CURRICULUM VITAE

Dr. Phasit Charoenkwan

17 Soi 12 Chotana Rd. Muang Chiang Mai 50300
Home: 053-213-590 Mobile: 08-6115-2008
e-mail: ple@dr.com

1 Education

September 2010 – August 2014:
Doctor of Philosophy (**Ph.D**) in Bioinformatics
National Chiao Tung University, Hsinchu, Taiwan
GPA: 4.28
Ranked first in the class of academic year 2010

June 2004 – September 2006:
Master of Science (**M.S.**) in Computer Science,
Chiang Mai University, Chiang Mai, Thailand
GPA: 3.88 (**1st in class)**
Ranked first in the class of academic year 2006

June 2000 – March 2004:
Bachelor of Science (**B.S.**) in Computer Science,
Chiang Mai University, Chiang Mai, Thailand
GPA: 3.59 (**1st class honors**)
Ranked first in the class of academic year 2004

2 Working

Dec 2015 – Present :
Lecturer at College of Arts, Media and Technology
Chiang Mai University, Chiang Mai, Thailand
Social Mining, Image Mining & Deep Learning

September 2014 – July 2015:
Postdoctoral at Intelligent Computing Lab
National Chiao Tung University, Hsinchu, Taiwan
Biological & Medical Image Analysis

October 2008 – March 2010:
Lecturer
MeaJo University, Chiang Mai, Thailand
Digital Communications

June 2007 – October 2008:
Lecturer
Mae Fah University, Chiang Rai, Thailand
Computer Science

September 2006 – June 2007:
Researcher
Chiang Mai University, Chiang Mai, Thailand
Bioinformatics

3 Research Interest & Expertise

- Bioinformatics
- Biomedical Informatics
- Precision Oncology Data Science
- Computational Liquid Biopsy
- QSAR
- Optimization, Feature Selection and Data Mining

4 Publications (2020 – Present)

Udomruk, S., Sutthitthasakul, S., Bunsermvicha, N., Pinyopornpanish, K., Charoenkwan, P., et al. Machine learning–based cfDNA fragmentation profiling using automated capillary electrophoresis for early detection of hepatocellular carcinoma. Communications Medicine (2026).

Nikom, J., Shoombuatong, W., Charoenkwan, P., Musikasuwan, S. GAXGB: A Two-Stage Ensemble Framework Integrating Genetic Algorithms and XGBoost for Anti-HIV Peptide Prediction. Trends in Sciences, 23(3), 11717 (2026).

Charoenkwan, P., Pipattanaboon, C., Schaduangrat, N., Mahmud, S. M. H., et al. Leveraging a Meta-Learning Strategy to Advance the Accuracy of Neutralizing Antibodies against Dengue Virus Serotype Prediction. ACS Omega, 10(50), 61296–61307 (2025).

Charoenkwan, P., Chumnanpuen, P., Schaduangrat, N., Shoombuatong, W. Accelerating the identification of the allergenic potential of plant proteins using a stacked ensemble-learning framework. Journal of Biomolecular Structure and Dynamics, 43(13), 6637–6649 (2025).

Charoenkwan, P., Schaduangrat, N., Chumnanpuen, P., Shoombuatong, W. PSR-MAPMS: A new approach for the interpretable prediction of myelin autoantigenic peptides in multiple sclerosis using multi-source propensity scores. Protein Science, 34(8), e70010 (2025).

Charoenkwan, P., Chumnanpuen, P., Schaduangrat, N., Shoombuatong, W. Stack-AVP: A stacked ensemble predictor based on multi-view information for fast and accurate discovery of antiviral peptides. Journal of Molecular Biology, 437(6), 168853 (2025).

Charoenkwan, P., Chumnanpuen, P., Schaduangrat, N., Shoombuatong, W. Deepstack-ACE: A deep stacking-based ensemble learning framework for the accelerated discovery of ACE inhibitory peptides. Methods, 234, 131–140 (2025).

Charoenkwan, P., Schaduangrat, N., Moni, M. A., Shoombuatong, W. iMRSA-Fuse: A fast and accurate computational approach for predicting anti-MRSA peptides by fusing multi-view information. IEEE Transactions on Computational Biology and Bioinformatics, 22(1), 2–12 (2025).

Charoenkwan, P., Schaduangrat, N., Manavalan, B., Shoombuatong, W. M3S-ALG: Improved and robust prediction of allergenicity of chemical compounds by using a novel multi-step stacking strategy. Future Generation Computer Systems, 162, 107455 (2025).

Kaewkamol, P., Arwatchananukul, S., Saengrayap, R., Charoenkwan, P. Automated defect classification of coffee beans using deep-stacking ensemble learning. International Journal of Science and Innovative Technology, 8(1), 1–9 (2025).

Arwatchananukul, S., Chaiwong, S., Charoenkwan, P., Punvichai, T., Chen, M., et al. Classification of translucent flesh defects in Phulae pineapples using stacking ensemble classifiers and deep neural networks. Applied Food Research, 101460 (2025).

Arwatchananukul, S., Xu, D., Charoenkwan, P., Moon, S. A., Saengrayap, R. Implementing a deep learning model for defect classification in Thai Arabica green coffee beans. Smart Agricultural Technology, 9, 100680 (2024).

Schaduangrat, N., Khemawoot, P., Jiso, A., Charoenkwan, P., et al. MetaCGRP is a high-precision meta-model for large-scale identification of CGRP inhibitors using multi-view information. Scientific Reports, 14(1), 24764 (2024).

Natsrita, P., Charoenkwan, P., Shoombuatong, W., Mahalapbutr, P., Faksri, K., et al. Machine-learning-assisted high-throughput identification of potent and stable neutralizing antibodies against all four dengue virus serotypes. Scientific Reports, 14(1), 17165 (2024).

Suanoi, P., Kaewman, N., Pekkoh, J., Charoenkwan, P., Pumas, C. A novel system for assessing paraquat toxicity using Desmodesmus maximus as a potential bio-indicator and deep learning-based approach. Algal Research, 77, 103370 (2024).

Charoenkwan, P., Schaduangrat, N., Pham, N.T., Manavalan, B., Shoombuatong, W.Pretoria: An effective computational approach for accurate and high-throughput identification of CD8+ t-cell epitopes of eukaryotic pathogens (2023) International Journal of Biological Macromolecules, 238, art. no. 124228, .

Charoenkwan, P., Chumnanpuen, P., Schaduangrat, N., Oh, C., Manavalan, B., Shoombuatong, W.PSRQSP: An effective approach for the interpretable prediction of quorum sensing peptide using propensity score representation learning (2023) Computers in Biology and Medicine, 158, art. no. 106784, .

Malang, C., Charoenkwan, P., Wudhikarn, R. Implementation and Critical Factors of Unmanned Aerial Vehicle (UAV) in Warehouse Management: A Systematic Literature Review (2023) Drones, 7 (2), art. no. 80, .

Charoenkwan, P., Pipattanaboon, C., Nantasenamat, C., Hasan, M.M., Moni, M.A., Lio, P., Shoombuatong, W.PSRTTCA: A new approach for improving the prediction and characterization of tumor T cell antigens using propensity score representation learning (2023) Computers in Biology and Medicine, 152, art. no. 106368, .

Schaduangrat, N., Anuwongcharoen, N., Moni, M.A., Lio’, P., Charoenkwan, P., Shoombuatong, W.StackPR is a new computational approach for large-scale identification of progesterone receptor antagonists using the stacking strategy(2022) Scientific Reports, 12 (1), art. no. 16435, .

Charoenkwan, P., Ahmed, S., Nantasenamat, C., Quinn, J.M.W., Moni, M.A., Lio’, P., Shoombuatong, W. AMYPred-FRL is a novel approach for accurate prediction of amyloid proteins by using feature representation learning (2022) Scientific Reports, .

Ahmad, S., Charoenkwan, P., Quinn, J.M.W., Moni, M.A., Hasan, M.M., Lio’, P., Shoombuatong, W. SCORPION is a stacking-based ensemble learning framework for accurate prediction of phage virion proteins (2022) Scientific Reports, .

Charoenkwan, P., Nantasenamat, C., Hasan, M.M., Moni, M.A., Lio', P., Manavalan, B., Shoombuatong, W. StackDPPIV: A novel computational approach for accurate prediction of dipeptidyl peptidase IV (DPP-IV) inhibitory peptides (2022) Methods, .

Charoenkwan, P., Schaduangrat, N., Moni, M.A., Lio’, P., Manavalan, B., Shoombuatong, W. SAPPHIRE: A stacking-based ensemble learning framework for accurate prediction of thermophilic proteins (2022) Computers in Biology and Medicine, .

Charoenkwan, P., Chiangjong, W., Hasan, M.M., Nantasenamat, C., Shoombuatong, W. Review and Comparative Analysis of Machine Learning-based Predictors for Predicting and Analyzing Anti-angiogenic Peptides (2022) Current Medicinal Chemistry, .

Charoenkwan, P., Schaduangrat, N., Hasan Mahmud, S.M., Thinnukool, O., Shoombuatong, W. RECENT DEVELOPMENT OF MACHINE LEARNING-BASED METHODS FOR THE PREDICTION OF DEFENSIN FAMILY AND SUBFAMILY (2022) EXCLI Journal, .

Charoenkwan, P., Schaduangrat, N., Hasan, M.M., Moni, M.A., Lió, P., Shoombuatong, W. EMPIRICAL COMPARISON AND ANALYSIS OF MACHINE LEARNING-BASED PREDICTORS FOR PREDICTING AND ANALYZING OF THERMOPHILIC PROTEINS (2022) EXCLI Journal, .

Kabir, M., Nantasenamat, C., Kanthawong, S., Charoenkwan, P., Shoombuatong, W. LARGE-SCALE COMPARATIVE REVIEW AND ASSESSMENT OF COMPUTATIONAL METHODS FOR PHAGE VIRION PROTEINS IDENTIFICATION (2022) EXCLI Journal, .

Charoenkwan, P., Schaduangrat, N., Lio', P., Moni, M.A., Manavalan, B., Shoombuatong, W. NEPTUNE: A novel computational approach for accurate and large-scale identification of tumor homing peptides (2022) Computers in Biology and Medicine, .

Wudhikarn, R., Charoenkwan, P., Malang, K. Deep Learning in Barcode Recognition: A Systematic Literature Review (2022) IEEE Access, .

Charoenkwan, P., Chiangjong, W., Nantasenamat, C., Moni, M.A., Lio’, P., Manavalan, B., Shoombuatong, W. SCMTHP: A New Approach for Identifying and Characterizing of Tumor-Homing Peptides Using Estimated Propensity Scores of Amino Acids (2022) Pharmaceutics, .

Charoenkwan, P., Chotpatiwetchkul, W., Lee, V.S., Nantasenamat, C., Shoombuatong, W. A novel sequence-based predictor for identifying and characterizing thermophilic proteins using estimated propensity scores of dipeptides (2021) Scientific Reports,

Charoenkwan, P., Nantasenamat, C., Hasan, M.M., Moni, M.A., Manavalan, B., Shoombuatong, W. Umpred-frl: A new approach for accurate prediction of umami

peptides using feature representation learning (2021) International Journal of Molecular Sciences, .

Charoenkwan, P., Chiangjong, W., Lee, V.S., Nantasenamat, C., Hasan, M.M., Shoombuatong, W. Improved prediction and characterization of anticancer activities of peptides using a novel flexible scoring card method (2021) Scientific Reports, .

Charoenkwan, P., Chiangjong, W., Nantasenamat, C., Hasan, M.M., Manavalan, B., Shoombuatong, W. StackIL6: a stacking ensemble model for improving the prediction of IL-6 inducing peptides (2021) Briefings in bioinformatics, .

Malik, A.A., Chotpatiwetchkul, W., Phanus-umporn, C., Nantasenamat, C., Charoenkwan, P., Shoombuatong, W. StackHCV: a web-based integrative machine-learning framework for large-scale identification of hepatitis C virus NS5B inhibitors (2021) Journal of Computer-Aided Molecular Design, .

Charoenkwan, P., Nantasenamat, C., Hasan, M.M., Manavalan, B., Shoombuatong, W. BERT4Bitter: A bidirectional encoder representations from transformers (BERT)-based model for improving the prediction of bitter peptides (2021) Bioinformatics, .

Charoenkwan, P., Nantasenamat, C., Hasan, M.M., Moni, M.A., Lio, P., Shoombuatong, W. Ibitter-fuse: A novel sequence-based bitter peptide predictor by fusing multi-view features (2021) International Journal of Molecular Sciences.

Charoenkwan, P., Shoombuatong, W., Nantasupha, C., Muangmool, T., Suprasert, P., Charoenkwan, K. Article ipmi: Machine learning-aided identification of parametrial invasion in women with early-stage cervical cancer (2021) Diagnostics.

Charoenkwan, P., Kanthawong, S., Nantasenamat, C., Hasan, M.M., Shoombuatong, W. iAMY-SCM: Improved prediction and analysis of amyloid proteins using a scoring card method with propensity scores of dipeptides (2021) Genomics.

Charoenkwan, P., Kanthawong, S., Schaduangrat, N., Yana, J., and Shoombuatong, W. (2020). Pvpred-scm: Improved prediction and analysis of phage virion proteins using a scoring card method. Cells, 9(2).

Charoenkwan, P., Schaduangrat, N., Nantasenamat, C., Piacham, T., & Shoombuatong, W. (2020). IQSP: A sequence-based tool for the prediction and analysis of quorum sensing peptides via chou's 5-steps rule and informative physicochemical properties. International Journal of Molecular Sciences, 21(1) doi:10.3390/ijms21010075

5 Teaching Experiences

At Chiang Mai University

Lecturer (Lecture and Lab)

- Enterprise Database Management System
- Advance Computer Programming
- Design and Analysis of Data Warehouse
- Design and Analysis of Business Intelligence

Guest Speaker for seminar class (graduated student)

- Text Mining

Guest Speaker for seminar class (graduated student)

- BioImage Informatics

Teaching assistant (Lecture and Lab):

- COMP 112 (Computer Programming)
- COMP 202 (IT2)
- COMP 211 (Computer Programming2)
- COMP 219 (Java)
- COMP 218 (Assembly)

At Mae Fah Luang University

Lecturer (Lecture and Lab)

- Object Oriented Programming
- Mobile Programming
- Computer Games Concept and Design
- Data Warehousing and Data Mining
- Artificial Intelligent
- System Analysis and Design (Lecture only)

At Mae Jo University

Lecturer (Lecture and Lab)

- Web Design

6 Skills

Languages:

Thai: Native speaker

English:	Listening	Reading	Speaking	Writing
	Excellent	Excellent	Good	Good

IELTS: **6.5**, Toeic: **840**

Chinese:	Listening	Reading	Speaking	Writing
	Good	-	Good	-

Computer Programming Language:

Currently:
C, C++, PyThon, R, MatLab, Php, RapidMiner, PowerBI, Tableau
Has an experience :
CUDA, HTML, CSS, CMS, Visual Basic.NET, Java, Java script, ASP.NET, ASP, SHELL script, XNA framework, C#.NET,Perl, Panda3D engine, Flash Actionscript, OpenGL, SystemML etc.

Cetificate:

Java Certified
IBM Scalable Data Science Course Certificate
IBM Advance Machine Learning and Signal Processing Course Certificate