HUANG Chen

Position:	Assistant Professor
Faculty ：	the Sate Key Laboratory of Mechanism and Quality of Chinese Medicine
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Teaching course: Medical Statistics, Pharmacological experimental methods, Experimental Methods of TCM Pharmacology, Progress in Biomedical Research

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

Dr. Chen Huang earned his Master's degree in Bioinformatics from the School of Bioinformatics Science and Technology at Harbin Medical University, and his Ph.D. in Biomedicine from the Institute of Chinese Medical Sciences at the University of Macau. He currently serves as an Assistant Professor at The State Key Laboratory of Mechanism and Quality of Chinese Medicine and the Dr. Neher’s Biophysics Laboratory for Innovative Drug Discovery at Macau University of Science and Technology. His primary research focuses on high-throughput sequencing data analysis to identify cancer-related molecular targets, mining feature genes from high-throughput sequencing data for cancer prognosis, leveraging high-throughput data analysis to guide precision oncology therapeutics and AI-assisted development and optimization of traditional Chinese medicine compounds. Dr. Huang has authored or co-authored over 30 SCI-indexed papers as first or corresponding author in renowned journals such as Briefings in Bioinformatics, Ultrasonics Sonochemistry, Clinical and Translational Medicine, International Journal of Biological Sciences, Journal of Cellular Physiology, and Genome Biology and Evolution.

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 Scienceand 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

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-κB 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 autho**r)
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 autho**r)
15. MIRS: An AI Scoring System for Predicting the Prognosis and Therapy of Breast Cancer. ***Iscience.*** 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 lopnorensis 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 Monopeptide 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. ***Ther 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.
51. 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.

Academic and social institutions

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