# Visanu Wanchai

4301 W. Markham St., #782 Little Rock, AR 72205-7199 (501) 686 6023 VWanchai@uams.edu

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Education Ph.D. Biomedical Informatics, University of Arkansas for Medical Sciences (UAMS), Little Rock, Arkansas	2017 – Pres.
M.S. Bioinformatics and Systems Biology King Mongkut's University of Technology Thonburi (KMUTT), Bangkok, Thailand	2011
B.S. Computer Science (summa cum laude) Mae Fah Luang University, Chiang Rai, Thailand	2008
Current Position Research Associate Arkansas Center for Genomic Epidemiology & Medicine (ArC-GEM) University of Arkansas for Medical Sciences (UAMS) Little Rock, Arkansas	2016 – Pres.
Professional Experience Programmer The BioEnergy Science Center (BESC) Oak Ridge National Laboratory Oak Ridge, Tennessee	2014 – 2016
Research Assistant Pilot Plant Development and Training Institute (PDTI) King Mongkut's University of Technology Thonburi (KMUTT) Bangkok, Thailand	2011 – 2014
Master's Student Intern Center for Biological Sequence Analysis (CBS) Technical University of Denmark (DTU) Copenhagen, Denmark	2010 – 2011
Intern Optimus Soft Company, Ltd. Bangkok, Thailand	2007 – 2008
Honors and Awards MCBIOS 2018 Student Travel Award, Supported from the Arkansas INBRE grant from NIGMS (P20 GM103429) at NIH	2018
Master's degree scholarship in Bioinformatics and Systems Biology King Mongkut's University of Technology Thonburi (KMUTT) Bangkok, Thailand	2008
Outstanding student award, Mae Fah Luang University, Thailand	2007

Educational Activities	
Invited speaker, BMIG 5003 Computational Methods for Informaticists, University of Arkansas for Medical Sciences (UAMS), Little Rock, Arkansas	2019
Invited speaker, UALR & UAMS Genomics Workshop, University of Arkansas for Medical Sciences (UAMS), Little Rock, Arkansas	2019
Invited speaker, BMIG 5101 Foundations of BMI: Sequences as Biological Information University of Arkansas for Medical Sciences (UAMS), Little Rock, Arkansas	2018
Invited speaker, UALR & UAMS Genomics Workshop, University of Arkansas for Medical Sciences (UAMS), Little Rock, Arkansas	2018
Invited speaker, Advanced course on Comparative Genomics & Metagenomics, Faculty of Medicine, Siriraj Hospital, Mahidol University, Thailand	2017
Organizer, Oxford Nanopore MinION workshop, Department of Biological Science, University of Arkansas, Fayetteville, Arkansas	2017
Invited speaker, UALR & UAMS Genomics Workshop, University of Arkansas for Medical Sciences (UAMS), Little Rock, Arkansas	2017
Invited speaker, PhD-course MOL8013 Bacterial genomics, Department of Laboratory Medicine, Children's and Women's Health, Faculty of Medicine, NTNU, Norway	2017
Invited speaker, PhD-course MOL8013 Bacterial genomics, Department of Laboratory Medicine, Children's and Women's Health, Faculty of Medicine, NTNU, Norway	2016

#### Patent

Charles Parker, George Garrity, David Ussery, <u>Visanu Wanchai</u>, and Intawat Nookaew. Method for Identification and Characterization of Prokaryotes Using Whole Genome DNA Sequence Data. US Provisional Patent Application No. 62/232,925. Filed September 25, 2015. Washington, DC: U.S. Patent and Trademark Office.

#### **Publications**

- 1. <u>Visanu Wanchai</u>, Jing Jin, Emine Bircan, Charis Eng and Mohammed Orloff. **Genome-wide tracts of homozygosity and exome analyses reveal repetitive elements with Barrets esophagus/esophageal adenocarcinoma risk.** BMC Bioinformatics. BioMed Central; 2019;20:98.
- 2. Trudy M. Wassenaar, <u>Visanu Wanchai</u>, Gregory S. Buzard and David W. Ussery. **In silico Selection of Amplification Targets for Rapid Polymorphism Screening in Ebola Virus Outbreaks.** Front. Microbiol. Frontiers; 2019;10:857.
- 3. Adriana Cabal, Se-Ran Jun, Piroon Jenjaroenpun, <u>Visanu Wanchai</u>, Intawat Nookaew, Thidathip Wongsurawat, Mary J. Burgess, Atul Kothari, Trudy M. Wassenaar and David W. Ussery. **Genome-Based Comparison of Clostridioides difficile: Average Amino Acid Identity Analysis of Core Genomes.** Microb. Ecol. Springer US; 2018;76:801–13.
- 4. Thidathip Wongsurawat, Piroon Jenjaroenpun, Trudy M. Wassenaar, Taylor D. Wadley, <u>Visanu Wanchai</u>, Nisreen S. Akel, Aime T. Franco, Michael L. Jennings, David W. Ussery and Intawat Nookaew. **Decoding the Epitranscriptional Landscape from Native RNA Sequences.** bioRxiv. 2018:17:487819.
- 5. Se-Ran Jun, Trudy M. Wassenaar, <u>Visanu Wanchai</u>, Preecha Patumcharoenpol, Intawat Nookaew and David W. Ussery. **Suggested mechanisms for Zika virus causing microcephaly: What do the genomes tell us?** BMC Bioinformatics. BioMed Central; 2017;18:471.
- 6. <u>Visanu Wanchai</u>, Preecha Patumcharoenpol, Intawat Nookaew and David W. Ussery. **dBBQs: DataBase of Bacterial Quality scores.** BMC Bioinformatics. BioMed Central; 2017;18:483.

- Se-Ran Jun, Trudy M. Wassenaar, Intawat Nookaew, Loren Hauser, <u>Visanu Wanchai</u>, Miriam Land, Collin M. Timm, Tse-Yuan S. Lu, Christopher W. Schadt, Mitchel J. Doktycz, Dale A. Pelletier and David W. Ussery. <u>Diversity of Pseudomonas Genomes, Including Populus-Associated Isolates, as Revealed by Comparative Genome Analysis.</u> Appl. Environ. Microbiol. American Society for Microbiology; 2016;82:375–83.
- 8. Se-Ran Jun, Michael R. Leuze, Intawat Nookaew, Edward C. Uberbacher, Miriam Land, Qian Zhang, Visanu Wanchai, Juanjuan Chai, Thomas D. Pedersen, Trudy M. Wassenaar and David W. Ussery. **Ebolavirus comparative genomics.** FEMS Microbiol. Rev. Oxford University Press; 2015;39:764–78.

## **Book Chapters**

- 1. Trudy M. Wassenaar, <u>Visanu Wanchai</u>, Duah Alkam, Intawat Nookaew and David W. Ussery. Conservation of Two-Component Signal Transduction Systems in E. coli, Salmonella, and Across 100,000 Bacteria of Various Bacterial Phyla. Mol. Mech. Microb. Evol. Springer, Cham; 2018. p. 153–74.
- 2. Trudy M. Wassenaar, Se-Ran Jun, <u>Visanu Wanchai</u>, Preecha Patumcharoenpol, Intawat Nookaew, Katrina Schlum, Michael R. Leuze and David W. Ussery. **Insights from Comparative Genomics of the Genus Salmonella.** Curr. Top. Salmonella Salmonellosis. InTech; 2017.

## **Published Abstracts, Meetings and Presentations**

## Meeting

#### National/International Meeting

The 21th Genomic Standards Consortium Meeting (GSC21), Vienna, Austria

2019

## **Oral Presentation**

## Local/Regional Meeting

The 14<sup>th</sup> Annual Midsouth Computational Biology and Bioinformatics society conference (MCBIOS2017), Little Rock, Arkansas

2017

<u>Visanu Wanchai</u>, Preecha Patumcharoenpol, Intawat Nookaew and David W. Ussery.
 dBBQs: DataBase of Bacterial Quality scores.

#### **Posters**

#### National/International Meetings

The Young Microbiologist Symposium (YMS2018), Queen's University, Belfast, UK

2018

• <u>Visanu Wanchai</u> and David W. Ussery. **What have we learned from 140,000 bacterial** genomes.

The 8<sup>th</sup> Global Summit on Regulatory Science Conference (GSRS17), Brasilia, Brazil

2017

• <u>Visanu Wanchai</u> and David W. Ussery. **Functional domain analyses of sigma factors** in *Vibrio* genomes.

## Local/Regional Meetings

The 5<sup>th</sup> Arkansas Bioinformatics Consortium Annual Meeting (AR-BIC), Little Rock, Arkansas 2019

- <u>Visanu Wanchai</u> and David W. Ussery. **Using 16S rRNA for Microbial Classification: A** Cautionary Tale.
- Skylar Connor, <u>Visanu Wanchai</u>, Michael Robeson, Trudy Wassenaar and David Ussery. **Ribosomal Proteins for Better Resolution in Microbial Taxonomy.**

The 15<sup>th</sup> Annual Midsouth Computational Biology and Bioinformatics society conference (MCBIOS2018), Starkville, Mississippi

2018

- <u>Visanu Wanchai</u>, Jing Jin, Emine Bircan, Tianjiao Shen, and Mohammed Orloff.
   <u>Identifying repetitive elements associated BE/EAC-related traits using exome sequencing data.</u>
- <u>Visanu Wanchai</u> and David W. Ussery. Analyses of genome quality scores across 120,000 genomes.
- Jing Jin, Emine Bircan, <u>Visanu Wanchai</u>, Tianjiao Shen, Ebrahim Jakoet and Mohammed Orloff. **Tracts of Homozygosity and Linkage Disequilibrium Profiles in Lung Cancer.**
- Tianjiao Shen, Jing Jin, Emine Bircan, <u>Visanu Wanchai</u> and Mohammed Orloff.
   Integrative Genomic Analysis of MARCO, EPAS1, SFTPB, KCNK3, ACADL with Lung Cancer.
- Skylar Connor, <u>Visanu Wanchai</u>, Michael Robeson, Trudy Wassenaar and David Ussery.
   Towards a Better Resolution in <u>Microbial Taxonomy</u>: 16S rRNA Trees vs
   Ribosomal Protein Trees.

The 4<sup>th</sup> Arkansas Bioinformatics Consortium Annual Meeting (AR-BIC), Little Rock, Arkansas

2018

• <u>Visanu Wanchai</u> and David W. Ussery. **Analyses of genome quality scores across** 120.000 genomes.

The South Central Branch of American Society for Microbiology Annual Meeting (ASM), Little Rock, Arkansas 2017

- <u>Visanu Wanchai</u> and David W. Ussery. What is Life? Conserved Functional Domains Across All Life.
- Kaleb Abram, <u>Visanu Wanchai</u>, Se-Ran Jun, Intawat Nookaew and David Ussery. **Pangenome Analysis Methodology Comparison Using** *Salmonella*.
- Skylar Connor, <u>Visanu Wanchai</u>, Michael Robeson, Trudy Wassenaar and David Ussery. **Ribosomal Proteins for Better Resolution in Microbial Taxonomy.**
- Duah Alkam, Thidathip Wongsurawat, Piroon Jenjaroenpun, <u>Visanu Wanchai</u>, Preecha Patumcharoenpol, Intawat Nookaew, David Ussery, Trudy Wassenaar, Michael Robeson and Se-Ran Jun. **Rapid Genome-Based Surveillance for the Mumps Virus**.