# **HUANG Chen**



**Position:** Assistant Professor

**Faculty:** State Key Laboratory of Quality

Research in Chinese Medicine

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**Research Areas**: Bioinformatics, data analysis of high throughput sequencing to investigate potential biomarkers involved in diverse diseases.

Dr. Huang Cheng worked as assistant professor State Key Laboratory of Quality Research in Chinese Medicine, Macau University of Science and Technology. He obtained a Bachelor's degree in Biotechnology in Life Science Institute, Nanchang University, 2007. He graduated with Master degree from Biological information science and technology institute, Harbin Medical University in 2010. During the master study, his research focused on using SVM to predict potential drug target from ion channel proteins. Then he worked in BGI Shenzhen as a data analyst on next generation sequencing (NGS) from 2010 to 2012. He obtained Ph.D with Biomedicine in ICMS, University of Macau (UM) at the end of 2016, and his study involved in mining potential bioactive polypeptides from transcriptome of corals based on NGS, prediction of gene clusters involved in biosynthesis of antibiotics from the novel bacterium using whole genome sequencing. Then he continue the post-doctoral study in faculty of Health and Science until 2020. His study mainly focused on the identification and functional investigation of novel lncRNAs implicated in diverse biological processes or diseases, including asthma, ABPA, zebrafish embryo development, DNA damage, cytotoxicity, etc.

## **Academic Qualifications**

2012-2017	Ph.D. in Biomedical Sciences, Area of Specialization:
	Bioinformatics Institute of Chinese Medical Sciences,
	University of Macau, China
2007-2010	M.E. in Bioinformatics, Biological information science and
	technology institute, Harbin Medical University, China
2003-2007	B.S. in Biotechnology (Biopharmaceuticals), College of Life
	Science, Nanchang University, China

## Working experiences

2020-present	Assistant Professor, State Key Laboratory of Quality
	Research in Chinese Medicine, Macau University of Science
	and Technology, Macao
2017-2020	Post-doctoral, Faculty of Health Sciences, University of Macau,
	Macao
2010-2012	Analyst, Beijing Genomics Institute at Shenzhen
	(BGI-shenzhen)

#### **Publications**

Selected articles published in SCI journals in the recent past years: (#Contribution equally)

- 1. Shixue Sun, <u>Chen Huang</u>, Dongliang Leng, Chang Chen, Teng Zhang, Kuan Cheok Lei, and Xiaohua Douglas Zhang (2021). Gene fusion of IL7 is involved in the regulation of idiopathic pulmonary fibrosis. *Therapeutic Advances in Respiratory Disease* (DOI: 10.1177/1753466621995045)
- 2. <u>Chen Huang</u>, Bo Zhu, Dongliang Leng, Wei Ge, Xiaohua Douglas Zhang (2020). Long noncoding RNAs implicated in embryonic development in Ybx1 knockout Zebrafish. *FEBS Open Bio* (DOI: 10.1002/2211-5463.13057).
- 3. Peiyan Zheng, \*Chen Huang, Dongliang Leng, Baoqing Sun, xiaohua Douglas Zhang (2020). Transcriptome analysis of Peripheral Whole Blood reveals key IncRNAs implicated in

childhood asthma. BMC Medical Genomics (doi:10.21203/rs.2.15948/v1).

- 4. Zhong-Yan Zhou, Wai-Rong Zhao, Ying Xiao, Xiang-Ming Zhou, **Chen Huang**, Wen-Ting Shi, Jing Zhang, Qing Ye, Xin-Lin Chen, Jing-Yi Tang (2020). Antiangiogenesis effect of timosaponin AIII on HUVECs in vitro and zebrafish embryos in vivo. **Acta Pharmacol Sin.** 2020 Feb;41(2):260-269. doi: 10.1038/s41401-019-0291-z.
- 5. <u>Chen Huang</u>, Dongliang Leng, Kuan Cheok Lei, Shixue Sun, Xiaohua Douglas Zhang (2019). Transcriptome analysis reveals IncRNA-mediated complex regulatory network response to DNA damage in the liver tissue of Rattus norvegicus. *Journal of Cellular Physiology*. https://doi.org/10.1002/jcp.28889.
- 6. Dongliang Leng, \*Chen Huang, Kuan Cheok Lei, Shixue Sun, Xiaohua Douglas Zhang (2019). Co-expression network analysis of IncRNAs and mRNAs in Rats liver tissue reveals the complex interactions in response to pathogenic cytotoxicity. *International Journal of Biological Sciences*. 2019; 15(11):2296-2307. doi:10.7150/ijbs.33735.
- 7. <u>Chen Huang</u>, Dongliang Leng, Shixue Sun, Xiaohua Douglas Zhang. (2019). Re-analysis of the coral Acropora digitifera transcriptome reveals a complex IncRNAs-mRNAs interaction network implicated in Symbiodinium infection. *BMC Genomics*. PMCID: PMC6335708 doi: 10.1186/s12864-019-5429-3.
- 8. Jean-Étienne R L Morlighem, <u>Chen Huang</u>, Qiwen Liao, Paula Braga Gomes, Carlos Daniel Pérez, Álvaro Rossan de Brandão Prieto-da-Silva, Simon Ming-Yuen Lee, Gandhi Rádis-Baptista (2018). The Holo-Transcriptome of the Zoantharian Protopalythoa variabilis (Cnidaria: Anthozoa): A Plentiful Source of Enzymes for Potential Application in Green Chemistry, Industrial and Pharmaceutical Biotechnology. *Marine Drugs*. PMID: 29899267.
- 9. Qiwen Liao, Shengnan Li, Shirley Weng In Siu, Binrui Yang, <u>Chen Huang</u>, Judy Yuet-Wa Chan, Jean-É tienne R. L. Morlighem, Clarence Tsun Ting Wong, Gandhi Radis-Baptista, Simon Ming-Yuen Lee. Novel Kunitz-like Peptides Discovered in the Zoanthid Palythoa caribaeorum through Transcriptome Sequencing (2018). *Journal of Proteome research*. PMID: 29285938.
- 10. <u>Chen Huang</u>, Jean-Étienne RL Morlighem, Jing Cai, Qiwen Liao, Carlos Daniel Perez, Paula Braga Gomes, Min Guo, Gandhi Rádis-Baptista, Simon Ming Yuen Lee. (2017). Identification of long non-coding RNAs in two anthozoan species and their possible implications for coral bleaching. *Scientific Reports*. PMCID: PMC5509713 DOI: 10.1038/s41598-017-02561-y.

- 11. Min Guo, Ruifu Yang, <u>Chen Huang</u>, Qiwen Liao, Guangyi Fan, Chenghang Sun and Simon Ming-Yuen Lee). Evolutionary gradient of predicted nuclear localization signals (NLS)-bearing proteins in genomes of family Planctomycetaceae (2017). *BMC Microbiology*. PMID: 28376722.
- 12. <u>Chen Huang</u>, Ross Ka-Kit Leung, Min Guo, Li Tuo, Lin Guo, Wing Wai Yew, Inchio Lou, Simon Ming Yuen Lee, Chenghang Sun (2016). Genome-guided Investigation of Antibiotic Substances produced by Allosalinactinospora lopnorensis CA15-2T from Lop Nor region, China. *Scientific Reports.* PMID: 26864220.
- 13. <u>Chen Huang</u>, Jean-Étienne RL Morlighem, Hefeng Zhou, Erica Patrícia Lima, Paula Braga Gomes, Jing Cai, Inchio Lou, Carlos Daniel Perez, Simon Ming Yuen Lee, Gandhi Rádis-Baptista (2016). The transcriptome of the zoanthid *Protopalythoa variabilis* (Cnidaria, Anthozoa) reveals several predicted toxin-like and venom-auxiliary polypeptides. *Genome Biology Evolution*. PMID: 2756675825.
- 14. Congyuan Cao, Inchio Lou, <u>Chen Huang</u>, Ming-Yuen Lee (2016). Metagenomic sequencing of activated sludge filamentous bacteria community using the Ion Torrent platform. *Desalination & Water Treatment*. Jan 2016, Vol. 57 Issue 5, p2175
- 15. ZaijunZhang, GuohuiLi, SamuelS.W.Szeto, CheongMengChong, QuanQuan, <u>Chen Huang</u>, WeiCui, BaojianGuo, YuqiangWang, YifanHan, K.W.MichaelSiu, Simon MingYuenLee, IvanK.Chu (2015). Examining the neuroprotective effects of protocatechuic acid and chrysin on in vitro and in vivo models of Parkinson disease. *Free Radical Biology and Medicine*. PMID: 25769424.
- 16. Nitin Udpa , Roy Ronen, Dan Zhou, Junbin Liang, Tsering Stobdan, Otto Appenzeller, Ye Yin, Yuanping Du, Lixia Guo, Rui Cao, Yu Wang, Xin Jin, <u>Chen Huang</u>, Wenlong Jia Vineet Bafna and Gabriel G Haddad (2015). Whole genome sequencing of Ethiopian highlanders reveals conserved hypoxia tolerance genes. *Genome Biology*. 2014 15:R36.
- 17. Alba F.C. Torres, \*Chen Huang, Cheong Meng Chong, Siu Wai Leung, Alvaro R. B. Prieto-da-Silva, Alexandre Havt, Yves P. Quinet, Alice M. C. Martins, Simon M. Y. Lee, Gandhi Radis-Baptista (2013). Transcriptome analysis in venom gland of the predatory giant ant Dinoponera quadriceps: insights into the polypeptide toxin arsenal of hymenopterans. *PLoS One.* PMID: 24498135.
- 18. Dan Zhou, Nitin Udpa, Roy Ronen, Tsering Stobdan, Junbin Liang, Otto Appenzeller,

Huiwen W. Zhao, Yi Yin, Yuanping Du, Lixia Guo, Rui Cao, Yu Wang, Xin Jin, <u>Chen Huang</u>, Wenlong Jia, Dandan Cao, Guangwu Guo, Jorge L. Gamboa, Francisco Villafuerte, David. Callacondo, Jin Xue, Siqi Liu, Kelly A. Frazer, Yingrui Li, Vineet Bafna, Gabriel G. Haddad (2013). Whole-Genome Sequencing Uncovers the Genetic Basis of Chronic Mountain Sickness in Andean Highlanders. *American Journal of Human Genetics*. PMID: 23954164.

19. <u>Chen Huang</u>, Ruijie Zhang, Zhiqiang Chen, Yongshuai Jiang, Zhenwei Shang, Peng Sun, Xuehong Zhang, Xia Lia (2009). Predict potential drug targets from the ion channel proteins based on SVM. *Journal of Theoretical Biology*. PMID: 19903486.

#### Academic and social institutions

2018-present, Macao Bioinformatics Association, member of a council