

黃琛



职称： 助理教授
学院/部门： 中药机制与质量全国重点实验室、
埃尔文内尔博士生物物理与创新
药物实验室
邮电地址： chuang@must.edu.mo
电话： (853) 6806-9981
传真： (853) 2882-5886
办公室： L503
邮寄地址： 澳门凼仔伟龙马路澳门科技大学

教学科目：医学统计学、药理实验方法、中药药理实验方法、生物医学研究进展

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、AI 辅助中药复方开发和优化

个人简介

黄琛博士，硕士毕业于哈尔滨医科大学生物信息科学与技术学院生物信息学专业，博士毕业于澳门大学中华医药学院生物医药专业。目前为澳门科技大学中药机制与质量全国重点实验室、埃尔文内尔博士生物物理与创新药物实验室助理教授，主要研究方向为高通量测序数据分析挖掘癌症相关分子靶标、高通量测序数据挖掘特征基因指导肿瘤预后、高通量数据分析指导肿瘤精准治疗、AI 辅助中药复方开发和优化等。以第一或通讯作者在 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。

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	数据分析工程师

学术成果

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- κ 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 quadriceps*: 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.* Jan2016, 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.

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