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	2020
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 Postdoctoral fellowship Department of Biomedical Informatics, College of Medicine University of Arkansas for Medical Sciences (UAMS) Little Rock, Arkansas	2021 – Pres.
Professional Experience Research Associate Department of Biomedical Informatics, College of Medicine University of Arkansas for Medical Sciences (UAMS) Little Rock, Arkansas	2016 – 2021
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
Professional Affiliations Member, American Society for Microbiology (ASM)	

Member, Genomic Standard Consortium (GSC)

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, UALR & UAMS Genomics Workshop, University of Arkansas for Medical Sciences (UAMS), Little Rock, Arkansas	2021
Invited speaker, SIRE-BIF co-seminar, Mahidol University & King Mongkut's University of Technology Thonburi, Thailand	2021
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

Provisional 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

- Wassenaar, Trudy M, Visanu Wanchai, Gregory Buzard, and David W Ussery. 2022. "The First Three Waves of the Covid-19 Pandemic Hint at a Limited Genetic Repertoire for SARS-CoV-2." FEMS Microbiology Reviews, January, fuac003. https://doi.org/10.1093/femsre/fuac003.
- Abram, Kaleb, Zulema Udaondo, Carissa Bleker, <u>Visanu Wanchai</u>, Trudy M. Wassenaar, Michael S. Robeson, and David W. Ussery. 2021. "Mash-Based Analyses of Escherichia Coli Genomes Reveal 14 Distinct Phylogroups." Communications Biology 4 (1): 117. https://doi.org/10.1038/s42003-020-01626-5.
- Jenjaroenpun, Piroon, <u>Visanu Wanchai</u>, Kikumi D. Ono-Moore, Jennifer Laudadio, Laura P. James, Sean H. Adams, Fred Prior, Intawat Nookaew, David W. Ussery, and Thidathip Wongsurawat. 2020.
 "Two SARS-CoV-2 Genome Sequences of Isolates from Rural U.S. Patients Harboring the D614G Mutation, Obtained Using Nanopore Sequencing." Microbiology Resource Announcements 10 (1). https://doi.org/10.1128/mra.01109-20.
- <u>Visanu Wanchai</u>, Intawat Nookaew, and David W. Ussery. 2020. "ProdMX: Rapid Query and Analysis of Protein Functional Domain Based on Compressed Sparse Matrices." Computational and Structural Biotechnology Journal 18: 3890–96. https://doi.org/10.1016/j.csbj.2020.10.023.
- Jenjaroenpun, Piroon, Thidathip Wongsurawat, Taylor D Wadley, Trudy M Wassenaar, Jun Liu, Qing Dai, <u>Visanu Wanchai</u>, et al. 2020. "Decoding the Epitranscriptional Landscape from Native RNA Sequences." Nucleic Acids Research, July. https://doi.org/10.1093/nar/gkaa620.
- Abram, Kaleb, Zulema Udaondo, Carissa Bleker, <u>Visanu Wanchai</u>, Trudy M. Wassenaar, and Dave W. Ussery. 2019. "What Can We Learn from over 100,000 Escherichia Coli Genomes?" BioRxiv, 708131. https://doi.org/10.1101/708131.
- Wassenaar, Trudy M., <u>Visanu Wanchai</u>, Gregory S. Buzard, and David W. Ussery. 2019. "In Silico Selection of Amplification Targets for Rapid Polymorphism Screening in Ebola Virus Outbreaks." Frontiers in Microbiology 10: 857. https://doi.org/10.3389/fmicb.2019.00857.
- 8. <u>Visanu Wanchai</u>, Jing Jin, Emine Bircan, Charis Eng, and Mohammed Orloff. 2019. "Genome-Wide Tracts of Homozygosity and Exome Analyses Reveal Repetitive Elements with Barrets Esophagus/Esophageal Adenocarcinoma Risk." BMC Bioinformatics 20 (S2): 98. https://doi.org/10.1186/s12859-019-2622-y.
- Cabal, Adriana, 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. 2018.
 "Genome-Based Comparison of Clostridioides Difficile: Average Amino Acid Identity Analysis of Core Genomes." Microbial Ecology 76 (3): 801–13. https://doi.org/10.1007/s00248-018-1155-7.
- Jun, Se Ran, Trudy M. Wassenaar, <u>Visanu Wanchai</u>, Preecha Patumcharoenpol, Intawat Nookaew, and David W. Ussery. 2017. "Suggested Mechanisms for Zika Virus Causing Microcephaly: What Do the Genomes Tell Us?" BMC Bioinformatics 18 (S14): 471. https://doi.org/10.1186/s12859-017-1894-3.
- Jun, Se-Ran, Trudy M. Wassenaar, Intawat Nookaew, Loren Hauser, <u>Visanu Wanchai</u>, Miriam Land, Collin M. Timm, et al. 2016. "Diversity of Pseudomonas Genomes, Including Populus-Associated Isolates, as Revealed by Comparative Genome Analysis." Applied and Environmental Microbiology 82 (1): 375–83. https://doi.org/10.1128/aem.02612-15.
- Jun, Se Ran, Michael R. Leuze, Intawat Nookaew, Edward C. Uberbacher, Miriam Land, Qian Zhang, <u>Visanu Wanchai</u>, et al. 2015. "Ebolavirus Comparative Genomics." Edited by Urs Greber. FEMS Microbiology Reviews 39 (5): 764–78. https://doi.org/10.1093/femsre/fuv031.
- <u>Visanu Wanchai</u>, Preecha Patumcharoenpol, Intawat Nookaew, and David Ussery. 2017. "DBBQs: DataBase of Bacterial Quality Scores." BMC Bioinformatics 18 (Suppl 14): 483. https://doi.org/10.1186/s12859-017-1900-9.

Book Chapters

- Wassenaar, Trudy M., <u>Visanu Wanchai</u>, Duah Alkam, Intawat Nookaew, and David W. Ussery. 2018. "Conservation of Two-Component Signal Transduction Systems in E. Coli, Salmonella, and Across 100,000 Bacteria of Various Bacterial Phyla." In Molecular Mechanisms of Microbial Evolution, 153–74. Springer, Cham. https://doi.org/10.1007/978-3-319-69078-0_7.
- Wassenaar, Trudy M., Se-Ran Jun, <u>Visanu Wanchai</u>, Preecha Patumcharoenpol, Intawat Nookaew, Katrina Schlum, Michael R. Leuze, and David W. Ussery. 2017. "Insights from Comparative Genomics of the Genus Salmonella." In Current Topics in Salmonella and Salmonellosis. InTech. https://doi.org/10.5772/67131.

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 th Annual Midsouth Computational Biology and Bioinformatics society conference (MCBIOS2017), Little Rock, Arkansas • Visanu Wanchai, Preecha Patumcharoenpol, Intawat Nookaew and David W. Ussery. dBBQs: DataBase of Bacterial Quality scores.	2017
Posters National/International Meetings The Young Microbiologist Symposium (YMS2018), Queen's University, Belfast, UK • <u>Visanu Wanchai</u> and David W. Ussery. What have we learned from 140,000 bacterial genomes.	2018
 The 8th Global Summit on Regulatory Science Conference (GSRS17), Brasilia, Brazil <u>Visanu Wanchai</u> and David W. Ussery. Functional domain analyses of sigma factors in Vibrio genomes. 	2017
 Local/Regional Meetings The 5th Arkansas Bioinformatics Consortium Annual Meeting (AR-BIC), Little Rock, Arkansas <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 15th Annual Midsouth Computational Biology and Bioinformatics society conference (MCBIOS2018), Starkville, Mississippi <u>Visanu Wanchai</u>, Jing Jin, Emine Bircan, Tianjiao Shen, and Mohammed Orloff. Identifying repetitive elements associated BE/EAC-related traits using exome sequencing data. <u>Visanu Wanchai</u> and David W. Ussery. Analyses of genome quality scores across 120,000 genomes. 	2018
 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, Visanu Wanchai and Mohammed Orloff 	

 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 Microbial Taxonomy: 16S rRNA Trees vs Ribosomal Protein Trees. 	
 The 4th Arkansas Bioinformatics Consortium Annual Meeting (AR-BIC), Little Rock, Arkansas <u>Visanu Wanchai</u> and David W. Ussery. Analyses of genome quality scores across 120,000 genomes. 	2018
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. 	
 The Genomic Science Contractors-Grantees Meeting XIV: USDA-DOE Plant Feedstock Genomics for Bioenergy Meeting, Washington, D.C. Visanu Wanchai, Se-Ran Jun, Intawat Nookaew, Miriam Land, Preecha Patumcharoinpol, Michael Leuze, and David W. Ussery. Plant-Microbe Interfaces: High-Throughput Comparative Genomics for Populusassociated Microbes. 	2016
 The Genomic Science Contractors-Grantees Meeting XIII: USDA-DOE Plant Feedstock Genomics for Bioenergy Meeting, Washington, D.C. Intawat Nookaew, Dan Olsen, Mirko Basen, Manesh Shah, <u>Visanu Wanchai</u>, Cong Trinh, Philip D. Hyatt, Steve D. Brown, Miriam L. Land, Michael R. Leuze, Robert L. Hettich, Robert M. Kelly, Mike Adams, Lee Lynd, David W. Ussery, and Paul Gilna. Integration of Multi-Omic Data for Advanced Consolidated Bioprocesses. Se-Ran Jun, Sanjeev Dahal, Qian Zhang, <u>Visanu Wanchai</u>, Tse-Yuan Lu, Miriam Land, Intawat Nookaew, Chris W. Schadt, Collin M. Timm, Dale A. Pelletier, and David W. Ussery. Plant-Microbe Interfaces: Comparative Genomics of Populus endosphere microbiomes. 	2015