

# 黃琛



**職稱：** 助理教授  
**學院/部門：** 中藥機製與質量全國重點實驗室、  
埃爾文內爾博士生物物理與創新  
藥物實驗室  
**電郵地址：** chuang@must.edu.mo  
**電話：** (853) 6806-9981  
**傳真：** (853) 2882-5886  
**辦公室：** L503  
**郵寄地址：** 澳門氹仔偉龍馬路澳門科技大学

**教學科目：** 醫學統計學、藥理實驗方法、中藥藥理實驗方法、生物醫學研究進展

**研究方向：** 生物信息分析挖掘腫瘤相關分子靶標、靶向代謝重編程輔助腫瘤免疫治療、AI/機器學習輔助腫瘤精準治療、AI 輔助中藥復方開發和優化

黃琛博士，碩士畢業於哈爾濱醫科大學生物信息科學與技術學院生物信息學專業，博士畢業於澳門大學中華醫藥學院生物醫藥專業。目前為澳門科技大學中藥機製與質量全國重點實驗室、埃爾文內爾博士生物物理與創新藥物實驗室助理教授，主要研究方向為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、AI 輔助中藥復方開發和優化等。以第一或通訊作者在 Briefings in bioinformatics、Clinical and Translational Medicine、Ultrasonics Sonochemistry、Iscience、Phytomedicine、International Journal of Biological Sciences、Journal of Cellular Physiology、Genome Biology and Evolution 等期刊发表 SCI 论文 30 余篇。

## 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	數據分析工程師

## 學術成果

### Representative Papers published as First author or Corresponding author

1. Prioritizing pathway signature using deep learning approach: a novel strategy for Traditional Chinese Medicine Formula generation and optimization. *Briefings in Bioinformatics*. Volume 26, Issue 4, July 2025, bbaf403. (Corresponding author)
2. Association between calcium intake and risk of congestive heart failure: a cross-sectional study from the 2003–2018 NHANES database. *BMC Cardiovascular Disorders*. 25, Article number: 518 (2025). (Corresponding author)
3. Ultrasound-responsive nanobubble-mediated sonodynamic therapy sensitizes disulfidptosis in the treatment of liver hepatocellular carcinoma. *Ultrasonics Sonochemistry*. Volume 118, July 2025, 107368. (Corresponding author)
4. Computational Tools for Studying Genome Structural Variation. *OMICS: A Journal of Integrative Biology*. 2025 Feb;29(2):36-48. (Corresponding author)
5. iDICss robustly predicts melanoma immunotherapy response by synergizing genomic and transcriptomic knowledge via independent component analysis. *Clinical and Translational Medicine*. 2025 Jan;15(1):e70183 (Corresponding author)
6. Discovering a novel glycosyltransferase gene CmUGT1 enhances main metabolites production of Cordyceps militaris. *Frontiers in Microbiology*. 2024 Oct;15, 1437963 (Co-first author)
7. Metabolic Reprogramming Induced by Aging Modifies the Tumor Microenvironment. *Cells*. 2024 Oct;13 (20), 1721 (Corresponding author)
8. Serum liver enzymes and risk of stroke: Systematic review with meta-analyses and Mendelian randomization studies. *European Journal of Neurology*. 2024 DOI: 10.1111/ene.16506 (Corresponding author)
9. A Neural Network–Based Scoring System for Predicting Prognosis and Therapy in Breast Cancer. *Current Protocols*. 2024 Aug;4(8):e1122 (Corresponding author)
10. Oxyimperatorin attenuates LPS-induced microglial activation in vitro and in vivo via suppressing NF- $\kappa$ B p65 signaling. *Biomedicine & Pharmacotherapy*. 2024 Apr;173:116379 (Co-first author)

11. Transcriptional Landscape of Immune-Response 3' -UTR Alternative Polyadenylation in Melanoma. *Int J Mol Sci.* 2024 Mar 6;25(5):3041. (**Corresponding author**)
12. 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.* 2024 Jun;128:155431 (**Co-first author**)
13. MMP3C: An in-silico framework to depict cancer metabolic plasticity using gene expression profiles. *Briefings in Bioinformatics.* 2023 Nov 22;25(1):bbad471 (**Corresponding author**)
14. Systemic Pharmacology and Bioinformatics: Exploring the Modern biological Mechanisms of Rhubarb in the Treatment of Papillary Thyroid Carcinoma. *MedComm - Future Medicine.* 2023 Volume2, Issue4 (**Corresponding author**)
15. MIRS: An AI Scoring System for Predicting the Prognosis and Therapy of Breast Cancer. *Isience.* 2023 Oct 26;26(11):108322. (**Co-first author**)
16. Metabolic Pathway Pairwise-Based Signature as a Potential Non-Invasive Diagnostic Marker in Alzheimer's Disease Patients. *Genes.* 2023 Jun 17;14(6):1285. (**Corresponding author**)
17. CDKN2A-mediated molecular subtypes characterize the hallmarks of tumor microenvironment and guide precision medicine in Triple Negative Breast Cancer. *Front Immunol.* 2022 Aug 16;13:970950. (**Corresponding author**)
18. Three patterns of sensitization to mugwort, timothy, birch and their major allergen components revealed by Latent class analysis. *Molecular Immunology.* 2022 May;145:59-66. (**Corresponding author**)
19. Landscape analysis of Matrix Metalloproteinases unveils key prognostic markers for patients with breast cancer. *Front Genet.* 2022 Jan 6;12:809600. (**Corresponding author**)
20. Comprehensive transcriptome analysis of peripheral blood unravels key lncRNAs implicated in ABPA and asthma. *PeerJ.* 2021 Jun 24;9:e11453. (**Co-first author**)
21. Long noncoding RNAs implicated in embryonic development in Ybx1 knockout Zebrafish. *FEBS Open Bio.* 2021 Apr;11(4):1259-1276. (**Co-first author**).
22. Transcriptome analysis of Peripheral Whole Blood reveals key lncRNAs implicated in childhood asthma. *BMC Medical Genomics.* 2020 Sep 18;13(1):136. (**Co-first author**).
23. Transcriptome analysis reveals lncRNA-mediated complex regulatory network response to DNA damage in the liver tissue of Rattus norvegicus. *J Cell Physiol.* 2019 Dec;234(12):23216-23231. (**Co-first author**)
24. Co-expression network analysis of lncRNAs and mRNAs in Rats liver tissue reveals the complex interactions in response to pathogenic cytotoxicity. *Int J Biol Sci.* 2019 Aug

- 22;15(11):2296-2307. (Co-first author)
- 25.Re-analysis of the coral *Acropora digitifera* transcriptome reveals a complex lncRNAs-mRNAs interaction network implicated in Symbiodinium infection. **BMC Genomics**. 2019 Jan 16;20(1):48. (Co-first author)
- 26.Identification of long non-coding RNAs in two anthozoan species and their possible implications for coral bleaching. **Sci Rep**. 2017 Jul 13;7(1):5333. (First author)
- 27.Genome-guided Investigation of Antibiotic Substances produced by *Allosalinactinospora lopnorenensis* CA15-2T from Lop Nor region, China. **Sci Rep**. 2016 Feb 11;6:20667. (Co-first author)
- 28.The transcriptome of the zoanthid *Protopalythoa variabilis* (Cnidaria, Anthozoa) reveals several predicted toxin-like and venom-auxiliary polypeptides. **Genome Biol Evol**. 2016 Oct 5;8(9):3045-3064. (Co-first author)
- 29.Transcriptome analysis in venom gland of the predatory giant ant *Dinoponera quadricaps*: insights into the polypeptide toxin arsenal of hymenopterans. **PLoS One**. 2014 Jan 31;9(1):e87556. (Co-first author)
- 30.Predict potential drug targets from the ion channel proteins based on SVM. *J Theor Biol*. 2010 Feb 21;262(4):750-6. (Co-first author)

#### Representative Papers published as Co-author

- 31.Hylocereus polyrhizus pomace polysaccharides for the treatment of obesity-induced intestinal mucosal injury. **International Journal of Biological Macromolecules**. Volume 333, Part 1, December 2025, 148768.
- 32.In Situ Assembly of Transformable Mono-peptide on Activated Neutrophils Attenuates NETs-Induced Hepatocellular Carcinoma Metastasis by Disrupting NE Nuclear Translocation. **Advanced Science**. 24 October 2025.
- 33.Pitaya stem polysaccharide promotes wound healing by modulating macrophage polarization via single-cell RNA sequencing evidence. **International Journal of Biological Macromolecules**. Volume 308, Part 3, May 2025, 142653.
- 34.Taurine and proline promote lung tumour growth by co-regulating Azgp1/mTOR signalling pathway. **NPJ Precision Oncology**. 9, Article number: 90 (2025)
- 35.Dietary polysaccharides from dragon fruit pomace, a co-product of the fruit processing industry, exhibit therapeutic potential in high-fat diet-induced metabolic disorders. **Food Research International**. Volume 203, February 2025, 115818.
- 36.Shared genetics and causal association between plasma levels of SARS - CoV - 2 entry receptor ACE2 and Alzheimer's disease. **CNS Neurosci Ther**. 2024 Jul;30(7):e14873.

37. RespirAnalyzer: an R package for analyzing data from continuous monitoring of respiratory signals. *Bioinform Adv.* 2024 Jan 13;4(1):vbae003.
  38. Interpretation of 10 years of Alzheimer's disease genetic findings in the perspective of statistical heterogeneity. *Briefings in Bioinformatics* 2024 Mar 27;25(3):bbae140.
  39. Comprehensive analysis of tumor microenvironment reveals prognostic ceRNA network related to immune infiltration in sarcoma. *Clin Cancer Res.* 2023 Oct 2;29(19):3986-4001.
  40. The difference in the composition of gut microbiota is greater among bats of different phylogenies than among those with different dietary habits. *Front Microbiol.* 2023 Jul 28;14:1207482.
  41. RABC: Rheumatoid Arthritis Bioinformatics center. *Nucleic Acids Res.* 2023 Jan 6;51(D1):D1381-D1387.
  42. Gene fusion of IL7 is involved in the regulation of idiopathic pulmonary fibrosis. *Thor Adv Respir Dis.* 2021 Jan-Dec;15:1753466621995045.
  43. Dissecting the heterogeneity and tumorigenesis of BRCA1 deficient mammary tumors via single cell RNA sequencing. *Theranostics.* 2021 Oct 25;11(20):9967-9987.
  44. Antiangiogenesis effect of timosaponin AIII on HUVECs in vitro and zebrafish embryos in vivo. *Acta Pharmacol Sin.* 2020 Feb;41(2):260-269.
  45. 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. *Mar Drugs.* 2018 Jun 13;16(6):207.
  46. Novel Kunitz-like Peptides Discovered in the Zoanthid *Palythoa caribaeorum* through Transcriptome Sequencing (2018). *J Proteome Res.* 2018 Feb 2;17(2):891-902
  47. Evolutionary gradient of predicted nuclear localization signals (NLS)-bearing proteins in genomes of family Planctomycetaceae (2017). *BMC Microbiol.* 2017 Apr 4;17(1):86.
  48. Metagenomic sequencing of activated sludge filamentous bacteria community using the Ion Torrent platform. *Desalination & Water Treatment.* Jan 2016, Vol. 57 Issue 5, p2175
  49. Examining the neuroprotective effects of protocatechuic acid and chrysin on in vitro and in vivo models of Parkinson disease. *Free Radic Biol Med.* 2015 Jul;84:331-343.
  50. Whole genome sequencing of Ethiopian highlanders reveals conserved hypoxia tolerance genes. *Genome Biol.* 2014 Feb 20;15(2):R36.
- Whole-Genome Sequencing Uncovers the Genetic Basis of Chronic Mountain Sickness in Andean Highlanders. *Am J Hum Genet.* 2013 Sep 5;93(3):452-62.

#### 學術及社會機構任職

擔任澳門生物信息學學會副會長