### **BIOGRAPHICAL SKETCH**

Provide the following information for the Senior/key personnel and other significant contributors. Follow this format for each person. DO NOT EXCEED FIVE PAGES.

NAME: Primerano, Donald Anthony

eRA COMMONS USER NAME (credential, e.g., agency login): primeran

POSITION TITLE: Professor and Interim Chair, Dept. of Biochemistry and Microbiology

EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
St. Vincent College, Latrobe PA	B.S.	05/1976	Biology
Duke University, Durham NC	Ph.D.	10/1982	Microbiology
Michigan State University	Postdoc	11/1988	Yeast gene regulation

### A. Personal Statement

My primary research interests are in the discovery of chronic disease susceptibility genes using next generation sequencing, expression profiling and bioinformatic approaches. I currently serve as the Co-Director of the Genomics and Bioinformatics Core Facility (GABC) and as a member of the WV-IDeA Network of Biomedical Research Excellence (WV-INBRE) Administrative Core and WV Cancer Genomics Steering Committee. I have served as the Genomics Core Director from 1999-2011. As Co-Director, I have experience in (1) developing sequencing strategies and service relationships between the GABC and research networks needing genomic analyses, (2) providing overall direction to a core with evolving technologies and institutional responsibilities, (3) assisting individual investigators in designing genomic experiments and (4) providing training in genomic technologies.

In the COBRE application (Obesity Research Center of Appalachia), the primary goal of the GABC will be to support the genomic research goals of project investigators and other Marshall investigators. The GABC provides the following services:

- 1) high throughput next generation sequencing (NGS) to support RNA-Seq, whole exome, whole genome, microbiome and methylation studies
- 2) bioinformatic and biostatistical support for NGS and microarray projects
- 3) automated Sanger DNA sequencing and genotyping and RNA/DNA quality assessment
- 4) access to real time thermal cyclers for quantitative PCR
- 5) workshops on next generation sequencing methods, bioinformatics and biostatistical methods central to investigator research projects.

During the period from 1999 to the present, the GABC has successfully supported to the goals of the several funded programs: WVBRIN, WV-INBRE Phase I, WV-INBRE phase II, COBRE Transcription Factors and Cancer, and the WV Cancer Genomics Network. Under my direction, the GABC has launched next generation sequencing as a state-wide service and completed several NGS projects including microbiome, RNA-Seq, whole exome sequencing and whole genome sequencing. These experiences and accomplishments will enable GABC staff and me to design RNA-Seq and other genomic studies to support the research objectives of projects within this COBRE application. The following publications illustrate the roles of the GABC in genomic analyses.

- 1. Cockburn AF, Dehlin JM, Ngan T, Crout R, Boskovic G, Denvir J, **Primerano D**, Plassman BL, Wu B, Cuff CF. (2012) High throughput DNA sequencing to detect differences in the subgingival plaque microbiome in elderly subjects with and without dementia. Investigative Genetics 3:19. PMCID: PMC3488532, PMID: 22998923.
- 2. **D. Primerano,** G. Boskovic, J. Fan, J. H. Kim and J.Denvir. (2012) Potential Susceptibility Variants for Obesity and Type 2 Diabetes in the TALLYHO Mouse. J Biomolecular Tech. 23(Suppl): S41. PMCID: PMC3630602.
- 3. LL Richards-Waugh, **DA Primerano**, Y Dementieva, JC Kraner, and GO Rankin. (2014) Fatal Methadone Toxicity: Potential Role of CYP3A4 Genetic Polymorphism. J Anal Toxicol. 38(8):541-7. doi: 10.1093/jat/bku091. PMID: 25217544. PMCID: PMC4229888
- 4. TB Salisbury, JK Tomblin, **DA Primerano**, G Boskovic, J Fan, J Fletcher, N Santanam, E Hurn, GZ Morris, and J Denvir. (2014) Endogenous aryl hydrocarbon receptor promotes basal and inducible expression of tumor necrosis factor target genes in MCF-7 cancer cells. Biochem Pharmacol 91:390-9. doi: 10.1016/j.bcp.2014.06.015. Epub 2014 Jun 24. PMID: 24971714 PMCID: PMC4157967.
- 5. Miranda B. Carper, James Denvir, Goran Boskovic, **Donald A. Primerano**, and Pier Paolo Claudio. RGS16, a novel p53 and pRb cross-talk candidate inhibits migration and invasion of pancreatic cancer cells. Genes and Cancer 5:420-435 (2014) [PMID: 25568667 [PubMed] PMCID: PMC4279439]
- 6. Denvir J, Neitch S, Fan J, Niles RM, Boskovic G, Schreurs BG, **Primerano DA**, and Alkon DL. Identification of the PS1 Thr147lle Variant in a Family with Very Early Onset Dementia and Expressive Aphasia. J Alzheimer's Dis. 2015 Mar 26. PMID: 25812849 [Epub ahead of print, in press]

#### **B.** Positions and Honors

# **Positions and Employment**

1975	Laboratory assistant in Microbiology at the Pittsburgh Public Health Labs
1975 - 1976	Teaching assistant in Microbiology at St. Vincent College.
1976 - 1982	Predoctoral fellow in Microbiology and Immunology (mentor, Dr. R. O. Burns) and member of
	the University Program in Genetics, Duke University
1982 - 1988	Research Associate, Department of Microbiology and Public Health (mentor, P.T. Magee)
	Michigan State University
1988 - 1994	Assistant Professor, Marshall University School of Medicine
1994 - 1998	Associate Professor, Marshall University School of Medicine
1998 - pres.	Professor, Joan C. Edwards School of Medicine at Marshall University
	Director of Marshall University Genomics Core Facility (1991- present)
	Director of Appalachian Cardiovascular Research Network (2000 – present)
2005 - pres.	Section Head, Division of Microbiology, Joan C. Edwards School of Medicine
2014 - pres.	Interim Chair, Department of Biochemistry and Microbiology

# Other Experience and Professional Memberships

1990-1999	Director of MU DNA Core Facility
1999-2011	Director of MU Genomics Core Facility
1999-	Member, WV-INBRE Steering Committee
2000-	Member, American Society of Human Genetics
2003 -2014	Director of the Appalachian Cardiovascular Research Network
2008-	Member, Association of Biomolecular Resource Facilities
2011-	Co-Director, Genomics and Bioinformatics Core Facility

# Honors:

1999: Professor of the Year given by the Medical School Class of 2001

2004: Graduate Faculty Achievement Award given by the MU Graduate Student Organization

2009: Certificate of Teaching Excellence awarded by the MU Joan C. Edwards School of Medicine

## C. Contributions to Science

Over the past five years in my capacity as co-director of the Genomics and Bioinformatics Core Facility, I have collaborated with biomedical investigators to identify and characterize global molecular and cellular responses as well as changes in microbial communities. These collaborations have involved the use of Next Generation Sequencing (such as RNA-Seq expression profiling, whole exome and microbiome analysis), microarray methods and variant genotyping.

[1] In collaboration with Travis Salisbury PhD, a set of 600 AHR-dependent genes (ADGs) whose expression is regulated by unliganded AHR were identified by RNA-Seq differential expression profiling. Ingenuity Pathway Analysis revealed that the ADGs were significantly enriched in dioxin and tumor necrosis factor (TNF) pathways. AHR was shown to be required for TNF induction of MNSOD and the cellular response to cytotoxicity in MCF-7 breast cancer cells. This latter result suggests a novel role for AHR in cancer progression as a mediator of TNF and antioxidant responses.

1. TB Salisbury, JK Tomblin, DA Primerano, G Boskovic, J Fan, J Fletcher, N Santanam, E Hurn, GZ Morris, and J Denvir. Endogenous aryl hydrocarbon receptor promotes basal and inducible expression of tumor necrosis factor target genes in MCF-7 cancer cells. Biochem Pharmacol 91:390-9 (2014). doi: 10.1016/j.bcp.2014.06.015. Epub 2014 Jun 24. PMID: 24971714 PMCID: PMC4157967.

[2] In collaboration with Christopher Cuff PhD, an association between oral microbiome and cognitive function was investigated by determining the relative abundance of bacterial species present in subgingival plaque from older adults with or without dementia. The V3 variable region of the microbial 16S bacterial ribosomal RNA gene was amplified from the genomic DNA of subgingival microbes and sequenced on an Illumina HiSeq1000 System. Quantitative Insights Into Microbial Ecology (QIIME) software was used to make taxonomic assignments and measurements of microbial diversity. Although taxa differences did not reach statistical significance, a consistently higher level of Fusobacteriaceae and a generally lower level of Prevotellaceae was seen in subjects without dementia.

1. Cockburn AF, Dehlin JM, Ngan T, Crout R, Boskovic G, Denvir J, Primerano D, Plassman BL, Wu B, Cuff CF. (2012) High throughput DNA sequencing to detect differences in the subgingival plaque microbiome in elderly subjects with and without dementia. Investigative Genetics 3:19. PMCID: PMC3488532, PMID: 22998923.

## Complete List of Published Work in MyBibliography:

Public URL (tested prior to submission) for the Complete List of my published work (MyBibliography) is <a href="http://www.ncbi.nlm.nih.gov/sites/myncbi/donald.primerano.1/bibliography/47150066/public/?sort=date&direction=ascending">http://www.ncbi.nlm.nih.gov/sites/myncbi/donald.primerano.1/bibliography/47150066/public/?sort=date&direction=ascending</a>

## D. Research Support

## **Ongoing Research Support**

Title: WV Cancer Genomics Network

Agency: WV Higher Education Policy Commission Research Challenge Grant

Period: 07/01/2012 to 06/30/2017 Role: Co-P.I. (PP Claudio P.I.)

Goal: The goal of the network is to develop a repository of cancer tissues and study the genomic and

epigenomic events that cause cancers prevalent in West Virginia

Grant #: 2P20GM103434-14

Title: West Virginia IDeA Networks of Biomedical Research Excellence Phase III

Subproject: Genomics and Bioinformatics Core (GABC)

Period: 9/19/14 - 7/31/19 Agency: NIH/NIGMS

Role: Co-P.I. (G. Rankin, P.I.)

Goal: The primary goal of the GABC is to enable the genomic research goals of individual and

program project research grants.

# **Completed Research Support**

Grant #: 2P20

Title: COBRE Administrative Supplement: WV Cancer Genetics Network

Period: 10/1/09 -08/31/2011

Agency: NIH/NCRR

Role: Co-P.I. (R. Niles, P.I.)

Grant #: NA

Title: Translational Genomic Research Institute (Next Generation Sequencing)

Agency: Health Resources and Services Administration

Role: Next Gen Sequencing Facility Director.

Goal: The goal of this supplement was to develop next generation sequencing which will aid in the

identification of cancer and cardiovascular susceptibility genes

Grant #: 2P20GM103434

Title: West Virginia IDeA Networks of Biomedical Research Excellence Phase II

Subproject: Appalachian Cardiovascular Research Network

Period: 5/1/09 - 7/30/14 Agency: NIH/NIGMS

Role: Co-P.I. (G. Rankin, P.I.)

Goal: The goal was to develop research projects which characterized the genetic and environmental

bases of vascular disease