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教学科目: 医学统计学、药理实验方法、中药药理实验方法

研究方向: 生物信息分析挖掘肿瘤相关分子靶标、靶向代谢重编程辅助肿瘤免疫治疗、AI/机器学习辅助肿瘤精准治疗

个人简介

黄琛博士于 2007 年毕业于南昌大学生命科学学院，获生物技术学士学位。2010 年毕业于哈尔滨医科大学生物信息科学与技术学院，获得生物信息学硕士学位。硕士期间研究方向为应用支持向量机挖掘离子通道蛋白潜在的药物靶点。2010 年至 2012 年在深圳华大基因组研究院进行二代测序数据研究与分析。2016 年在澳门大学中华医药学院获得生物医药博士学位。博士期间研究方向包括基于高通量转录组测序分析挖掘珊瑚虫体内潜在药用价值的活性肽，全基因测序挖掘放线菌新型的体内新型抗生素合成相关的基因簇。2017 年至 2020 年在澳门大学健康学院进行博士后研究，研究方向主要为基于高通量转录组测序数据分析挖掘与呼吸道过敏性疾病，如哮喘、过敏性支气管肺曲霉病等发病相关的长链非编码 RNA。2020 年受聘于澳门科技大学中药质量研究国家重点实验室担任助理教授。

学历

2012-2017 澳门大学中华医药学院生物医药博士
2007-2010 哈尔滨医科大学生物信息科学与技术学院生物信息学硕士
2003-2007 南昌大学生命科学学院生物技术学学士

工作经历

2020-至今	澳门科技大学中药质量研究国家重点实验室	助理教授
2017-2020	澳门大学健康学院	博士后
2010-2012	深圳华大基因研究院	数据分析员

学术成果

Representative Papers published as Co-first author[#] or Corresponding author*

1.Changcheng Lu[#], **Chen Huang[#]**, Shuhui Qu, Huiyuan Lin, Hai-Jing Zhong, Cheong-Meng Chong (2024). Oxyimperatorin attenuates LPS-induced microglial activation in vitro and in vivo via suppressing NF-κB p65 signaling. *Biomedicine & Pharmacotherapy* (<https://doi.org/10.1016/j.biopha.2024.116379>)

2.Xiao Yang, Yingyi Wu, Xingyu Chen, Jiayue Qiu, **Chen Huang*** (2024). The Transcriptional Landscape of Immune-Response 3' -UTR Alternative Polyadenylation in Melanoma. *Int. J. Mol. Sci.* (<https://doi.org/10.3390/ijms25053041>)

3.Yi-Zhong Zhang[#], Huan-Ling Lai[#], **Chen Huang[#]**, Ze-Bo Jiang, Hao-Xin Yan, Xuan-Run Wang, Chun Xie, Ju-Min Huang, Wen-Kang Ren, Jia-Xin Li, Zhi-Ran Zhai, Xiao-Jun Yao, Qi-Biao Wu, Elaine Lai-Han Leung (2024). Tanshinone IIA induces ER stress and JNK activation to inhibit tumor growth and enhance anti-PD-1 immunotherapy in non-small cell lung cancer. *Phytomedicine* (<https://doi.org/10.1016/j.phymed.2024.155431>)

4.Xingyu Cheng, Min Deng, Zihan Wang, **Chen Huang*** (2024). MMP3C: An in-silico framework to depict cancer metabolic plasticity using gene expression profiles. *Briefings in Bioinformatics* (DOI: 10.1093/bib/bbad471)

5. Wang Zihan, Chen Xingyu, Si Weichen, **Chen Huang*** (2023). Systemic Pharmacology and Bioinformatics: Exploring the Modern biological Mechanisms of Rhubarb in the Treatment of Papillary Thyroid Carcinoma. *MedComm - Future Medicine* (DOI:10.1002/mef2.69)

6.**Chen Huang**, Min Deng, Dongliang Leng, Baoqing Sun, Peiyan Zheng, Xiaohua Douglas Zhang (2023). MIRS: An AI Scoring System for Predicting the Prognosis and Therapy of Breast Cancer. *Isience* (DOI: 10.1016/j.isci.2023.108322)

7.Yunwen Feng, Xingyu Chen, Xiaohua Douglas Zhang*, **Chen Huang*** (2023). Metabolic

Pathway Pairwise-Based Signature as a Potential Non-Invasive Diagnostic Marker in Alzheimer's Disease Patients. *Genes* (doi.org/10.3390/genes14061285)

8. Tianyi Cheng, Yingyi Wu, Zhiyu Liu, Yi Yu, Shixue Sun, Min Guo, Baoqing Sun*, **Chen Huang*** (2022). CDKN2A-mediated molecular subtypes characterize the hallmarks of tumor microenvironment and guide precision medicine in Triple Negative Breast Cancer. *Frontiers in Immunology* (DOI 10.3389/fimmu.2022.970950)

9. LitingWu, XiangqingHou, WentingLuo, HaishengHu, XianhuiZheng, YueminChen, Zhangkai J.Cheng, **Chen Huang***, Baoqing Sun* (2022). Three patterns of sensitization to mugwort, timothy, birch and their major allergen components revealed by Latent class analysis. *Molecular Immunology* (https://doi.org/10.1016/j.molimm.2022.03.009)

10. Tianyi Cheng, Peiyong Chen, Jingyi Chen, Yingtong Deng, **Chen Huang*** (2022). Landscape analysis of Matrix Metalloproteinases unveils key prognostic markers for patients with breast cancer. *Frontiers in Genetics* (https://doi.org/10.3389/fgene.2021.809600)

11. **Chen Huang**, Dongliang Leng, Peiyan Zheng, Min Deng, Baoqing Sun, Xiaohua Douglas Zhang (2021). Comprehensive transcriptome analysis of peripheral blood unravels key lncRNAs implicated in ABPA and asthma. *PeerJ* (DOI 10.7717/peerj.11453)

12. **Chen Huang**, Bo Zhu, Dongliang Leng, Wei Ge, Xiaohua Douglas Zhang (2021). Long noncoding RNAs implicated in embryonic development in Ybx1 knockout Zebrafish. *FEBS Open Bio* (DOI: 10.1002/2211-5463.13057).

13. 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).

14. **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.

15. 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.

16. 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.

17. Chen Huang, 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*. PMID: PMC5509713 DOI: 10.1038/s41598-017-02561-y.

18. 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.

19. 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 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.

20. 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.

21. 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.

Representative Papers published as Co-author

22.Teng Zhang, Xinzheng Dong, Dandan Wang, **Chen Huang**, Xiaohua Douglas Zhang (2024). RespirAnalyzer: an R package for analyzing data from continuous monitoring of respiratory signals. *Bioinformatics Advances* (<https://doi.org/10.1093/bioadv/vbae003>)

23.Dongliang Leng, Ziyi Yang, Heng Sun, Chengcheng Song, **Chen Huang**, Ka U Ip, Guokai Chen, Chu-Xia Deng, Xiaohua Douglas Zhang, Qi Zhao (2023). Comprehensive analysis of tumor microenvironment reveals prognostic ceRNA network related to immune infiltration in sarcoma. *Clinical Cancer Research* (DOI: 10.1158/1078-0432.CCR-22-3396)

24.Min Guo, Siwei Xie, Junhua Wang, Yuzhi Zhang, Xiangyang He, Pengfei Luo, Jin Deng, Chunhui Zhou, Jiao Qin, **Chen Huang**, Libiao Zhang (2023). The difference in the composition of gut microbiota is greater among bats of different phylogenies than among those with different dietary habits. *Frontiers in Microbiology* (doi: 10.3389/fmicb.2023.1207482)

25.Haiyan Chen, Jing Xu, Siyu Wei, Zhe Jia, Chen Sun, Jingxuan Kang, Xuying Guo, Nan Zhang, Junxian Tao, Yu Dong, Chen Zhang, ... **Chen Huang**, Fanwu Kong, Guoping Tang, Yongshuai Jiang, Mingming Zhang (2023). RABC: Rheumatoid Arthritis Bioinformatics. *Nucleic Acids Research* (doi.org/10.1093/nar/gkac850)

26.Shixue Sun, **Chen Huang**, 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)

27.Heng Sun, JM Zeng, ZQ Miao, KC Lei, **Chen Huang**, LL Hu, Sek Man Su, Un In Chan, Kai Miao, Xu Zhang, Aiping Zhang, Sen Guo, Si Chen, Ya Meng, Min Deng ,..., Xiaohua Douglas Zhang, Xiaoling Xu, Chu-Xia Deng (2021). Dissecting the heterogeneity and tumorigenesis of BRCA1 deficient mammary tumors via single cell RNA sequencing. *Theranostics* (DOI: 10.7150/thno.63995).

28.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.

29. 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 Rádís-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.

30. 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.

31. 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.

32. 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

33. Zaijun Zhang, Guohui Li, Samuel S.W. Szeto, Cheong Meng Chong, Quan Quan, **Chen Huang**, Wei Cui, Baojian Guo, Yuqiang Wang, Yifan Han, K.W. Michael Siu, Simon Ming Yuen Lee, Ivan K. 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.

34. 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.

35. 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, ... 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.

学术及社会机构任职

担任澳门生物信息学学会理事会理事