Matthew Shirley, Ph.D.

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Education

2013 - Ph.D. Biochemistry, Cellular, and Molecular Biology, Johns Hopkins School of Medicine, Baltimore MD

2008 - B.S. Biochemistry, University of Missouri, Columbia MO

Research

- **2013-Current** - Postdoctoral Fellow, Department of Oncology, Johns Hopkins School of Medicine, Baltimore MD

  Working in the labs of Drs. Sarah Wheelan and Vasan Yegnasubramanian I developed computational tools for the analysis of novel high-dimensional sequencing methods. We applied these tools to prostate cancer biomarker discovery.

- **2008-2013** - Ph.D. Candidate, Department of Biochemistry, Cellular, and Molecular Biology, Johns Hopkins School of Medicine, Baltimore MD

  *As a graduate student I started research with Drs. Jin Zhang and Heng Zhu in the Department of Pharmacology at Johns Hopkins School of Medicine. Using the protein microarrays pioneered by the Zhu lab we interrogated the kinome for novel kinase-substrate interactions. I continued my graduate research in the lab of Dr. Jonathan Pevsner at Kennedy Krieger Institute where I characterized the extent of genetic variability in lymphoblast cell lines. My research culminated in the discovery of a somatic mutation in **GNAQ** which is found only in affected tissues from patients with the Sturge-Weber syndrome. This work spanned wet-lab and computational work involving microarray design and analysis as well as DNA resequencing assay design, high-dimensional data analysis, and tool development.*

- **2006-2008** - Research Assistant, Department of Biochemistry, University of Missouri, Columbia MO

  *In my third year of college at the University of Missouri I joined the lab of Dr. Judy Wall in the Department of Biochemistry. In the Wall lab I worked on characterizing the molecular genetics of the bacterium **Desulfovibrio vulgaris** Hildenborough for its potential in heavy metal bioremediation. My work involved characterizing a Tn5 transposon mediated mutant library, as well as operation and configuration of a gas chromatagraph.*

Peer-Reviewed Publications

See a full of publications at Google Scholar.

- **Shirley MD**, Tang H, Gallione CJ, Baugher JD, Frelin LP, Cohen B, North PE, Marchuk DA, Comi AM, Pevsner J. *Sturge–Weber Syndrome and Port-Wine Stains Caused by Somatic Mutation in GNAQ*. New England Journal of Medicine. 2013. PMID: 23656586.

- R.H. Newman, J. Hu, H. Rho, Z. Xie, C. Woodard, J. Neiswinger, C. Cooper, **M. Shirley** et al. *Construction of human activity-based phosphorylation networks*. Molecular Systems Biology. 2013. PMID: 23549483 Open Access.

- Stevens EL, Baugher JD, **Shirley MD**, Frelin LP, Pevsner J. *Unexpected Relationships and Inbreeding in HapMap Phase III Populations*. PLoS ONE. 2012. PMID: 23185369.

- **Shirley MD**, Baugher JD, Stevens EL, Tang Z, Gerry N, Beiswanger CM, Berlin DS, Pevsner J. *Chromosomal variation in lymphoblastoid cell lines*. Human Mutation. 2012. PMID: 22374857

Software

- pyfaidx: efficient pythonic random access to fasta subsequences. figshare. 10.6084/m9.figshare.972933

- fastqp: Simple FASTQ and SAM read quality assessment and plotting using Python.

- hamstring: Python module for generating Hamming7,4 error-correcting DNA barcodes. Based on work by Leonid Bystrykh.

- triPOD: web interface for the triPOD analysis developed by Joe Baugher et al.

- sra toolkit: Galaxy tool definitions for NCBI SRA Toolkit

- ncbi epigenomics: Galaxy interface to NCBI Epigenomics

Grants

- 2013 - AWS in Education Grant, supporting *Introduction to Python* short course in the Center for Computational Genomics

Teaching

- **2013-Current** - Instructor, Center for Computational Genomics, Johns Hopkins School of Medicine, Baltimore MD

- **2013-Current** - Instructor, Bioinformatics & Computational Biology Department, Foundation for Advanced Education in the Sciences, Bethesda MD

Titles of talks link to slides.

- Biotrac45: Bioinformatic Analysis of Next Generation Sequencing Data, Galaxy for Next Generation Sequencing Analysis, April 8, 2014, FAES, Bethesda MD

- Introduction to Pythonˆ: data structures and flow control, October 28 2013, Center for Computational Genomics, Baltimore MD

- Introduction to Pythonˆ: functions, classes, and I/O, October 30 2013, Center for Computational Genomics, Baltimore MD
  ˆ *Supported by AWS in Education Grant award*

- BIOF503: Make Striking Figures and Analyze Data with R, Spoon-Fed R, October 24 2013, FAES, Bethesda MD

- BIOF309: Introduction to Python, Interfacing R and Python using Rpy2, May 2 2013, FAES, Bethesda MD

- BIOF309: Introduction to Python, Hello web: Accessing databases and APIs using Biopython, April 25 2013, FAES, Bethesda MD

- BIOF309: Introduction to Python, Reading, processing, and writing high throughput sequencing data, April 18 2013, FAES, Bethesda MD

- BIOF521: Bioinformatics for analysis of data generated by NGS, Galaxy for Next Generation Sequencing Analysis, February 6 2013, FAES, Bethesda MD

- Biotrac45: Bioinformatic Analysis of Next Generation Sequencing Data, Galaxy for Next Generation Sequencing Analysis, July 9 2013, FAES, Bethesda MD

- Biotrac45: Bioinformatic Analysis of Next Generation Sequencing Data, Galaxy for Next Generation Sequencing Analysis, November 12 2012, FAES, Bethesda MD

Seminars

- Computational Genomics Young Investigators Symposium, Deep amplicon sequencing reveals GNAQ 548G>A as the causal somatic mutation in Sturge-Weber syndrome and common port-wine stains, October 17 2013, Center for Computational Genomics, Johns Hopkins School of Medicine, Baltimore MD

- Thesis Seminar, Sturge–Weber syndrome & port-wine stain: Genomic analysis reveals somatic activating mutation in GNAQ as genetic basis for neurocutaneous disorder, May 22 2013, Department of Biochemistry, Cellular, and Molecular Biology, Johns Hopkins School of Medicine, Baltimore MD

- Graduate Student Colloquium, Chromosomal Variation in Lymphoblastoid Cell Lines, December 10 2012, Department of Biochemistry, Cellular, and Molecular Biology, Johns Hopkins School of Medicine, Baltimore MD

Posters

- Graduate Student Association Poster Session, Chromosomal Variation in Lymphoblastoid Cell Lines, April 25 2012, Johns Hopkins School of Medicine, Baltimore MD

- Undergraduate Research Day at the Capitol, Rapid Automated Characterization of Transposon Insertion Mutants in *Desulfovibrio vulgaris* Hildenborough by srnPCR, April 2008, Jefferson City MO

- Undergraduate Research and Creative Achievements Forum, Rapid Automated Characterization of Transposon Insertion Mutants in *Desulfovibrio vulgaris* Hildenborough by srnPCR, 2007, Winner of Chancellor's Award for Excellence in Research, University of Missouri, Columbia MO

- Environmental Stress Pathway Project, Rapid Automated Characterization of Transposon Insertion Mutants in *Desulfovibrio vulgaris* Hildenborough by srnPCR, 2007, Virtual Institute for Microbial Stress and Survival, Lawrence Berkeley National Laboratories, Berkeley CA

Awards

- 2007 - Chancellor's Award for Excellence in Research, Undergraduate Research and Creative Achievements Forum, University of Missouri, Columbia MO