

# 黃琛



職稱: 助理教授

學院/部門: 中藥質量研究國家重點實驗室

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**研究方向:** 高通量測序數據分析挖掘癌癥相關分子靶標、高通量測序數據挖掘特征基因指導腫瘤預後、高通量數據分析指導腫瘤精準治療

黃琛博士于 2007 年畢業于南昌大學生命科學學院，獲生物技術學士學位。2010 年畢業于哈爾濱醫科大學生物信息科學與技術學院，獲得生物信息學碩士學位。碩士期間研究方向為應用支持向量機挖掘離子通道蛋白潛在的藥物靶點。2010 年至 2012 年在深圳華大基因組研究院進行二代測序數據研究與分析。2016 年在澳門大學中華醫藥學院獲得生物醫藥博士學位。博士期間研究方向包括基於高通量轉錄組測序分析挖掘珊瑚蟲體內潛在藥用價值的活性肽，全基因測序挖掘放線菌新型的體內新型抗生素合成相關的基因簇。2017 年至 2020 年在澳門大學健康學院進行博士後研究，研究方向主要為基於高通量轉錄組測序數據分析挖掘過與呼吸道過敏性疾病，如哮喘、過敏性支氣管肺曲霉病等發病相關的長鏈非編碼 RNA。2020 年受聘于澳門科技大學中藥質量研究國家重點實驗室擔任助理教授。

## 學歷

2012-2017 澳門大學中華醫藥學院生物醫藥博士

2007-2010 哈爾濱醫科大學生物信息科學與技術學院生物信息學碩士

2003-2007 南昌大學生命科學學院生物技術學學士

## 工作履歷

2020-至今	澳門科技大學中藥質量研究國家重點實驗室	助理教授
2017-2020	澳門大學健康學院	博士後
2010-2012	深圳華大基因研究院	數據分析師

## 學術成果

### 近年發表的主要 SCI 期刊論文(#Contribution equally)

1. **Chen Huang**, 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).
2. Peiyan Zheng, **#Chen Huang**, Dongliang Leng, Baoqing Sun, xiaohua Douglas Zhang (2020). Transcriptome analysis of Peripheral Whole Blood reveals key lncRNAs implicated in childhood asthma. *BMC Medical Genomics* (doi:10.21203/rs.2.15948/v1).
3. 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.
4. **Chen Huang**, Dongliang Leng, Kuan Cheok Lei, Shixue Sun, Xiaohua Douglas Zhang (2019). Transcriptome analysis reveals lncRNA-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>.
5. Dongliang Leng, **#Chen Huang**, Kuan Cheok Lei, Shixue Sun, Xiaohua Douglas Zhang (2019). Co-expression network analysis of lncRNAs 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.
6. **Chen Huang**, Dongliang Leng, Shixue Sun, Xiaohua Douglas Zhang. (2019). Re-analysis of

the coral *Acropora digitifera* transcriptome reveals a complex lncRNAs-mRNAs interaction network implicated in Symbiodinium infection. *BMC Genomics*. PMID: PMC6335708 doi: 10.1186/s12864-019-5429-3.

7. Jean-Étienne R L Morlighem, **Chen Huang**, Qiwen Liao, Paula Braga Gomes, Carlos Daniel Pérez, Álvaro Rossan de Brandão Prieto-da-Silva, Simon Ming-Yuen Lee, Gandhi Radis-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.

8. Qiwen Liao, Shengnan Li, Shirley Weng In Siu, Binrui Yang, **Chen Huang**, Judy Yuet-Wa Chan, Jean-Étienne 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.

9. **Chen Huang**, Jean-Étienne RL Morlighem, Jing Cai, Qiwen Liao, Carlos Daniel Perez, Paula Braga Gomes, Min Guo, Gandhi Radis-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*. PMID: PMC5509713 DOI: 10.1038/s41598-017-02561-y.

10. Min Guo, Ruifu Yang, **Chen Huang**, 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.

11. **Chen Huang**, 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 lopnorenensis* CA15-2T from Lop Nor region, China. *Scientific Reports*. PMID: 26864220.

12. **Chen Huang**, Jean-Étienne RL Morlighem, Hefeng Zhou, Erica Patrícia Lima, Paula Braga Gomes, Jing Cai, Inchio Lou, Carlos Daniel Perez, Simon Ming Yuen Lee, Gandhi Radis-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.

13. Congyuan Cao, Inchio Lou, **Chen Huang**, Ming-Yuen Lee (2016). Metagenomic sequencing of activated sludge filamentous bacteria community using the Ion Torrent platform. *Desalination & Water Treatment*. Jan2016, Vol. 57 Issue 5, p2175
14. ZaijunZhang, GuohuiLi, SamuelS.W.Szeto, CheongMengChong, QuanQuan, **Chen Huang**, 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.
15. Nitin Udpa , Roy Ronen, Dan Zhou, Junbin Liang, Tsering Stobdan, Otto Appenzeller, Ye Yin, Yuanping Du, Lixia Guo, Rui Cao, Yu Wang, Xin Jin, **Chen Huang**, 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.
16. 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.
17. 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, **Chen Huang**, 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.
18. **Chen Huang**, 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.

#### 學術及社會機構任職

擔任澳門生物信息學學會理事會理事

