

# **Curriculum Vitae**

## **Intawat Nookaew, Ph.D.**

### **About myself**

I have strong skills in computational biology, bioinformatics and systems biology as demonstrated across a rich and diverse publication and research record. Unlike classically trained computational biologists/bioinformaticians, I have broad experiences in different areas spanning biomedical, clinical, and nutritional research, as well as biotechnology, bioprocess, metabolic engineering, and chemical engineering. I also have experiences in high-performance computing in super computer environment. With this portfolio of expertise includes extensive experimental work and computational analysis. I am uniquely able to successfully collaborate with biologists, clinicians, bioprocess engineers, and computational scientists.

My research has two sides. First is the development of novel advanced algorithms and frameworks to accelerate the utilization and mining for biological interpretation of large-scale data. This would ultimately result in a range of computational tools made available to the research community. I have developed many software packages for large-scale data modeling, integration and visualization. I have provided a web services and two databases that are available in World Wide Web to serve the research community in biologist user-friendly fashions. Moreover, I have also developed several computational analysis pipelines for tailor made analyses in different projects that I have contributed. All of them are open source that have been shared in the research community. Second, to apply the developed tools and pipelines in different research areas. I have gained extensive experiences in collaborations with biomedical researchers, clinical, both nationally and internationally. I have discovered through these collaborations that data analysis is neither sufficient nor satisfying. It is necessary that I become a proficient translator who converts the mathematical-like results to biologist- friendly results. This leads to concrete biological interpretations/understanding that are further evolved to novel findings in various subjects.

### **Personal Data**

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### **Employment**

March 2016 – Present, Associate Professor, Department Biomedical Informatics, University of Arkansas for Medical Sciences, Little Rock, Arkansas, USA.

March 2017 – 2018, Adjunct Associate Professor, Center of Applied Thai Traditional Medicine, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, Thailand.

March 2014 – March 2016, Senior R&D Staff Scientist in Computational Biology/Bioinformatics, Biosciences Division, Oak Ridge National Laboratory (ORNL), Oak Ridge, Tennessee, USA.

Feb 2014 – October 2016, Associate Professor, Chalmers University of Technology, Department of Chemical & Biological Engineering, Sweden.

Nov 2012 – Jan 2014: Assistant Professor, Department of Chemical and Biological Engineering, Chalmers University of Technology, Sweden.

June 2012 – Feb 2014: Bioinformatics Infrastructure for Life Science (BILS) expert, Sweden (Bioinformatics expert).

June 2010 – Oct 2012: Project Leader, Systems Biology, Department of Chemical and Biological Engineering, Chalmers University of Technology, Sweden.

Nov 2008 – June 2010: Postdoctoral Researcher, Systems Biology, Department of Chemical and Biological Engineering, Chalmers University of Technology, Sweden.

Jan 2008 – Oct 2008: Researcher, Pilot Plant Development and Training Institute, King Mongkut's University of Technology Thonburi, Bangkok, Thailand.

### **Education**

Doctor of Engineering (Chemical Engineering) King Mongkut's University of Technology Thonburi, Bangkok, Thailand (30<sup>th</sup> October 2007) *Thesis*: "Unveiling Regulatory and Control Mechanisms of Yeast Lipid Metabolism by Systems Biology Approach"

Doctoral research internship at Center for Microbial Biotechnology (CMB), Technical University of Denmark, Lyngby, Denmark, 2005-2006

Bachelor of Engineering (Chemical Engineering) Suranaree University of Technology, Nakhon Ratchasima, Thailand, 2000

### **Teaching experiences**

Experience from teaching at Master's/PhD's level for 8 years in Systems Biology, Metabolic Engineering, Comparative Genomics, Omics biology, Computational Biology and Bioinformatics subject as listed below.

- Chalmers University of Technology, KMG060 Systems Biology ~50 students, Master/PhD degree course, Fall 2012
- Chalmers University of Technology, KMG060 Systems Biology ~50 students, Master/PhD degree course, Fall 2011
- Chalmers University of Technology, KMG060 Data Acquisition and Handling in Systems Biology ~40 students, Master/PhD degree course, Fall 2010

- Chalmers University of Technology, KMG060 Data Acquisition and Handling in Systems Biology ~40 students, Master/PhD degree course, Fall 2009
- Chalmers University of Technology, KKR063 Metabolic Engineering: design of microbial metabolism ~15 students, Master/PhD degree course, Spring 2011
- Chalmers University of Technology, KKR063 Metabolic Engineering: design of microbial metabolism ~15 students, Master/PhD degree course, Spring 2010
- Chalmers University of Technology, UCM010 Introduction to cell and molecular biology ~40 students, undergraduate course, Spring 2012
- Chalmers University of Technology, KMB065 Molecular Biotechnology ~50 students, undergraduate course, 2012
- Gothenburg university, Advanced course in NGS data analysis, ~40 students graduate course, 2012
- Gothenburg university, Introduction in Bioinformatics ~20 students, graduate course, 2009
- King Mongkut's University of Technology, Thonburi (Thailand), Introduction to Bioinformatics and Systems biology, ~30 students, graduate course, 2008
- Liden University (Netherland), NBIC Metagenomics approaches and data analysis course ~30 students, 2013.
- FEBS International PhD course: Systems Medicine, ~25 students, graduate course, summer 2010
- FEBS International course: Yeast systems biology, ~30 students, graduate course, summer 2011
- University of Tennessee, LFSC615 - Journal Club for Genome science/Technology. 15 students, graduate course, fall 2014
- University of Tennessee, LFSC520 - Genome Science and Technology I, ~30 students, graduate course, fall 2014
- University of Tennessee, LFSC696 - Advanced Topics in Genome science/Technology: Computational Biology in Omics, ~20 students, graduate course, spring 2015
- University of Tennessee, LFSC615 - Journal Club for Genome science/Technology. 15 students, graduate course, fall 2015
- University of Tennessee, LFSC520 - Genome Science and Technology I, ~30 students, graduate course, fall 2015
- University of Tennessee, LFSC696 - Advanced Topics in Genome science/Technology: Computational Biology in Omics, ~15 students, graduate course, spring 2016
- Universidad Autónoma del Estado de Morelos in Mexico, International Course on Systems Biology at Summer 2016
- University of Arkansas for Medical Sciences BIMG6111 – Comparative Microbial genomics, graduate course, Spring 2018, 2019.

### **Supervision experiences**

Supervised/supervising 18 Ph.D. students, 8 Master of Science students, 3 Post-doctoral researchers and 5 research engineers/software engineers. He also obtained a pedagogic

certificate in 2012 in the subject of “Supervision of Research” from Chalmers University of Technology

***PhD student***

- Marta Papini (PhD 2012, Chalmers University of Technology)
- Pramote Chumnanpuen (PhD 2012, Chalmers University of Technology)
- Rasmus Ågren (PhD 2013, Chalmers University of Technology)
- Tobias Österlund (PhD 2014, Chalmers University of Technology)
- Fredrik Karlsson (PhD 2014, Chalmers University of Technology)
- Christoph Knuf (PhD 2014, Chalmers University of Technology)
- Natapol Pornputtpong (PhD 2014, Chalmers University of Technology)
- Kwanjeera Wanichthanarak (PhD 2014, Chalmers University of Technology)
- Kaisa Thorell (PhD 2014, Gothenburg University)
- Fancesco Gatto (PhD 2015, Chalmers University of Technology)
- Saeed Shoaie (PhD 2015, Chalmers University of Technology)
- Leif Väremo (PhD 2016, Chalmers University of Technology)
- Soni Nikulkumar (PhD 2017, Chalmers University of Technology)
- Suresh Poudel (2014 – 2016, PhD Student, University of Tennessee)
- Sanjeev Dahal(2014 – 2016, PhD Student, University of Tennessee)
- Skylar Connor (2016- Present, PhD Student, University of Arkansas for Medical Sciences)
- Duah Alkam (2017- Present, PhD Student, University of Arkansas for Medical Sciences)
- Sangkam Kandel (2016- Present, PhD Student, University of Arkansas Little Rock)
- Taylor D Wadley (2017 - Present, PhD Student, University of Arkansas for Medical Sciences)
- Daniel Acheampong (2018- Present, PhD Student, University of Arkansas Little Rock)
- Pattapon Kunadireck (2019- Present, PhD Student, Chulalongkorn University)

***Visiting PhD student***

- Kanthida Kosonmano (2011, University of Innsbruck)
- Ibrahim El-Semman (2012, Assiut University)

***Master student***

- Hnin Yu (Master thesis 2009, Chalmers University of Technology)
- Leif Väremo Yu (Master thesis 2010, Chalmers University of Technology)
- Kemal Sanli (Master thesis 2010, Chalmers University of Technology)
- Elias Björnson (Master thesis 2013, Chalmers University of Technology)
- Hedieh Nasser (Master thesis 2011, Gothenburg University)
- Shaghayegh Hosseini (Master thesis 2012, Gothenburg University)
- Selam Tesfaye (Master thesis 2012, Chalmers University of Technology)
- Qian Zhang (Master thesis 2016, University of Tennessee)

- Pantakan Puengrang (Master thesis 2018, King Monkut's University of Technology, Thonburi)

### ***Bachelor student***

- Conor Purvis (2017, Harding University)
- Joseph A Koon (2017, University of Arkansas for Medical Science)
- Ana Swaringen (2018, Harding University)

### ***Post Doctoral researcher***

- Pirroon Jenjaroenpun (2017 – Present, University of Arkansas for Medical Sciences)
- Thidathip Wongsurawat (2017 – Present, University of Arkansas for Medical Sciences)
- Se-Ran Jun (2014 – 16, Oak Ridge National Laboratory)
- Partho SenPhD (2014-2017, Chalmers University of Technology)
- Manuel Gracia PhD (2012-2014, Chalmers University of Technology)
- Subazini Tankaswamy PhD (2012-2014, Chalmers University of Technology)

### ***Research Engineer***

- Manesh Shah (2014 – Present, Oak Ridge National Laboratory)
- Visanu Wanchai (2014 – Present, Oak Ridge National Laboratory/University of Arkansas for Medical Sciences)
- Preecha Patumcharoenpol (2015 – 2017, Oak Ridge National Laboratory University of Arkansas for Medical Sciences)
- Shaghayegh Hosseini (2013-2014, Chalmers University of Technology)
- Avlant Nilsson (2012-2013, Supervisor, Chalmers University of Technology)

### **Reviewer and editor for journals**

- GigaScience (reviewer)
- Briefing in Bioinformatics (reviewer)
- Bioinformatics (reviewer)
- PLOS computational biology (reviewer)
- Molecular Biosystems (reviewer)
- Microbiology (reviewer)
- Nucleic Acids Research (reviewer)
- PLOS one (reviewer)
- Genomics Proteomics and Bioinformatics (reviewer)
- Bioprocess and Biosystems Engineering (reviewer)
- Molecular Biology Reports (reviewer)
- Protein and peptides Letter (reviewer)
- BMC systems Biology (reviewer)
- BMC Bioinformatics (reviewer)
- BMC Genomics (reviewer)

- BioMedical Research International (reviewer)
- ISME (reviewer)
- Biotechnology and Biofuel (reviewer)
- Standard in Genomics Science (reviewer)
- npj Systems Biology and Applications (reviewer)
- International Journal of Genomics (guest editor)
- Bioenergy Research (guest editor)
- BioMed Research International (guest editor)
- Advances in Biochemical Engineering/Biotechnology (volume editor)
- Molecular Genetics and Genomics (reviewer)
- Infection, Genetics and Evolution (reviewer)
- Siriraj Medical Journal (International Editorial Board)
- Frontiers in Cellular and Infection Microbiology (reviewer)

### **Reviewer for National and International Research Grant Application**

- Portuguese research council (Fundação para a Ciência e a Tecnologia), 2012
- The Netherlands Organisation for Scientific Research (NWO), 2014
- Bioinformatics Pilot Project Reviewer for South Carolina IDeA Networks of Biomedical Research Excellence (SC INBRE), 2016
- Reviewer for Research Development Proposals for Arkansas IDeA Networks of Biomedical Research Excellence (AR INBRE), 2017
- Reviewer for pilot grant for the Center for Translational Pediatric Research (CTPR) in systems biology research area (CROBRE, Arkansas), 2017
- Reviewer for Research Development Proposals for Arkansas IDeA Networks of Biomedical Research Excellence (AR INBRE), 2018
- Reviewer for The Clinical and Translational Science Awards (CTSA) Inter-Institutional Pilot Project Award: UNM HSC, UK, UU Health, & UAMS, 2018

### **Research Grants**

#### **Ongoing Research Support**

**Cancer Prevention and Population Science (CPPS) program Pilot project Award 2018-2019:** *Oral and Gut Microbiome Analysis during PepCan Injections in Head and Neck Cancer Patients.* 12K My role: PI

**Cancer Prevention and Population Science (CPPS) program Pilot project Award 2018-2019:** *Epigenome and Epitranscriptional Landscape Analysis of During Initiation of Lung Tumor using Native RNA/DNA Sequencing,* 10K. My role: Co-PI

**NIH-MIGMS-P20GM125503 O'Brian CA. (PI) 02/2018 – 01/2022**

#### ***Center for Musculoskeletal Diseases Research***

The central theme of the proposed Center for Musculoskeletal Disease Research (CMDR) at the University of Arkansas for Medical Sciences (UAMS) is that molecular

analysis of diseases that involve the skeleton will lead to a better understanding of their causes and will support development of novel therapies.

My Role: Co-I. Funded by National Institute of Health ~ \$13M

**PTC2017-02 Jun SR (PI) 05/2017 – 04/2018**

Genome-based mumps surveillance system using third generation sequencing technology.

My Role: CoI. Funded by UAMS Translational Research Institute ~ \$40K

**PTC2017-02 Kothari A (PI) 05/2017 – 04/2018**

Molecular and Epidemiology and Transmission of *C. difficile* Infection.

My Role: CoI. Funded by UAMS Translational Research Institute ~ 50K

**PTC2017-02 Kothari A (PI) 05/2017 – 04/2018**

Molecular and Epidemiology and Transmission of *C. difficile* Infection.

My Role: CoI. Funded by UAMS Translational Research Institute ~ 50K

**AR Tobacco Research Intawat Nookaew (PI) 07/01/2018-06/30/19**

12K

### **Completed Research Support**

**VR-2013-4504 Nookaew I (PI) 01/01/2014 – 12/31/2018**

#### ***Systems biology analysis of in vitro human colon ecosystem***

The objective of this project is to Apply systems biology to identify mechanisms of interrelationships among gut bacteria, colon cell and diet in the developed in vitro colon ecosystem. Living cells are complex and needs a holistic approach such as systems biology to understand its behaviors and discover novel mechanisms. The human gut ecosystem, contains diverse of bacteria community called microbiome and imbalance of the microbiota is associated with human diseases. However, detailed characterizations on the gut ecosystems are limited because of its high degree of complexity. Consequently, we need a simplified system that has flexible features that allow for modulation of the system following specific hypotheses testing. For this purpose we will develop an advanced bioreactor to mimic the human colon ecosystem. The bioreactor will be composed of matured polarized colonic cells that can directly interact with specific bacteria/bacteria community and specific dietary compounds under an anaerobic environment on the apical side of the mucus layer. Three key components of the bioreactor are i) a polarized mucosal surface built by a human colonic cell line appropriate for investigation of colon and bacteria interaction, ii) a simplified bacterial community selected from the most abundant strains in human gut and iii) in vitro digested food to mimic the food that enter to the colon from the small intestine. We will use the developed system as a model coupling with metabolomic and transcriptomic monitoring of cellular responses to evaluate effects of different diets and dietary compounds on the composition and metabolic activity of the intestinal microbiota and investigate structural changes in the simplified human colon ecosystem. In this project a healthy Nordic diet, a high fat diet, and the Nordic diet enriched with plant foods high in phenolics will be elucidated together with the simplified bacteria in the developed system. Furthermore, the simplified bacteria community will be replaced by isolated microbiota in fecal samples from humans. The large-scale data generated in this project will be analyzed by systems biology approaches on the basis of advanced integrative analysis and mathematical modeling/simulation of genome-scale metabolic models. The results will uncover interrelationships and interaction mechanisms to gain insight into our understanding of the human colon ecosystem as well as the importance of diet in maintaining health. These lead to accelerate the development of novel prebiotic, probiotic, drug and clinical food for diseases prevention and treatment.

My Role: PI. Funded by Swedish Research council ~ \$500K

**IMI\_JU\_2010\_3 Lewis, D.J. (PI) 03/01/2012 – 02/28/2017**

#### ***Bioacsafe - Biomarker for enhanced vaccines immune safety***

Biovacsafe is a concise consortium of three vaccine manufacturers together with selected academic, public, and SME participants used to co-working in industry-led projects, organized into focused workpackages to generate knowledge and tools to benchmark licensed vaccine reactogenicity, and create practical and generalizable guidelines and techniques to enhance immunosafety of novel vaccines from pre- development to post-marketing surveillance. A compact interlocking structure based on conceptual —Activity Cores— provides efficient and cost-effective goal delivery, while offering the full spectrum of functionality and capacity to match the needs for developing predictive biomarkers and models of inflammation/autoimmunity and clinical events classification. A Technology Core has transcriptomics, genotyping, proteomics, metabolomics and data mining, with depth and capacity to discover, validate and distribute novel biomarkers. A Models Core has a full range of ex vivo/in vivo murine, small animal and non-human primate models of inflammation and biomarker discovery, with advanced immunology and imaging. A Clinical Core has capability to safely and efficiently distribute clinical studies of vaccine immunosafety for biomarker discovery from small intensive trials to large- scale studies of adult, paediatric and other populations. A Populations Core has population-scale biobank discovery, clinical cohorts (with globalization capability, autoimmune, chronic, inflammatory and infectious disease groups), large-scale genotyping and sequencing, and a safely accessible central database for online analyses of large datasets. A Regulatory Core with expertise to synthesize outputs to generate and disseminate classifications, guidelines, reference standards for vaccine development, and inform EFPIA activities. A Management Core with track record of successful public-private projects ensures work packages interoperate to maximize discovery - validation - application - re-discovery cycles, to deliver project goals on time, within budget, while enhancing interactions with other closely integrated actors such as FDA, EMA.

My Role: co-PI, Funded by Innovative Medicine Initiative under European Research Council ~ \$660K (total \$32M)

**DOE-SFA-PMI      Doktycz M. (PI)      05/01/2014 – 06/28/2016**

***Plant Microbe Interface***

The goal of the PMI SFA is to understand the genome-dependent molecular and cellular events involved in establishing and maintaining beneficial interactions between plants and microbes. Populus and its associated microbial community serves as the experimental system for understanding how these molecular events manifest themselves within the spatially, structurally, and temporally complex scales of natural systems. To achieve this goal, we focus on 1) characterizing host and environmental drivers for diversity and function in the Populus microbiome, 2) utilizing microbial model system studies to elucidate Populus-microbial interactions at the molecular level and dissecting the signals and pathways responsible for initiating and maintaining microbial relationships and 3) develop metabolic and genomic modeling of these interactions to aid in interpreting the molecular mechanisms shaping the Populus-microbial interface.

My Role: co-PI, Funded by Department of Energy ~ \$400K

**DOE- BRCs-BESC Gilna P. (PI) 05/01/2014 – 10/31/2017**

***BioEnergy Science Center***

The BioEnergy Center (BESC) is focused on the fundamental understanding and elimination of biomass recalcitrance. BESC's approach to improve accessibility to the sugars within biomass involves (1) designing plant cell walls for rapid deconstruction and (2) developing multi-talented microbes or converting plant biomass into biofuels in a single step [consolidated bioprocessing (CBP)]. BESC researchers provide enabling technologies in characterization, 'omics, modeling and data management in order to (1) understand chemical and structural changes within biomass and (2) to provide insights into biomass formation and conversion.

My Role: co-PI, Funded by Department of Energy ~ \$400K

**DNA2Face Tokola R.A. (PI)      05/01/2015 – 10/31/2015**

***An Approach for Correlating Facial Structure and DNA***

The reduction in cost of DNA sequencing and genotyping technology is leading to the availability of massive datasets of human genome sequences and human genotypes representing mutational variation among people. These large-scale data provide for the first time the potential to correlate an individual specific genetic code



with susceptibility to disease, behavior, physical appearance, and more. This project we explore computational genetics, computer vision, and machine learning to establish a relationship between variation in an individuals specific genetic code (DNA) and facial appearance.

My Role: Co-PI, Funded by Intelligence Advanced Research Projects Activity ~ \$100K

**BILS-NOOKAEW Nookaew (PI) 06/01/2012 – 06/012014**

***BILS (Bioinformatics Infrastructure for Life Sciences)***

BILS is a distributed national research infrastructure supported by the Swedish Research Council (Vetenskapsrådet) providing bioinformatics support to life science researchers in Sweden. In the projects, the BILS persons are working close to the research group, and they spend part of their time to teach the users in order to propagate the bioinformatics knowledge. Furthermore, BILS provides infrastructure and tools for bioinformatics analyses in order to facilitate these analyses for the users.

My Role: PI, Funded by Swedish Research council ~ \$140K

**eScience-2012 Kristiansson E. (PI) 06/01/2012 – 06/012013**

***A distributed framework for quantitative analysis of very large metagenomes***

Develop, a program for efficiently scale-up on bioinformatics analysis of metagenome in high performance computing cluster.

My Role: Co-PI, Funded by Chalmers University of Technology ~ \$24K

**Scholarship and Awards**

Allbio bioinformatics project (EU project). Bioinformatics Workshop “Evaluation of Test Cases” (2012)

National Institute of Health (NIH) travel awards (2012)

Knut and Alice Wallenbergs foundation travel awards (2010)

Thai Graduate Institute of Science and Technology (TGIST), Ph.D. Scholarship

**Private company collaboration experiences**

Sandoz, Novozyme, Mascoma, Sanofi Pasteu, Novartis Vaccines, GlaxoSmithKline Biologicals, Islensk Erfdagreining

**Other**

Founding member of Goteborg Bioinformatics Network (GOTBIN), non-profit bioinformatics network in Sweden (<http://www.chalmers.se/en/departments/math/research/gotbin/Pages/default.aspx> )

Affiliated member of Advance Immunization Technologies (ADITEC), European Union funded project (<http://www.aditecproject.eu/>).

**Referee**

Prof. David Ussery (PhD), Oak Ridge National Laboratory, Oak Ridge, Tennessee, USA.

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Prof. Jens Nielsen (PhD), Chalmers University of Technology, Gothenburg, Sweden.

Email: [nielsenj@chalmers.se](mailto:nielsenj@chalmers.se)

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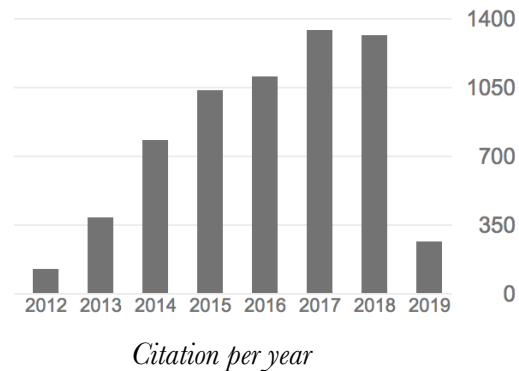
### **Patent application**

Method for Identification and Characterization of Prokaryote using Whole Genome Sequencing Data. George M. Garrity, Charles T Parker Jr., Dawid W. Ussery, Visanu Wanchai, **Intawat Nookaew**. USA patent.

### **Publications**

Published more than **100** peer-review research articles/book chapter, 2 peer-review conference proceeding, 6 international talks, more than 50 poster presentations. **H-index = 34**, **i10-index = 65**, **Total citation > 6,500**, **Total impact factor > 600**.

<http://scholar.google.se/citations?user=RUkyizkAAAAJ&hl=en>



### **Research articles**

1. **Nookaew, I.**, Meechai, A., Thammarongtham, C., Laoteng, K., Ruanglek, V., Cheevadhanarak, S., . . . Bhumiratana, S. (2007). Identification of flux regulation coefficients from elementary flux modes: A systems biology tool for analysis of metabolic networks. *Biotechnology and Bioengineering*, 97(6), 1535-1549. doi: 10.1002/bit.21339. *IF = 4.16*
2. **Nookaew, I.**, Jewett, M. C., Meechai, A., Thammarongtham, C., Laoteng, K., Cheevadhanarak, S., . . . Bhumiratana, S. (2008). The genome-scale metabolic model iIN800 of *Saccharomyces cerevisiae* and its validation: a scaffold to query lipid metabolism. *BMC Systems Biology*, 2, 71. doi: 10.1186/1752-0509-2-71. *IF = 2.44*
3. Bordel, S., & **Nookaew, I.** (2010). Systems biology or just biology? A report of the 11th International Conference on Systems Biology. *Biotechnology Journal*, 5(12), 1257-1260. doi: 10.1002/biot.201000390. *IF = 3.49*
4. Cvijovic, M., Olivares-Hernandez, R., Agren, R., Dahr, N., Vongsangnak, W., **Nookaew, I.**, . . . Nielsen, J. (2010). BioMet Toolbox: genome-wide analysis of metabolism. *Nucleic Acids Research*, 38(Web Server issue), W144-149. doi: 10.1093/nar/gkq404. *IF = 9.11*
5. **Nookaew, I.**, Gabrielsson, B. G., Holmang, A., Sandberg, A. S., & Nielsen, J. (2010). Identifying molecular effects of diet through systems biology: influence of herring diet on sterol metabolism and protein turnover in mice. *Plos One*, 5(8),

- e12361. doi: 10.1371/journal.pone.0012361. *IF* = 3.53
6. Papini, M., **Nookaew, I.**, Scalcinati, G., Siewers, V., & Nielsen, J. (2010). Phosphoglycerate mutase knock-out mutant *Saccharomyces cerevisiae*: physiological investigation and transcriptome analysis. *Biotechnology Journal*, 5(10), 1016-1027. doi: 10.1002/biot.201000199. *IF* = 3.49
  7. Vongsangnak, W., **Nookaew, I.**, Salazar, M., & Nielsen, J. (2010). Analysis of genome-wide coexpression and coevolution of *Aspergillus oryzae* and *Aspergillus niger*. *Omics-a Journal of Integrative Biology*, 14(2), 165-175. doi: 10.1089/omi.2009.0118. *IF* = 2.36
  8. Karlsson, F. H., **Nookaew, I.**, Petranovic, D., & Nielsen, J. (2011). Prospects for systems biology and modeling of the gut microbiome. *Trends in Biotechnology*, 29(6), 251-258. doi: 10.1016/j.tibtech.2011.01.009. *IF* = 11.95
  9. Karlsson, F. H., Ussery, D. W., Nielsen, J., & **Nookaew, I.** (2011). A closer look at bacteroides: phylogenetic relationship and genomic implications of a life in the human gut. *Microbial Ecology*, 61(3), 473-485. doi: 10.1007/s00248-010-9796-1. *IF* = 2.97
  10. Lindqvist, M., **Nookaew, I.**, Brinkenber, I., Samuelson, E., Thorn, K., Nielsen, J., & Harandi, A. M. (2011). Unraveling molecular signatures of immunostimulatory adjuvants in the female genital tract through systems biology. *Plos One*, 6(6), e20448. doi: 10.1371/journal.pone.0020448. *IF* = 3.53
  11. **Nookaew, I.**, Olivares-Hernandez, R., Bhumiratana, S., & Nielsen, J. (2011). Genome-scale metabolic models of *Saccharomyces cerevisiae*. *Methods Mol Biol*, 759, 445-463. doi: 10.1007/978-1-61779-173-4\_25. *IF* = NA
  12. Agren, R., Bordel, S., Mardinoglu, A., Pornputtapong, N., **Nookaew, I.**, & Nielsen, J. (2012). Reconstruction of genome-scale active metabolic networks for 69 human cell types and 16 cancer types using INIT. *Plos Computational Biology*, 8(5), e1002518. doi: 10.1371/journal.pcbi.1002518. *IF* = 4.83
  13. Caspeta, L., Shoaie, S., Agren, R., **Nookaew, I.**, & Nielsen, J. (2012). Genome-scale metabolic reconstructions of *Pichia stipitis* and *Pichia pastoris* and in silico evaluation of their potentials. *BMC Systems Biology*, 6, 24. doi: 10.1186/1752-0509-6-24. *IF* = 2.44
  14. Chumnanpuen, P., Zhang, J., **Nookaew, I.**, & Nielsen, J. (2012). Integrated analysis of transcriptome and lipid profiling reveals the co-influences of inositol-choline and Snf1 in controlling lipid biosynthesis in yeast. *Molecular Genetics and Genomics*, 287(7), 541-554. doi: 10.1007/s00438-012-0697-5. *IF* = 2.73
  15. Karlsson, F. H., Fak, F., **Nookaew, I.**, Tremaroli, V., Fagerberg, B., Petranovic, D., . . . Nielsen, J. (2012). Symptomatic atherosclerosis is associated with an altered gut metagenome. *Nature Communications*, 3, 1245. doi: 10.1038/ncomms2266. *IF* = 11.47
  16. Khoomrung, S., Chumnanpuen, P., Jansa-ard, S., **Nookaew, I.**, & Nielsen, J. (2012). Fast and accurate preparation fatty acid methyl esters by microwave-assisted derivatization in the yeast *Saccharomyces cerevisiae*. *Appl Microbiol Biotechnol*, 94(6), 1637-1646. doi: 10.1007/s00253-012-4125-x. *IF* = 3.34
  17. Larsson, E., Tremaroli, V., Lee, Y. S., Koren, O., **Nookaew, I.**, Fricker, A., . . . Backhed, F. (2012). Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88. *Gut*, 61(8), 1124-1131. doi: 10.1136/gutjnl-2011-301104. *IF* = 14.66

18. **Nookaew, I.**, Papini, M., Pornputtpong, N., Scalcinati, G., Fagerberg, L., Uhlen, M., & Nielsen, J. (2012). A comprehensive comparison of RNA-Seq-based transcriptome analysis from reads to differential gene expression and cross-comparison with microarrays: a case study in *Saccharomyces cerevisiae*. *Nucleic Acids Research*, 40(20), 10084-10097. doi: 10.1093/nar/gks804. *IF* = 9.11
19. Osterlund, T., **Nookaew, I.**, & Nielsen, J. (2012). Fifteen years of large scale metabolic modeling of yeast: developments and impacts. *Biotechnology Advances*, 30(5), 979-988. doi: 10.1016/j.biotechadv.2011.07.021. *IF* = 9.02
20. Papini, M., **Nookaew, I.**, Siewers, V., & Nielsen, J. (2012). Physiological characterization of recombinant *Saccharomyces cerevisiae* expressing the *Aspergillus nidulans* phosphoketolase pathway: validation of activity through <sup>13</sup>C-based metabolic flux analysis. *Appl Microbiol Biotechnol*, 95(4), 1001-1010. doi: 10.1007/s00253-012-3936-0. *IF* = 3.34
21. Papini, M., **Nookaew, I.**, Uhlen, M., & Nielsen, J. (2012). *Scheffersomyces stipitis*: a comparative systems biology study with the Crabtree positive yeast *Saccharomyces cerevisiae*. *Microbial Cell Factories*, 11, 136. doi: 10.1186/1475-2859-11-136. *IF* = 4.22
22. Agren, R., Liu, L., Shoaie, S., Vongsangnak, W., **Nookaew, I.**, & Nielsen, J. (2013). The RAVEN toolbox and its use for generating a genome-scale metabolic model for *Penicillium chrysogenum*. *Plos Computational Biology*, 9(3), e1002980. doi: 10.1371/journal.pcbi.1002980. *IF* = 4.83
23. Chumnanpuen, P., **Nookaew, I.**, & Nielsen, J. (2013). Integrated analysis, transcriptome-lipidome, reveals the effects of INO-level (INO2 and INO4) on lipid metabolism in yeast. *BMC Systems Biology*, 7 Suppl 3, S7. doi: 10.1186/1752-0509-7-S3-S7. *IF* = 2.44
24. Hussain, A., **Nookaew, I.**, Khoomrung, S., Andersson, L., Larsson, I., Hulthen, L., . . . Holmang, A. (2013). A maternal diet of fatty fish reduces body fat of offspring compared with a maternal diet of beef and a post-weaning diet of fish improves insulin sensitivity and lipid profile in adult C57BL/6 male mice. *Acta Physiol (Oxf)*, 209(3), 220-234. doi: 10.1111/apha.12130. *IF* = 4.38
25. Hussain, A., Olausson, H., Nilsson, S., **Nookaew, I.**, Khoomrung, S., Andersson, L., . . . Holmang, A. (2013). Maternal beef and postweaning herring diets increase bone mineral density and strength in mouse offspring. *Exp Biol Med (Maywood)*, 238(12), 1362-1369. doi: 10.1177/1535370213506436. *IF* = 2.17
26. Jernas, M., Hou, Y., Stromberg Celind, F., Shao, L., **Nookaew, I.**, Wang, Q., . . . Olsson, B. (2013). Differences in gene expression and cytokine levels between newly diagnosed and chronic pediatric ITP. *Blood*, 122(10), 1789-1792. doi: 10.1182/blood-2013-05-502807. *IF* = 10.45
27. Jernas, M., Malmstrom, C., Axelsson, M., **Nookaew, I.**, Wadenvik, H., Lycke, J., & Olsson, B. (2013). MicroRNA regulate immune pathways in T-cells in multiple sclerosis (MS). *BMC Immunology*, 14, 32. doi: 10.1186/1471-2172-14-32. *IF* = 2.48
28. Jernas, M., Malmstrom, C., Axelsson, M., Olsson, C., **Nookaew, I.**, Wadenvik, H., . . . Olsson, B. (2013). MS risk genes are transcriptionally regulated in CSF leukocytes at relapse. *Mult Scler*, 19(4), 403-410. doi: 10.1177/1352458512455466. *IF* = 4.82
29. Jernas, M., **Nookaew, I.**, Wadenvik, H., & Olsson, B. (2013). Differential

- expression of T-cell genes in blood and bone marrow between ITP patients and controls. Thromb Haemost, 109(1), 112-117. doi: 10.1160/TH12-07-0468. *IF* = 5.76
30. Jernas, M., **Nookaew, I.**, Wadenvik, H., & Olsson, B. (2013). MicroRNA regulate immunological pathways in T-cells in immune thrombocytopenia (ITP). Blood, 121(11), 2095-2098. doi: 10.1182/blood-2012-12-471250. *IF* = 10.45
  31. Jewett, M. C., Workman, C. T., **Nookaew, I.**, Pizarro, F. A., Agosin, E., Hellgren, L. I., & Nielsen, J. (2013). Mapping condition-dependent regulation of lipid metabolism in *Saccharomyces cerevisiae*. G3 (Bethesda), 3(11), 1979-1995. doi: 10.1534/g3.113.006601. *IF* = 3.20
  32. Karlsson, F. H., Tremaroli, V., **Nookaew, I.**, Bergstrom, G., Behre, C. J., Fagerberg, B., . . . Backhed, F. (2013). Gut metagenome in European women with normal, impaired and diabetic glucose control. Nature, 498(7452), 99-103. doi: 10.1038/nature12198. *IF* = 41.46
  33. Khoomrung, S., Chumnannpuen, P., Jansa-Ard, S., Stahlman, M., **Nookaew, I.**, Boren, J., & Nielsen, J. (2013). Rapid quantification of yeast lipid using microwave-assisted total lipid extraction and HPLC-CAD. Analytical Chemistry, 85(10), 4912-4919. doi: 10.1021/ac3032405. *IF* = 5.64
  34. Knuf, C., **Nookaew, I.**, Brown, S. H., McCulloch, M., Berry, A., & Nielsen, J. (2013). Investigation of malic acid production in *Aspergillus oryzae* under nitrogen starvation conditions. Appl Environ Microbiol, 79(19), 6050-6058. doi: 10.1128/AEM.01445-13. *IF* = 3.67
  35. Mardinoglu, A., Agren, R., Kampf, C., Asplund, A., **Nookaew, I.**, Jacobson, P., . . . Nielsen, J. (2013). Integration of clinical data with a genome-scale metabolic model of the human adipocyte. Molecular Systems Biology, 9, 649. doi: 10.1038/msb.2013.5. *IF* = 10.87
  36. **Nookaew, I.**, Svensson, P. A., Jacobson, P., Jernas, M., Taube, M., Larsson, I., . . . Carlsson, L. M. (2013). Adipose tissue resting energy expenditure and expression of genes involved in mitochondrial function are higher in women than in men. J Clin Endocrinol Metab, 98(2), E370-378. doi: 10.1210/jc.2012-2764. *IF* = 6.21
  37. **Nookaew, I.**, Thorell, K., Worah, K., Wang, S., Hibberd, M. L., Sjovall, H., . . . Lundin, S. B. (2013). Transcriptome signatures in *Helicobacter pylori*-infected mucosa identifies acidic mammalian chitinase loss as a corpus atrophy marker. BMC Medical Genomics, 6, 41. doi: 10.1186/1755-8794-6-41. *IF* = 2.87
  38. Osterlund, T., **Nookaew, I.**, Bordel, S., & Nielsen, J. (2013). Mapping condition-dependent regulation of metabolism in yeast through genome-scale modeling. BMC Systems Biology, 7, 36. doi: 10.1186/1752-0509-7-36. *IF* = 2.44
  39. Sanli, K., Karlsson, F. H., **Nookaew, I.**, & Nielsen, J. (2013). FANTOM: Functional and taxonomic analysis of metagenomes. BMC Bioinformatics, 14, 38. doi: 10.1186/1471-2105-14-38. *IF* = 2.58
  40. Shoaie, S., Karlsson, F., Mardinoglu, A., **Nookaew, I.**, Bordel, S., & Nielsen, J. (2013). Understanding the interactions between bacteria in the human gut through metabolic modeling. Sci Rep, 3, 2532. doi: 10.1038/srep02532. *IF* = 5.58
  41. Thiele, I., Swainston, N., Fleming, R. M., Hoppe, A., Sahoo, S., Aurich, M. K., . . . **Nookaew, I.** . Palsson, B. O. (2013). A community-driven global reconstruction of human metabolism. Nature Biotechnology, 31(5), 419-425. doi: 10.1038/nbt.2488. *IF* = 41.51

42. Varemo, L., Nielsen, J., & **Nookaew, I.** (2013). Enriching the gene set analysis of genome-wide data by incorporating directionality of gene expression and combining statistical hypotheses and methods. Nucleic Acids Research, 41(8), 4378-4391. doi: 10.1093/nar/gkt111
43. Varemo, L., **Nookaew, I.**, & Nielsen, J. (2013). Novel insights into obesity and diabetes through genome-scale metabolic modeling. Front Physiol, 4, 92. doi: 10.3389/fphys.2013.00092. *IF* = 9.11
44. Vesth, T., Ozen, A., Andersen, S. C., Kaas, R. S., Lukjancenko, O., Bohlin, J., . . . **Nookaew, I.** . . . Ussery, D. W. (2013). Veillonella, Firmicutes: Microbes disguised as Gram negatives. Standards in Genomic Sciences, 9(2), 431-448. doi: 10.4056/sigs.2981345. *IF* = 3.18
45. El-Semman, I. E., Karlsson, F. H., Shoaie, S., **Nookaew, I.**, Soliman, T. H., & Nielsen, J. (2014). Genome-scale metabolic reconstructions of Bifidobacterium adolescentis L2-32 and Faecalibacterium prausnitzii A2-165 and their interaction. BMC Systems Biology, 8, 41. doi: 10.1186/1752-0509-8-41. *IF* = 2.44
46. Garcia-Albornoz, M., Thankaswamy-Kosalai, S., Nilsson, A., Varemo, L., **Nookaew, I.**, & Nielsen, J. (2014). BioMet Toolbox 2.0: genome-wide analysis of metabolism and omics data. Nucleic Acids Research, 42(Web Server issue), W175-181. doi: 10.1093/nar/gku371. *IF* = 9.11
47. Gatto, F., **Nookaew, I.**, & Nielsen, J. (2014). Chromosome 3p loss of heterozygosity is associated with a unique metabolic network in clear cell renal carcinoma. Proc Natl Acad Sci U S A, 111(9), E866-875. doi: 10.1073/pnas.1319196111. *IF* = 9.67
48. Karlsson, F. H., **Nookaew, I.**, & Nielsen, J. (2014). Metagenomic data utilization and analysis (MEDUSA) and construction of a global gut microbial gene catalogue. Plos Computational Biology, 10(7), e1003706. doi: 10.1371/journal.pcbi.1003706. *IF* = 4.83
49. Knuf, C., **Nookaew, I.**, Remmers, I., Khoomrung, S., Brown, S., Berry, A., & Nielsen, J. (2014). Physiological characterization of the high malic acid-producing Aspergillus oryzae strain 2103a-68. Appl Microbiol Biotechnol, 98(8), 3517-3527. doi: 10.1007/s00253-013-5465-x. *IF* = 3.34
50. Pornputtpong, N., Wanichthanarak, K., Nilsson, A., **Nookaew, I.**, & Nielsen, J. (2014). A dedicated database system for handling multi-level data in systems biology. Source Code Biol Med, 9, 17. doi: 10.1186/1751-0473-9-17. *IF* = NA
51. Svahn, S., Grahnmemo, L., Palsdottir, V., **Nookaew, I.**, Wendt, K., Gabriellsson, B., Jansson, J. O. (2014). Dietary polyunsaturated fatty acids increase survival and decrease bacterial load during septic S. aureus infection, and improve neutrophil function in mice. Infect Immun. doi: 10.1128/IAI.02349-14. *IF* = 3.73
52. Wanichthanarak, K., **Nookaew, I.**, & Petranovic, D. (2014). yStreX: yeast stress expression database. Database (Oxford), 2014. doi: 10.1093/database/bau068. *IF* = 3.37
53. Nielsen J., Bordel S., **Nookaew I.** (2014), Genome-Scale Metabolic Models: A Link between Bioinformatics and Systems Biology, Pages 165-173 Comprehensive Biomedical Physics, ISBN: 978-0-444-53633-4. *IF* = NA
54. Land M., Hauser L., Jun S.-R., **Nookaew I.**, Leuze M.R., Ahn T.-H., Karpinets T., Lund O., Kora G., Wassenaar T., Poudel S., Ussery D.W. Insights from twenty years of bacterial genome sequencing. Funct Integr Genomics. 2015



- Mar;15(2):141-61. doi: 10.1007/s10142-015-0433-4. *IF* = 2.48
55. Goossens KV, Ielasi FS, **Nookaew I**, Stals I, Alonso-Sarduy L, Daenen L, Van Mulders SE, Stassen C, van Eijnsden RG, Siewers V, Delvaux FR, Kasas S, Nielsen J, Devreese B, Willaert RG. Molecular mechanism of flocculation self-recognition in yeast and its role in mating and survival. *MBio*. 2015 Apr 14;6(2). pii: e00427-15. doi: 10.1128/mBio.00427-15. *IF* = 6.78
  56. Sommer F., **Nookaew I**, Adam N., Fogelstrand P., Bäckhed F. Site-specific programming of the host epithelial transcriptome by the gut microbiota. *Genome Biol*. 2015 Mar 28;16:62. doi: 10.1186/s13059-015-0614-4. *IF* = 10.81
  57. Våremo L, Scheele C, Broholm C, Mardinoglu A, Kampf C, Asplund A, **Nookaew I**, Uhlén M, Pedersen BK, Nielsen J. Proteome- and transcriptome-driven reconstruction of the human myocyte metabolic network and its use for identification of markers for diabetes. *J. Cell Rep*. 2015 May 12;11(6):921-33. doi: 10.1016/j.celrep.2015.04.010. *IF* = 8.36
  58. Jun S.R., Leuze M.R., **Nookaew I**, Uberbacher E.C., Land M., Zhang Q., Wanchai V., Chai J., Nielsen M., Trolle T., Lund O., Buzard G., Pedersen T.D., Wassenaar T.M., Ussery D.W. Ebolavirus comparative genomics, *FEMS Microbiol Rev*. 2015 Jul 14. pii: fuv031. *IF* = 13.24
  59. Soni N.K., **Nookaew I**, Sandberg A.S., Gabrielsson B.G. Eicosapentaenoic and docosahexaenoic acid-enriched high fat diet delays the development of fatty liver in mice. *Lipids Health Dis*. 2015 Jul 22;14(1). *IF* = 2.22
  60. Pornputtpong N., **Nookaew I**, Nielsen J. Human Metabolic Atlas: An online resource for human metabolism. *Database (Oxford)*. 2015 Jul 24;2015. pii: bav068. doi: 10.1093/database/bav068. *IF* = 3.37
  61. Zurawski J.V., Conway J.M., Lee L.L., Simpson H., Izquierdo J.A. Blumer-Schuette S., **Nookaew I**, Adams M. WW. , Kelly R.M. Comparative analysis of extremely thermophilic Caldicellulosiruptor species reveals common and differentiating cellular strategies for plant biomass utilization. *Appl Environ Microbiol*. 2015 Aug 7. pii: AEM.01622-15. *IF* = 3.67
  62. Jun S. R. , Wassenaar T.W., **Nookaew I** , Hauser L, Wanchai V., Land M., Timm C., Lu T.Y.S., Schadt C.W., Doktycz M.J. , Pelletier D.A., Ussery D.W. Comparative genome analysis of Pseudomonas genomes including Populus-associated isolates. *Appl Environ Microbiol*. 2015 Oct 30. pii: AEM.02612-1. *IF* = 3.67
  63. Abraham P.E., Wang X., Ranjan P., **Nookaew I**, Zhang B, Tuskan G.A., Hettich R.L. Integrating mRNA and Protein Sequencing for the Identification of Natural Protein Sequence Variants: A Case Study for two genotypes of Populus trichocarpa. *J Proteome Res*. 2015 Oct 30. *IF* = 4.25
  64. Jernas M., Céline F.S., **Nookaew I**, Mellgren K., Wadenvik H., Olsson B. Normalized autoimmune expression in remission of pediatric ITP. *Thromb Haemost*. 2016 Feb 4;115(6). *IF* = 5.72
  65. Pedersen L, Idorn M, Andersen GH, Lauenborg B, **Nookaew I**, Hansen RH, Johannesen HH, Becker JC, Pedersen KS, Dethlefsen C, Nielsen J, Gehl J, Pedersen BK, Straten PT, Hojman P. Voluntary running suppresses tumor growth through epinephrine- and IL-6-dependent NK cell mobilization and redistribution. *Cell Metab*. 2016 Feb 15. pii: S1550-4131(16)30003-1. doi: 10.1016/j.cmet.2016.01.011. *IF* = 17.57

66. Thorell K, Hosseini S, Gonzales RVP, Chaotham C, Graham DY, Paszat L, Rabeneck L, Lundin SB, **Nookaew I**, Sjöling A. Identification of a Latin American-specific BabA adhesin variant through whole genome sequencing of *Helicobacter pylori* patient isolates from Nicaragua. BMC Evol Biol. 2016 Feb 29;16(1):53. doi: 10.1186/s12862-016-0619-y. *IF* = 3.37
67. Svahn SL, Väre L, Gabrielsson BG, Peris E, **Nookaew I**, Grahne L, Sandberg AS, Wernstedt Asterholm I, Jansson JO, Nielsen J, Johansson ME. Six Tissue Transcriptomics Reveals Specific Immune Suppression in Spleen by Dietary Polyunsaturated Fatty Acids. PLoS One. 2016 May 11;11(5):e0155099. doi: 10.1371/journal.pone.0155099. *IF* = 3.53
68. Gatto F, Volpi N, Nilsson H, **Nookaew I**, Maruzzo M, Roma A, Johansson ME, Stierner U, Lundstam S, Basso U, Nielsen J. Glycosaminoglycan Profiling in Patients' Plasma and Urine Predicts the Occurrence of Metastatic Clear Cell Renal Cell Carcinoma. Cell Rep. 2016 May 11. pii: S2211-1247(16)30500-9. doi: 10.1016/j.celrep.2016.04.056. *IF* = 8.36
69. Timm, C.M., Pelletier, D.A., Jawdy S. A., Gunter L.E., Henning, J.A., Engle, N., Aufrecht, J., Gee, E., **Nookaew, I.**, Yang, Z., Lu, T-Y., Tschaplinski T.J., Doktycz, M.J., Tuskan G.A., Weston, D.J., Two poplar-associated bacterial isolates induce additive favorable responses in a constructed plant-microbiome system. Front Plant Sci. 2016 Apr 26;7:497. doi: 10.3389/fpls.2016.00497. *IF* = 3.98
70. Nguy L., Shubbar E., Jernas M., **Nookaew I.**, Lundgren J., Olsson B., Nilsson H., Guron G. Adenine-induced chronic renal failure in rats decreases aortic relaxation rate and alters expression of proteins involved in vascular smooth muscle calcium handling. Acta Physiol (Oxf). 2016 May 30. doi: 10.1111/apha.12724. *IF* = 4.07
71. Soni N, Ross AB, Scheers N, Savolainen OI, **Nookaew I**, Gabrielsson BG, Sandberg AS. Eicosapentaenoic and docosahexaenoic acid - enriched high fat diet delays skeletal muscle degradation in mice. Nutrients. 2016 Sep 3;8(9). pii: E543. doi: 10.3390/nu8090543. *IF* = 3.80
72. Thompson RA, Dahal S, Garcia S, **Nookaew I**, Trinh CT. Exploring complex cellular phenotypes and model-guided strain design with a novel genome-scale metabolic model of *Clostridium thermocellum* DSM 1313 implementing an adjustable cellulosome. Biotechnol Biofuels. 2016 Sep 6;9(1):194. doi: 10.1186/s13068-016-0607-x. eCollection 2016. *IF* = 6.44
73. Karlsson R, Thorell K, Hosseini S, Kenny D, Sihlbom C, Karlsson A, Sjöling Å, and **Nookaew I**. Comparative proteomes of two *Helicobacter pylori* strains using genomics and mass spectrometry-based proteomics. Front Microbiol. 2016 Nov 11;7:1757. eCollection 2016. *IF* = 4.17
74. Olafsdottir TA, Lindqvist M, **Nookaew I**, Andersen P, Maertzdorf J, Persson J, Christensen D, Zhang Y, Anderson J, Khoomrung S, Sen P, Agger EM, Coler R, Carter D, Meinke A, Rappuoli R, Kaufmann SH, Reed SG, Harandi AM. Comparative Systems Analyses Reveal Molecular Signatures of Clinically tested Vaccine Adjuvants. Sci Rep. 2016 Dec 13;6:39097. *IF* = 5.58
75. Pedersen TL, **Nookaew I**, Wayne Ussery D, Månsson M. PanViz: interactive visualization of the structure of functionally annotated pangenomes. Bioinformatics. 2017 Jan 5. pii: btw761. *IF* = 7.37
76. Soni NK, Ross AB, Scheers N, Savolainen OI, **Nookaew I**, Gabrielsson BG,



- Sandberg AS. Splenic Immune Response Is Down-Regulated in C57BL/6J Mice Fed Eicosapentaenoic Acid and Docosahexaenoic Acid Enriched High Fat Diet. Nutrients. 2017 Jan 10;9(1). . *IF* = 3.76
77. Poudel S, Giannone RJ, Rodriguez M Jr, Raman B, Martin MZ, Engle NL, Mielenz JR, **Nookaew I**, Brown SD, Tschaplinski TJ, Ussery D, Hettich RL. Integrated omics analyses reveal the details of metabolic adaptation of *Clostridium thermocellum* to lignocellulose-derived growth inhibitors released during the deconstruction of switchgrass. Biotechnol Biofuels. 2017 Jan 10;10:14. *IF* = 5.2
78. Zhang Q, Jun SR, Leuze M, Ussery D, **Nookaew I**. Viral Phylogenomics Using an Alignment-Free Method: A Three-Step Approach to Determine Optimal Length of k-mer. Sci Rep. 2017 Jan 19;7:40712. *IF* = 4.26
79. Thankaswamy-Kosalai S, Sen P, **Nookaew I**, Evaluation and assessment of read-mapping by multiple next-generation sequencing aligners based on genome-wide characteristics. Genomics. 2017 Mar 9. pii: S0888-7543(17)30020-4. doi: 10.1016/j.ygeno.2017.03.001. *IF* = 3.33
80. Hu G, Di Paola L, Pullara F, Liang Z, Nookaew **I**. **Network** Proteomics: From Protein Structure to Protein-Protein Interaction. Biomed Res Int. 2017. *IF* = 2.48
81. Larson-Prior L.J., Azhar G., Davila D.G. Jun S-R., Kemp A.S., Nookaew I., Wei J.Y., Wassenaar T.M. Neurobiology of Sleep and Microbiomics in Aging. OBM Neurobiology. *IF* = NA
82. Alkam A., Wongsurawat T., Jenjaroenpun P, Connor S, Hobbs C, Wassenaar T, Jun SR, **Nookaew I**, Ussery DW, J. Three Complete Genome Sequences of Genotype G Mumps Virus from the 2016 outbreak in Arkansas. Genome Announc. 2017 Aug 10;5(32). pii: e00555-17. *IF* = 1.18
83. Khoomrung S., Wanichthanarak K., **Nookaew I**, Thamsermsang O, Seubnooch P, Laohapand T, Akarasreenont P, Metabolomics and Integrative Omics for the Development of Thai Traditional Medicine. Front Pharmacol. 2017 Jul 18;8:474. *IF* = 4.44
84. Thorell K, Bengtsson-Palme J, Liu O H-F, Victoria R, Gonzales P, **Nookaew I**, Rabeneck L, Paszat L, Graham DY, Nielsen J, Lundin SB, Sjöling A. In vivo analysis of the viable microbiota and *Helicobacter pylori* transcriptome in gastric infection and early stages of carcinogenesis. Infect Immun. 2017 Sep 20;85(10). pii: e00031-17. *IF* = 3.73
85. Jun SR, **Nookaew I**, Hauser L, Gorin A. Assessment of Genome Annotation using Gene Function Similarity within Gene Neighborhood. BMC Bioinformatics. 2017 Jul 19;18(1):345. *IF* = 2.45
86. Thammarongtham C, **Nookaew I**, Vorapreeda T, Srisuk T, Land ML, Jeenor S, Laoteng K. Genome Characterization of Oleaginous *Aspergillus oryzae* BCC7051: A Potential Fungal-Based Platform for Lipid Production. Curr Microbiol. 2018 Jan;75(1):57-70. doi: 10.1007/s00284-017-1350-7. Epub 2017 Sep 1.
87. Wang J, Jenjaroenpun P, Bhinge A, Angarica VE, Del Sol A, **Nookaew I**, Kuznetsov VA, Stanton LW, Single-cell gene expression analysis reveals regulators of distinct cell subpopulations among developing human neurons Genome Res. 2017 Oct 13. doi: 10.1101/gr.223313.117. *IF* = 11.35
88. Sjöberg F., Barkman C., **Nookaew I**, Östman S., Adlerberth I., Saalman R., Wold A.E. Low Complexity of the Duodenal Microbiota in Children with Newly

- Diagnosed Ulcerative Colitis. PLoS One. 2017 Oct 19;12(10):e0186178. *IF* = 2.86
89. Srinivas N, Tokola R, Mikkilineni A, Nookaew I, Leuze M, Boehnen Biometrics (IJCB), 2017 IEEE International Joint Conference. (2017) DNA2FACE: An approach to correlating 3D facial structure and DNA, Biometrics (IJCB), 2017 IEEE International Joint Conference.
  90. Jun S-R., Wassenaar T., Wanchai V., Patumcharoenpol P., **Nookaew I**, Ussery DW Suggested mechanisms for Zika Virus causing microcephaly: what do the genomes tell us? BMC Bioinformatics. 2017 18(Suppl 14):47. *IF* = 2.45
  91. Wanchai V., Patumcharoenpol P., **Nookaew I**, Ussery DW., dBBQs : dataBase of Bacterial Quality scores. BMC Bioinformatics. 2017 18(Suppl 14):483. *IF* = 2.45
  92. Jenjaroenpun P., Wongsurawat T., Pereira R., Patumcharoenpol P., Ussery D.W., Nielsen J., **Nookaew I**. Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of *Saccharomyces cerevisiae* CEN.PK113-7D. Nucleic Acids Res. 2018 Jan 13. doi: 10.1093/nar/gky014. *IF* = 10.2
  93. Timm C.M., Carter K.R., Carrell A.A., Jun S-R., Jawdy S.S., Vélez J.M., Gunter L.E., Yang Z., **Nookaew I**, Engle N.L., Lu T-Y. S., Schadt C.W., Tschaplinski T.J., Doktycz M.J., Tuskan G.A., Pelletier D.A., Weston D.J. Abiotic Stresses Shift Belowground Populus-Associated Bacteria Toward a Core Stress Microbiome. mSystems. January/February 2018 Volume 3 Issue 1 e00070-17. *IF*=NA.
  94. Wongsurawat T, Woo C.C., Giannakakis A, Lin X.Y., Cheow E.S.H, Lee C.N., Richards M., Sze S.W., **Nookaew I**, Kuznetsov V.A, Sorokin V. Distinctive molecular signature and activated signaling pathways in aortic smooth muscle cells of patients with myocardial infarction. Atherosclerosis. 10.1016/j.atherosclerosis.2018.01.024. *IF*=4.24
  95. Wongsurawat T, Woo C.C., Giannakakis A, Lin X.Y., Cheow E.S.H, Lee C.N., Richards M., Sze S.W., **Nookaew I**, Kuznetsov V.A, Sorokin V. Transcriptome alterations of vascular smooth muscle cells in aortic wall of myocardial infarction patients. Data in Brief. Volume 17, April 2018, Pages 1112-1135
  96. Cabal A, Jun SR, Jenjaroenpun P, Wanchai V, **Nookaew I**, Wongsurawat T, Burgess MJ, Kothari A, Wassenaar TM, Ussery DW. Genome-Based Comparison of *Clostridioides difficile*: Average Amino Acid Identity Analysis of Core Genomes. Microb Ecol. 2018 Feb 14. doi: 10.1007/s00248-018-1155-7. *IF*=3.63
  97. Poudel S, Giannone RJ, Basen M, Nookaew I, Poole FL, Kelly RM, Adams MWW, Hettich RL. The diversity and specificity of the extracellular proteome in the cellulolytic bacterium *Caldicellulosiruptor bescii* is driven by the nature of the cellulosic growth substrate. Accepted Biotechnol Biofuels. *IF* = 5.2
  98. Wongsurawat T, Athipanyasilp N, Jenjaroenpun P, Jun SR, Kaewnapan B, Wassenaar TM, Leelahakorn N, Angkasekwinai N, Kantakamalakul W, Ussery DW, Sutthent R, **Nookaew I**, Horthongkham N., Case of Microcephaly after Congenital Infection with Asian Lineage Zika Virus, Thailand. Emerg Infect Dis. 2018 Sep 17;24(9). doi: 10.3201/eid2409.180416. *IF*=7.42
  99. Piccolo BD, Graham JL, Stanhope KL, **Nookaew I**, Mecer KE, Chintapalli SV, Wankhade UD, Shankar K, Havel PJ, Adams SH. Diabetes-Associated Alterations in the Cecal Microbiome and Metabolome are Independent of Diet or Environment in the UC Davis Type 2-Diabetes Mellitus Rat Model. Am J Physiol Endocrinol Metab. 2018 Jul 17. doi: 10.1152/ajpendo.00203.2018. *IF*=4.02

100. Apopa PL, Alley L, Penney RB, Arnaoutakis K, Steliga MA, Jeffus S, Bircan E, Gopalan B, Jin J, Patumcharoenpol P, Jenjaroenpun P, Wongsurawat T, Shah N, Boysen G, Ussery D, **Nookaew I**, Fagan P, Bebek G, Orloff MS. PARP1 Is Up-Regulated in Non-small Cell Lung Cancer Tissues in the Presence of the Cyanobacterial Toxin Microcystin. *Front Microbiol.* 2018 Aug 6;9:1757. doi: 10.3389/fmicb.2018.01757. eCollection 2018. *IF=4.02*
101. Wongsurawat T, Jenjaroenpun P, Athipanyasilp N, Kaewnapan B, Leelahakorn N, Angkasekwina N, Kantakamalakul W, Sutthent R, Ussery DW, Horthongkham N, **Nookaew I**. Genome Sequences of Zika Virus Strains Recovered from Amniotic Fluid, Placenta, and Fetal Brain of a Microcephaly Patient in Thailand, 2017. *Microbiol Resour Announc.* 2018 Sep 20;7(11).
102. Jenkins SV, Vang KB, Gies A, Griffin RJ, Jun SR, **Nookaew I**, Dings RPM. Sample storage conditions induce post-collection biases in microbiome profiles. *BMC Microbiol.* 2018 Dec 27;18(1):227. doi: 10.1186/s12866-018-1359-IF=2.23
103. Joffre E., Nicklasson M. , Álvarez-Carretero S., Xiao X., Sun L., **Nookaew I**, Zhu. , Sjöling Å (2019), The bile salt glycocholate induces global changes in gene and protein expression and activates virulence in enterotoxigenic *Escherichia coli*, *Sci Rep.* 2019 Jan 14;9(1):108. doi: 10.1038/s41598-018-36414-z.
104. Wongsurawat, T., P. Jenjaroenpun, M. K. Taylor, J. Lee, A. L. Tolardo, J. Parvathareddy, S. Kandel, T. D. Wadley, B. Kaewnapan, N. Athipanyasilp, A. M. Skidmore, D. Chung, C. Chaimayo, M. Whitt, W. Kantakamalakul, R. Sutthent, N. Horthongkham, D. W. Ussery, C. B. Jonsson, **Nookaew. I.** (2018). "Rapid Sequencing of Multiple RNA Viruses in their Native Form. Accepted in *Frontiers in Microbiology*. IF = 4.02.
105. Wadley TD, Jenjaroenpun P, Wongsurawat T, Ussery DW, **Nookaew I**. Complete Genome and Plasmid Sequences of *Escherichia coli* Type Strain ATCC 11775. Accepted in *Microbial Resource Annocement*.
106. Kovatcheva-Datchary P, Shoaie S, Lee S, Wahlström A, **Nookaew I**, Hallen A, Perkins R, Nielsen J, Bäckhed F, Simplified intestinal microbiota to study microbe-diet-host interactions in a mouse model. Accepted in *Cell Reports*. IF = 8.03.
107. Sjöberg F, **Nookaew I**, Yazdanshenas S, Adlerberth I, Wold. AE, Are all faecal bacteria detected with equal efficiency? A study using next-generation sequencing, T-RFLP and quantitative culture of infants' faecal samples. Under revision **PLoSone**.
108. Cheng WC, Ting LW, Yun LX, Dorajoo R, Richards M, Neng LC, Wongsurawat T, **Nookaew I**, Sorokin V, The miRNA 30b-5p - mRNA MBNL1 interaction is novel association involve in human VSMC differentiation process in patient with coronary atherosclerosis. Under revision **Molecular Sciences**
109. Jana A, **Nookaew I**, Singh J, Behkam B, Franco A, Nain A. Crosshatch nanofiber networks of tunable inter-fiber spacing induce plasticity in cell migration and cytoskeletal response. Under revision in **FASEB J**.

#### Peer-reviewed conference contributions

1. Meechai, A., **Nookaew, I.**, Thamarongtham, C., Laoteng, K., Ruanglek, V., Cheevadhanarak, S., and Bhumiratana, S. (2003) Pathway analyses of yeast metabolic reaction network for potential improvement of fatty acids production. at the 6th Asia Pacific Biochemical Engineering Conference 03, Australia.
2. **Nookaew, I.**, Liamprawat, C., Meechai, A., Laoteng, K., Cheevadhanarak, S., and Bhumiratana, S. Elementary flux mode analysis of fatty acid metabolism in *Saccharomyces cerevisiae*. The International Conference on Bioinformatics 2002: North-South Networking, Thailand

### **International talk**

1. Quantitative analysis of shotgun metagenomes through systems biology: Lessons from the human microbiome (2013). NBIC Metagenomics approaches and data analysis. Liden University, Netherland.
2. Systems biology analysis of sepsis prevention by polyunsaturated n-3 fatty acids (2012). 10<sup>th</sup> Nordic Nutrition Conference, Iceland.
3. Uncovering global impact of fish and enriched-polyunsaturated fatty acids diet in mice by systems biology (2011). 41<sup>st</sup> West European Fish Technologists Association, Sweden.
4. Is fat of women and men are difference ? *Integration analysis of gene expression and energy expenditure* (2011). Conference Enabling Systems Biology, UK.
5. Identifying molecular effects in metabolically active tissues in mouse through systems biology: Influence of herring diet on sterol metabolism and protein turnover in mouse (2010). 10<sup>th</sup> Swedish Bioinformatics Workshop, Sweden.
6. Biomarker discovery through integrative analysis of omic data - case study: kidney cancer (metabolite) and type 2 diabetes (microbiome) (2017). National Cancer Institute, National Institutes of Health, Bethesda, Maryland, USA
7. Transcriptional landscapes analysis through direct RNA sequencing. Nanopore Community (2017). New York, USA
8. Nookaew Intawat. What we learn from native RNA sequencing? The application of transcriptomics and genome sequencing of RNA viruses. September 10 2018. University of Tennessee Health Sciences Center, Memphis TN, USA
9. Nookaew Intawat. Direct RNA Sequencing for Genome-wide Expression and transcriptional landscape analysis. ADETEC meeting, October 1-3 2018. University of Siena, Siena Italy

### **Open-access computer programs and web services/databases**

#### **Published**

1. Platform for Integrated Analysis of Omics data (PIANO)
2. Functional and taxonomic analysis of metagenomes (FANTOM)
3. Reconstruction Analysis and Visualization of Metabolic Networks (RAVEN)
4. Genome and Transcriptome Sequencing Browser (Yseq Browser)
5. Genome-wide analysis of metabolism (Biomet toolbox)
6. Human Metabolic Atlas (HMA)
7. Metagenomics Data utilization and Analysis (MEDUSA) : Quantitative shot gun metagenomics analysis package

8. Populous multi-omics data (SNP, RNAseq, Proteomics) integration and visualization.

### **Developing**

- Ondine: web application for light weight ZUI multilevel omics data visualization
- Cloud computing of NGS data analysis through Galaxy platform
- Parallelization computing for shot gun metagenomics analysis
- Gap Kmers for rapid identification of DNA sequence (KALI)
- Dtree: Zoomable Phylogenetics tree visualization.
- FG-FBA: Probabilistic factor graph flux balance analysis.

### **Organizing workshop/conference**

Comparative Microbial Genomics Workshop, Bangkok, Thailand, 2008.

Swedish Bioinformatics Workshop (SBW2010), Gothenburg, Sweden, 2010.

3<sup>rd</sup> Generation Sequencing Workshop, 2016-2019

### **Skills summary**

#### **Computational skills**

- Computational language: R, MATLAB, python, perl, SQL, ruby, UNIX/Linux
- Database design and development: mySQL, mongoDB
- Large-scale data mining and statistics
- High performance computing.
- Multilevel omics data analysis, integration and visualization
- Genome-scale metabolic modeling and simulation
- C-13 labeled metabolic flux analysis and traditional metabolic flux analysis
- Genome analysis: comparative genomics, genome annotation, genome assembly, SNP/CNV analysis (high density arrays and NGS data)
- Metagenomics analysis: Shotgun sequencing analysis, 16S (amplicon) sequencing analysis
- Transcriptome analysis: Microarray, NGS data(RNA-seq) (reference genome mapping and *de novo* transcriptome assembly)
- Proteome analysis: LC-MS/MS data analysis
- Metabolome analysis: LC-MS/TOF data analysis, GC-MSq/TOF data analysis
- Gene-set Enrichment analysis
- Genome-wide association (GWAS) analysis
- 3D facial image analysis
- Machine learning
- Biological network modeling and analysis
- Systems Biology
- Large-scale data visualization.

#### **Experimental skills**

- Metabolic Engineering
- Bioengineering/Biotechnology
- Microarray analysis
- Fermentation
- Lipidomics analysis
- Metabolomics analysis

- Molecular biology
- Analytical chemistry
- Microbiology
- Molecular biology
- Genome/transcriptome sequencing
- Chemical and Biological Reactor Engineering