**Desiree S. Wilson**

**Education**

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| Doctorate of Philosophy in Biomedical Sciences | UT Health San Antonio | August 2011 – June 2017 |
| Bachelor of Science in Biology | Univ. Houston-Downtown | August 2007 – May 2011 |

**Certifications**

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| Basic Life Support (BLS)  |  | exp: Jan. 2020 |

**Skills**

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| Environmental safety | HIPAA and patient privacy | CPR/First-aid certified | Medical records |
| Unix/Linux | R programming | C++/Java programming | Git/GitHub |
| Microsoft Office Suite | OS: Linux/Mac/Windows | iPhone + Android | Technology |
| Next-gen seq. analysis | Health informatics analysis | Data analysis | Research |
| DNA/RNA/Protein isolation | ELISA | Immunoblotting | Immunohistochemistry |
| Polymerase chain reaction | Basic cell culture | Cell transfection | Genotyping |
| Team player | Strong organizational skills | Willingness to learn | Patient satisfaction |

**Work Experience**

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| Postdoctoral research fellow | UT Health San Antonio, San Antonio, TX | September 2018 – August 2019 |
| The goal for this project was to identify novel genes directly involved in amelogenesis. I isolated enamel organ epithelial tissue from post mortem C57BL/6 mouse pups from day 0, 2, 5 and 11. After I isolated the RNA from these tissues, the RNA samples were sent to the RNA sequencing core. I used Samtools, FastQC, cutadapt, HT-Seq, and DESeq2 to identify genes differentially expressed at these different developmental time points during amelogenesis (day 0, 2, 5 and 11). Lastly, GSEA and TopGO were used to identify enriched pathways and GO terms. |
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| Postdoctoral research fellow | UT Health San Antonio, San Antonio, TX | June 2017 – August 2018 |
| For this project, I worked closely with a cardiovascular surgeon to identify social determinants associated with poor surgical outcomes in University Hospital System and Audie L. Murphy Memorial VA Hospital patients. Using SQL, I queried Sunrise and CPRS electronic medical records databases to retrieve 11,000+ medical records. Using ArcGIS and R, I linked US Census socioeconomic data to 11,000+ electronic medical records. In R, I built a statistical model that incorporated US Census socioeconomic data to identify variables in the US Census data associated with frailty. My efforts resulted in a $3 million grant from NIH. |
| Graduate research assistant | UT Health San Antonio, San Antonio, TX | August 2011 – June 2017 |
| During my PhD graduate years, I worked with Drs. Ian Thompson and Robin Leach on identifying gene expression differences between men with metastatic prostate cancer and men who are in remission for prostate cancer post-prostatectomy. I isolated RNA and DNA from frozen prostatectomy samples. Illumina microarray was used for whole transcriptome analysis. GWAS was performed on DNA and I isolated methylated regions in the DNA to perform MBDcap sequencing. Using R on the RNA data, we identified 28 genes significantly different between remission vs metastatic prostate cancer patient groups. Project resulted in publications as well as federal funding from NIH. Additionally, we found two SNPs associated with Gleason in our preliminary GWAS data. Regarding the MBDcap sequencing data, we created a new tool to analyze MBDCap sequencing data. |
| Undergrad research assistant | MD Anderson, Houston, TX | January 2011–July 2011  |
| Investigated miRNA regulation of IGF1R expression. Using immunoblotting, PCR, ChIP, cell transfection, I worked with Dr. Hesham Amin and we investigated the regulation of IGF-IR and IGF-IIR in the insulin-like growth factor system of lymphoma and leukemia cell lines. No IGF2R mutations were discovered in these cell lines. Results of these projects were published in peer-reviewed journals.  |
| Undergrad research assistant | Baylor College of Medicine, Houston, TX | August 2010 – December 2010  |
| Screened for mutations in ZPBP1 and KLHL-10 genes in idiopathic infertile male human patient samples to determine whether such mutations give rise to male infertility. I transferred to a different lab before receiving the sequence. |
| Baylor SMART Fellow | Baylor College of Medicine, Houston, TX | May 2010 – August 2010  |
| Screened for mutations in SPAG 16 gene in idiopathic infertile male patient samples to determine if such mutations contribute to male infertility. One male infertile patient exhibited one amino acid change however could be a polymorphism that occurs in the normal fertile male patient samples. |
| Welch scholar | Univ. of Houston-Downtown, Houston, TX | June 2008 to August 2008 |
| Created nickel hydroxide films to sense different chemicals in alkaline media. The purpose of this research was to create an effective, cost efficient film to detect various chemicals in alkaline media. Results revealed the film could possibly make rocket launches and hydrogen peroxide fuel cells more efficient |
| Undergrad research assistant | San Jacinto College-North, Houston, TX | June 2007 – July 2007 |
| Located alluvial fans in the Uinta Basin in Northeastern Utah. Searched for burn horizons in the alluvial fans. Located charcoal in the burn horizons to find quantitative evidence of frequent fires and debris deposits in the alluvial fans. Discovered chronological inversion in two of the eleven alluvial fan locations. |

**Funding**

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| August 2011 to August 2012 | Initiative for Maximizing Student Development Grant Awardee #1R25GM095480-01 | National Institutes of Health | Amount: $30,100.00 |
| January 2010 | LSA1/LSMA: Alliance for Minority Participation | University of Houston-Downtown | Amount: $1,110.00 |
| August 2009 to August 2010 | National SMART Grant | U.S. Department of Education | Amount $6,000.00 |
| August 2009 to August 2010 | Red Rose Scholarship | University of Houston-Downtown | Amount: $3,000 |
| January 2009 to May 2011 | MARC U\*STAR scholarship | National Institutes of Health | Amount: $4,500.00 |
| August 2007 to August 2009 | Scholars Academy STEP Grant | US Army Research Office-Infrastructure Support Program-Urban Center for Student Success (UCSS) | Amount: $8,000.00 |
| January 2008 | Rising to the Challenge Scholarship | University of Houston-Downtown | Amount: $500.00 |
| August 2008 | Jones Scholarship | University of Houston-Downtown | Amount: $750.00 |

**Presentations**

**Wilson D**, Livi C, Chen Y, Hernandez J, Thompson IM, and Leach RJ. (June 2014) Gene Expression Profiling of Definitive Prostate Cancer Outcomes. Bioinformatics & Pharmacogenomics: Managing and Analyzing Big Data Conference. (poster)

**Wilson D**, Livi C, Chen Y, Hernandez J, Thompson IM, and Leach RJ. (October 2014) Gene Expression Profiling of Definitive Prostate Cancer Outcomes. National Cancer Institute Early Detection Research Network 9th Annual Scientific Workshop. (poster)

**Publications**

Hariharan N, Ashcraft K, Svatek RS, Livi C, **Wilson D**, Kaushik D, Leach RJ and Johnson-Pais TL. Adipose tissue secreted factors alter bladder cancer cell migration. Journal of Obesity, 2018; 2018:9247864.

Liu Y, **Wilson** D, Leach RJ, Chen Y. MBDDiff: an R package designed specifically for processing MBDcap-seq datasets. BMC Genomics, 2016; 17(Suppl 4):432.

Wang Y, Jadhav RR, Liu J, **Wilson D**, Chen Y, Thompson IM, Troyer DA, Hernandez J, Shi H, Leach RJ, Huang TH, Jin VX. Roles of Distal and Genic Methylation in the Development of Prostate Tumorigenesis Revealed by Genome-wide DNA Methylation Analysis. Scientific Reports, 2016; 6:22051.

Blackburn A, **Wilson D,** Gelfond J, Yao L, Hernandez J, Thompson IM, Leach RJ, Lehman DM. Validation of copy number variants associated with prostate cancer risk and prognosis. Urologic Oncology, 2014; Jan;32(1):44.e15-20

Vishwamitra D, Shi P, **Wilson D**, Manshouri R, Vega F, Schlette EJ, Amin HM. [MicroRNA 96 is a post-transcriptional suppressor of anaplastic lymphoma kinase expression.](http://www.ncbi.nlm.nih.gov/pubmed/22414602) The American Journal of Pathology, 2012; 180(5):1772-1780.

Vishwamitra D, Li Y, **Wilson D**, Manshouri R, Curry CV, Shi B, Tang XM, Sheehan AM, Wistuba II, Shi P, Amin HM. Expression and Effects of Inhibition of IGF-IR Tyrosine Kinase in Mantle Cell Lymphoma. Haematologica, 2011; 96(6):871-880.

**Organizations**

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| 2012 to 2016 | Association for Computing Machinery (ACM). |