterization. Developed and executed strategies to clone genes of interest for functional analysis.

M.S. Thesis Degree Research Project January 1998-December 2000

East Carolina University, Greenville, NC

Employed molecular biology-based techniques to obtain the genomic sequence of a *Hox* gene region on the *HoxBa* cluster in the *Teleost* fish *Morone saxatilis*. Performed various evolutionary analyses using multiple bioinformatics techniques with the resulting data.

Research Associate May-August 1998

Novartis Biotechnology Inc., RTP, NC

Research associate in Bioinformatics lab. Responsible for PCR amplifying an *Arabadopsis thaliana* EST library to be put on micro array chips. Performed standard molecular techniques using 96 well format protocols in order to achieve high-throughput results.

Research Assistant May-August 1997 and May-August 1996

Glaxo Wellcome (currently GSK), RTP, NC

Completed two clinical studies for 5-alpha reductase inhibitor class drug using high-throughput robotic sample processing and HPLC/APCI/MS/MS detection. Assisted in the completion of several other clinical studies for various other compounds. Analyzed the resulting data and co-authored the Bioanalytical Reports resulting from these studies.

GRANT FUNDING

- American Diabetes Association Pathway to Stop Diabetes Program, Career Initiator Award, Grant #1-14-INI-07 (2014-2020) $1.625M total.
  "Deconstructing type 2 diabetes using genome-wide high-density multi-tissue 'omics' profiling"

- NIH/NIDDK K99DK099240 (2013-2018) $750k total over three years during R00 phase.
  "Synthesizing genome, epigenome, and transcriptome datasets in type 2 diabetes."

- NIH/NIGMS Pharmacology Research Associate (PRAT) Fellowship (2011-2014) $285k

- NIH/NHGRI/NISC Pilot Project Sequencing Award (2014) $10k
  "Cell-type specific epigenome and transcriptome signatures of alpha and beta cells in rat islets." Co-author

- NIH/NHGRI/NISC Pilot Project Sequencing Award (2014) $10k

"Allelic and cross-species signatures of functional chromatin architecture in diabetes relevant cells." Primary author

- NIH/NHGRI/NISC Pilot Project Sequencing Award (2013) $10k
  "Genome-wide regulatory element mapping at DNA binding site resolution in frozen samples." Primary author

- NIH/NHGRI/NISC Pilot Project Sequencing Award (2013) $10k
  "Enhancer RNA-seq to measure regulatory element activity in type 2 diabetes." Primary author

- NIH/NHGRI/NISC Flagship Project Sequencing Award (2012) $175k
  "Determining effects of diabetes variants on the transcriptome of human pancreatic islets." Co-author

RESEARCH SKILLS

- Utilization of high-performance UNIX computing environments.
- Proficient at operating large parallel computing clusters for bioinformatics analyses.
- Skilled at performing various molecular-based laboratory techniques.

Programming Languages	Operating Systems
Perl	Linux/UNIX
R	Mac OS X
UNIX shell	Windows NT/2000/XP
MySQL	
HTML, XHTML, CSS, CGI	

HONORS AND AWARDS

- Distinguished Postbac Mentor Award, NIH (2014)
- Trainee of the Year Award, NIH/NHGRI (2013)
- Selected participant to invitation-only Cold Spring Harbor Banbury conference on "Enhancer Biology in Health and Disease" (2013)
- Fellows Award for Research Excellence (FARE), NIH (2013)
- Pharmacology Research Associate (PRAT) Program Fellow, NIH/NIGMS (2011-2014)
- Genome Technology Young Investigators of the Year Award (2010)
- Boston University Bioinformatics Innovative Teaching Award (2009)
- Associate Faculty Member, Faculty of 1000 Biology (2008 – present)
- National Academies, Ford Foundation Dissertation Fellowship (2008 – 2009)
- Genome Research Best Poster Award (Biology of Genomes Meeting, 2007)
- Boston University Presidential Fellowship (2004 – 2005)
- East Carolina University Mary C. Helms Scholarship for outstanding graduate student (2000)
- East Carolina University Research Day Best Poster Presentation Award (2000)
- East Carolina University James S. McDaniel Scholarship for outstanding graduate student (1999)
- East Carolina University Chancellor's List, Dean's List, and Honor Roll (1994 – 1998)
- East Carolina University soccer team

SCIENTIFIC SERVICE

- Admissions Committee Member, University of Michigan Department of Computational Medicine and Bioinformatics (2014)
- Panel member, University of Michigan BF 527 discussion about the future of bioinformatics as a domain of data science (2014)
- Panel member, University of Michigan BF 527 discussion about the future of genomics (2014)
- Panel member, NHGRI Advances in Genomics Research Summer Program (2014)
- Reviewer, Fellows Award for Research Excellence (FARE), NIH (2014)
- Member, NHGRI, NIH Retreat Planning Committee (2013)
- Panel member, NHGRI, NIH Summer Intern Career Development Panel Discussion (2012)
- Member, NHGRI, NIH Genome Trainee Advisory Committee (GTAC) (2011 – 2013)
- Scientific Judge, NIH Graduate Student Research Symposium (2011 - 2013)
- Scientific Ambassador, DNA Day (2010 – 2013)
- Graduate Student Organization Travel Grant Review Committee Member (2009)
- National Center for Scientific Education, Project Steve Member (2009 – present)
- Manuscript reviewer: *Genome Research*, *Nucleic Acids Research, BMC Bioinformatics, Computers in Biology and Medicine, Diabetes, Database, Human Heredity, and Advances in Nutrition*
- Scientific Judge and Moderator, Boston University Regional High School Science Bowl (2007 – 2009)
- Organizing Committee Member, Boston University student-run Bioinformatics and Systems Biology Research Symposium (2007)

TEACHING EXPERIENCE

Mentor

National Human Genome Research Institute, National Institutes of Health, Bethesda, MD

Daniel Quang	July 2014-present; Best Speaker Award at Tsukuba Global Science week in Tuskuba, Japan; currently preparing manuscript.
Brooke Wolford	August 2013-present; Best Poster Award at NIH Postbac Research Day; Best Poster Award at NHGRI Research Symposium; primary author for successful NHGRI pilot grant; currently preparing manuscripts.
Leland Taylor	August 2012-2013; awarded NSF Fellowship; accepted to NIH-Oxford/Cambridge Doctoral Program; co-authored manuscript.
Rachel Goldfeder	2010-2011; co-authored manuscript, currently PhD student at Stanford.

Boston University, Boston, MA May 2005-May 2009

Mentored research projects for high school and undergraduate students. Supervised the research for eight students. Designed the project, performed interviews and screened applications, and helped select candidates. Trained all students the required molecular biology, chemistry, and computer science skills.

Instructor

Spring and Fall 2008

Boston University, Boston, MA
Co-developed, organized, and taught course material for a semester-long graduate-level Bioinformatics Applications course (ENG BF 527) designed to introduce students to concepts and tools used for genomic and computational biology research.

Head Graduate Teaching Assistant 1999
Graduate Teaching Assistant 1998
East Carolina University, Greenville, NC
Performed all duties associated with teaching freshman level biology labs and served as a mentor to novice teaching assistants.

Independent Teaching Lectures

1. "How to give a successful chalk talk" S.C.J. Parker. Invited seminar sponsored by NHGRI/NIH, Bethesda, MD. October 20, 2014.

2. "Computational Comparative Genomics: Insights into Human Disease" S. C. J. Parker. Invited DNA Day lecture for the Smithsonian National Museum of Natural History, Washington, DC. April 25, 2014.

3. "Comparative genomics: insights into biological variation (with a focus on non-coding regions)" S. C. J. Parker. Invited lecture at Mt. Vernon High School, Alexandria, VA. February 26, 2013.

4. "My life during the Boston University Bioinformatics Program" S. C. J. Parker. Boston University Bioinformatics Program Recruitment Weekend, Boston, MA. February 16, 2013.

5. "Comparative genomics: insights into biological variation (with a focus on non-coding regions)" S. C. J. Parker. DNA Day lecture at Annandale High School, Annandale, VA. April 24, 2012.

6. "Comparative genomics: insights into biology (with a focus on non-coding DNA)" S. C. J. Parker. Hood College Department of Biology. Frederick, MD. March 1, 2012.

7. "My life during the Boston University Bioinformatics Program" S. C. J. Parker. Boston University Bioinformatics Program Recruitment Weekend, Boston, MA. February 18, 2012.

8. "Genome Sequencing" S. C. J. Parker. University of the District of Columbia, Washington DC. September 21, 2011.

9. "Beyond genes: The hidden landscapes of your DNA. (non-coding DNA is important!)" S. C. J. Parker. DC Science Café Lecture Series at Busboys and Poets, Washington DC. August 8, 2011.

10. "Comparative Genomics: Evolution to Human Disease" S. C. J. Parker. DNA Day lecture at Annandale High School, Annandale, VA. April 11, 2011.

11. "My life during the Boston University Bioinformatics Program" S. C. J. Parker. Boston University Bioinformatics Program Recruitment Weekend, Boston, MA. February 19, 2011.

12. "Comparative Genomics: From Evolution to Human Disease" S. C. J. Parker. DNA Day lecture at Wilde Lake High School, Columbia, MD. April 23, 2010.

13. "My life during the Boston University Bioinformatics Program" S. C. J. Parker. Boston University Bioinformatics Program Recruitment Weekend, Boston, MA. February 19, 2010.

RESEARCH ACTIVITY

Publications

1. "Stretch-Enhancers Delineate Disease-Associated Regulatory Nodes in T Cells." J. O'Shea, G. Vahedi, Y. Kanno, Y. Furumoto, K. Jiang, **S.C.J. Parker**, M. Erdos, S. Davis, R. Roychoudhuri, N. Restifo, M. Gadina, Z. Tang, Y. Ruan, F. Collins, and V. Sartorelli. *Nature* (in press)

2. "GBshape: a genome browser database for DNA shape annotations." T.P. Chiu, L. Yang, T. Zhou, B.J. Main, **S.C.J. Parker**, S.V. Nuzhdin, T.D. Tullius, and R. Rohs. *Nucleic Acids Res.* (2014) *Pubmed link*

3. "Comparative analysis of metazoan chromatin architecture" The modENCODE Project Consortium*. *Nature* (2014) *Pubmed link*
   [* lead analyst]

4. "Chromatin stretch enhancer states drive cell-specific gene regulation and harbor human disease risk variants" **S. C. J. Parker***, M. L. Stitzel*, D. L. Taylor, J. M. Orozco, M. R. Erdos, J. A. Akiyama, K. Lammerts van Bueren, P. S. Chines, N. Narisu, NISC Comparative Sequencing Program, B. L. Black, A. Visel, L. A. Pennacchio, F. S. Collins. *PNAS* (2013) *Pubmed link*
   [* co first author]

5. "Somatic Mutations in MAP3K5 Attenuate Its Proapoptotic Function in Melanoma through Increased Binding to Thioredoxin." T. D. Prickett*, B. Zerlanko*, J. J. Gartner, **S. C. J. Parker**, K. Dutton-Regester, J. C. Lin, J. K.Teer, X. Wei, J. Jiang, NISC Comparative Sequencing Program, G. Chen, M. A. Davies, J. E. Gershenwald, W. Robinson, S. Robinson, N. K. Hayward, S. A. Rosenberg, E. H. Margulies, Y. Samuels. *Journal of Investigative Dermatology* (2013) *Pubmed link*

6. "Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma" J. J. Gartner*, **S. C. J. Parker***, T. D. Prickett, K. Dutton-Regester, M. L. Stitzel, J. C. Lin, V. L. Simhadri, S. Jha, N. Katagiri, V. Gotea, J. K. Teer, X. Wei, M. A. Morken, U. K. Bhanot, NISC Comparative Sequencing Program, G. Chen, L. Elnitski, M. A. Davies, J. E. Gershenwald, H. Carter, R. Karchin, W. Robinson, S. Robinson, S. A. Rosenberg, F. S. Collins, A. A. Komar, C. Kimchi-Sarfaty, N. K. Hayward, E. H. Margulies, Y. Samuels. *PNAS* (2013) *Pubmed link*
   [* co first author]

7. "An Integrated Encyclopedia of DNA Elements in the Human Genome." The ENCODE Project Consortium*. *Nature* (2012) *Pubmed link*
   [* lead analyst]

8. "Mutational signatures of de-differentiation in functional non-coding regions of melanoma genomes." **S. C. J. Parker**, J. Gartner, I. Cardenas-Navia, X. Wei, H. Ozel Abaan, S. S. Ajay, N. F. Hansen, L. Song, U. K. Bhanot, J. K. Killian, Y. Gindin, R. Walker, P. S. Meltzer, J. C. Mullikin, T. S. Furey, G. E. Crawford, S. A. Rosenberg, Y. Samuels, and E. H. Margulies. *PLoS Genetics* 8(8) (2012) *Pubmed link*

9. "Extensive evolutionary changes in regulatory element activity during human origins are associated with altered gene expression and positive selection." Y. Shibata*, N. C. Sheffield*, O. Fedrigo, C. C. Babbitt, M. Wortham, D. London, L. Song, A. K. Tewari, **S. C. J. Parker**, E. H. Margulies, G. A. Wray, T. S. Furey, and G. E. Crawford. *PLoS Genetics* 8(6) (2012) *Pubmed link*

10. "A map of minor groove shape and electrostatic potential from hydroxyl radical cleavage patterns." E. P. Bishop*, R. Rohs*, **S. C. J. Parker***, S. M. West, P. Liu, R. S. Mann, B. Honig, and T. D. Tullius. *ACS Chemical Biology* (2011) *Pubmed link*
[* co first author]

11. "Accurate and comprehensive sequencing of personal genomes." S. S. Ajay, **S. C. J. Parker**, H. Ozel Abaan, K. Fuentes Fajardo, and E. H. Margulies. *Genome Research* (2011) *Pubmed link*

12. "A computational method to search for DNA structural motifs in functional genomic elements." **S. C. J. Parker**, A. Harlap, and T. D. Tullius. *Methods in Molecular Biology: Yeast Systems Biology, Humana Press, USA* (2011) *Pubmed link*

13. "Evolutionary constraint on DNA shape in the human genome." T. D. Tullius, **S. C. J. Parker**, and E. H. Margulies. *Evolutionary Biology: 14th Meeting 2010, P. Pontarotti, ed. Springer Heidelberg* (2011) *Book chapter link*

14. "A bioinformatics approach to determining sample identity from pooled lanes of high-throughput sequencing data." R. L. Goldfeder*, **S. C. J. Parker***, S. S. Ajay, H. Ozel Abaan, and E. H. Margulies. *PLoS ONE* (2011) *Pubmed link*
[* co first author]

15. "A User's Guide to the Encyclopedia of DNA Elements (ENCODE)." The ENCODE Project Consortium. *PLoS Biology*. 9(4):e1001046 (2011) *Pubmed link*

16. "DNA shape, genetic codes, and evolution." **S. C. J. Parker** and T. D. Tullius. *Current Opinion in Structural Biology.* Advanced online publication (2011) *Pubmed link*

17. "Global epigenomic analysis of primary human pancreatic islets provides insights into type 2 diabetes susceptibility loci" M. L. Stitzel, P. Sethupathy, D. S. Pearson, P. S. Chines, L. Song, M. R. Erdos, R. Welch, **S. C. J. Parker**, A. P. Boyle, L. J. Scott, NISC Comparative Sequencing Program, E. H. Margulies, M. Boehnke, T. S. Furey, G. E. Crawford, and F. S. Collins. *Cell Metabolism* 12(5):443-55 (2010) *Pubmed link*

18. "Human NPY Promoter Variation rs16147 as a Moderator of Prefrontal NPY Gene Expression and Negative Affect" W. H. Sommer, J. Lidström, H. Sun, D. Passer, R. Eskay, **S. C. J. Parker**, S. H. Witt, U. Zimmermann, V. Nieratschker, M. Rietschel, E. H. Margulies, M. Palkovits, M. Laucht, and M. Heilig. *Human Mutation*. Online publication (2010) *Pubmed link*

19. "Family-based analysis of candidate genes for polycystic ovary syndrome" K. G. Ewens, D. R. Stewart, W. Ankener, M. Urbanek, J. M. McAllister, C. Chen, K. M. Baig, **S. C. J. Parker**, E. H. Margulies, R. S. Legro, A. Dunaif, J. F. Strauss III, and R. S. Spielman. *Journal of Clinical Endocrinology and Metabolism* 95:2306-2315 (2010) *Pubmed link*

20. "Local DNA Topography Correlates with Functional Non-coding Regions of the Human Genome" **S. C. J. Parker**, L. Hansen, H. Ozel Abaan, T. D. Tullius, and E. H. Margulies. *Science* 324:389-392 (2009) *Pubmed link*

21. "The Relationship Between Fine Scale DNA Structure, GC Content, and Functional Elements in 1% of the Human Genome" **S. C. J. Parker**, E. H. Margulies, and T. D. Tullius. *Genome Informatics* 20:199-211 (2008) *Pubmed link*

22. "Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project" The ENCODE Project Consortium. *Nature* 447:799-816 (2007) *Pubmed link*

23. "Detection of DNA structural motifs in functional genomic elements" J.A. Greenbaum, **S. C. J. Parker**, and T.D. Tullius. *Genome Research* 17:940-6 (2007) *Pubmed link*

24. "Towards the identification of essential genes using targeted genome sequencing and comparative analysis" A. Gustafson, E. Snitkin, **S. C. J. Parker**, C. DeLisi and S. Kasif. *BMC Genomics* 7:265 (2006) *Pubmed link*

25. "DNA Sequence and Analysis of Human Chromosome 8" C. Nusbaum*, et al*. *Nature* 439:331-5 (2006) *Pubmed link*

26. "Finishing the euchromatic sequence of the human genome" International Human Genome Sequencing Consortium. *Nature* 431:931-45 (2004) *Pubmed link*

Selected Oral Presentations

1. The University of Michigan, Bioinformatics Workshop, Ann Arbor, MI. October 13, 2014.
2. The University of Michigan, Department of Human Genetics, Ann Arbor, MI. September 9, 2014.
3. The Jackson Laboratory, Bar Harbor, ME. March 13, 2014.
4. Vanderbilt University School of Medicine, Department of Medicine, Nashville, TN. March 4, 2014.
5. The National Institutes of Health, National Institute on Aging, Earl Stadtman Investigator talk, Baltimore, MD. February 24, 2014.
6. Case Western Reserve University, Department of Genetics and Genome Sciences, Cleveland, OH. February 19, 2014.
7. The University of Massachusetts Medical School, Program in Bioinformatics & Integrative Biology, Worcester, MA. February 3, 2014.
8. The Jackson Laboratory for Genomic Medicine, Farmington, CT. Janurary 29, 2014.

9. The University of Michigan, Department of Computational Medicine & Bioinformatics, Ann Arbor, MI. January 15, 2014.

10. Duke University, Department of Biostatistics and Bioinformatics, Durham, NC. January 8, 2014.

11. The National Institutes of Health, Earl Stadtman tenure track investigator search: Symposium on Computational Biology, Bioinformatics, Biostatistics, and Mathematics. Bethesda, MD. December 2, 2013.

12. Banbury Meeting on Enhancer Biology in Health and Disease, Cold Spring Harbor, NY. October 27-30, 2013.

13. The Biology of Genomes Meeting, Cold Spring Harbor, NY. May 7-11, 2013.

14. FUSION Study Meeting. Ann Arbor, MI. November 27, 2012.

15. The National Institutes of Health, Chromatin DECODE Meeting, Bethesda, MD. November 13, 2012.

16. The 17th Conversation: Journal of Biomolecular Structure and Dynamics; Invited under young investigator program. Albany, NY. June 14-18, 2011.

17. Annual Retreat for the National Human Genome Research Institute, National Institutes of Health, Cambridge, MD. November 15-16, 2010.

18. The ENCODE Consortium Meeting, Bethesda, MD. March 11, 2010.

19. Friday Floor Forums at the National Human Genome Research Institute, National Institutes of Health, Bethesda, MD. January 29, 2010.

20. Helicos BioSciences Corporation, Cambridge, MA. May 14, 2009.

21. Doctoral Dissertation Defense. Boston University, Boston, MA. April 9, 2009.

22. 8th International Workshop on Bioinformatics and Systems Biology. Zeuthen, Germany. June 9-11, 2008

23. Boston University Chemistry and Biology Seminar Series. April 23, 2008.

24. The ENCODE Consortium Chromatin and Replication Subgroup Meeting. Seattle, WA. October 28-30, 2005.

25. Master of Science Thesis Seminar. East Carolina University, Greenville, NC. February 16, 2001

26. NCAS (North Carolina Academy of Sciences) Meeting. Raleigh, NC. March 31-April 2, 2000

Selected Poster Presentations

1. The ENCODE and modENCODE Consortia Meeting, Crystal City, VA. May 23-25, 2011

2. The Biology of Genomes Meeting, Cold Spring Harbor, NY. May 10-14, 2010

3. The Genome Informatics Meeting, Hinxton, UK. September 14-18, 2010
4. The Biology of Genomes Meeting, Cold Spring Harbor, NY. May 11-15, 2010
5. The ENCODE Consortium Meeting. Bethesda, MD. March 12, 2010.
6. National Human Genome Research Institute, National Institutes of Health, Scientific Retreat, Gettysburg, PA. November 17-18, 2009.
7. The 16th Conversation: Journal of Biomolecular Structure and Dynamics. Albany, NY. June 16-20, 2009
8. National Institutes of Health, National Graduate Student Research Festival. Bethesda, MD. September 10-12, 2008
9. Boston University Science and Engineering Symposium. Boston, MA. March 31, 2008
10. The 15th Conversation: Journal of Biomolecular Structure and Dynamics 24(6):716. Albany, NY. June 19-23, 2007
11. The Biology of Genomes Meeting, Cold Spring Harbor, NY. May 8-12, 2007 (**Genome Research Best Poster Award**)
12. 6th International Workshop on Bioinformatics and Systems Biology. Boston, MA. July 24-26, 2006
13. ENCODE Consortium Meeting. Bethesda, MD. July 5-7, 2006 (two posters)
14. 5th International Workshop on Bioinformatics and Systems Biology. Berlin, Germany. August 22-25, 2005
15. ENCODE Consortium Meeting. Gaithersburg, MD. July 18-19, 2005
16. The 14th Conversation: Journal of Biomolecular Structure and Dynamics 22(6):828. Albany, NY. June 14-17, 2005
17. SICB (Society for Integrative and Comparative Biology) meeting. Chicago, IL. January 3-7, 2001
18. East Carolina University Research Day. Greenville. NC, April 3, 2000 (**Best Poster Award**)
19. SICB (Society for Integrative and Comparative Biology) meeting. Atlanta, GA. January 4-8, 2000