

# 王倩雯

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## 教育背景

博士 | 香港中文大学 | **2015.08-2021.02**

- 专业: 分子生物技术

学士 | 东北大学 | **2010.09-2014.06**

- 专业: 计算机科学与技术

## 研究经历

讲师 | 南方医科大学 | **2021.06 – 现在**

- 基础医学院, 生物信息学系

副研究员 | 香港中文大学 | **2021.04 – 2022.05**

- 生命科学院

研究助理 | 香港中文大学(深圳研究院) | **2014.10 - 2015.05**

- 生命科学院

## 教学经历

讲师 | 南方医科大学 | **2021.06 – 现在**

- 基础医学院, 生物信息学系

助教 | 香港中文大学 | **2015.08 – 2019.08**

- 生命科学院

研究生顾问 | 香港中文大学(联合书院) | **2016.08 – 2017.08**

- 联合书院

## 技能特长

### 编程技能

- Bash/Shell, R, Python, MySQL, C++, HTML5

### 多组学生物信息分析

- 全基因组甲基化测序, 染色质免疫沉淀测序, 小 RNA 测序, 染色质开放性测序, 纳米孔可直接 RNA 链测序和转录组测序

## 语言

- 流利的使用中文与英文

## 获奖

研究生发表论文奖 | School of Life Sciences, 香港中文大学 | 2020-2021

学术报告 | 2020-2021 Science Faculty Postgraduate Research Day, 香港中文大学 | 2021.01

最佳报告演讲奖 | 2020 SKLA/ IPMBAB Seminar Series, 香港中文大学 | 2020.11

青年学者竞赛优胜奖 | WUN Symposium cum Research Summit on Impacts of Grain Legume Research and Development in Developing Countries, 香港中文大学 | 2017.06

## 论文

10. Xiao Z<sup>#</sup>, **Wang Q**<sup>#</sup>, Li M, Huang M, Wang Z, Xie M, Varshney RK, Nguyen HT, Chan T, Lam H<sup>\*</sup>. 2022. Wildsoydb DataHub : an online platform for accessing soybean multiomic datasets across multiple reference genomes. *Plant Physiology* (accpeted)
9. Feng T<sup>#</sup>, Wu T<sup>#</sup>, Zhang, Y<sup>#</sup> Zhou L<sup>#</sup>, Liu S<sup>#</sup>, Li L, Li M, Hu E, **Wang Q**, Fu X, Zhan L, Xie Z, Xie W, Huang X, Shang X & Yu G, 2022, Stemness Analysis Uncovers That The Peroxisome Proliferator-Activated Receptor Signaling Pathway Can Mediate Fatty Acid Homeostasis In Sorafenib-Resistant Hepatocellular Carcinoma Cells, *Frontiers in Oncology* 12(July), 1–14
8. Zhou L<sup>#</sup>, Feng T<sup>#</sup>, Xu S, Gao F, Lam TT, **Wang Q**, Wu T, Huang H, Zhan L, Li L, Guan Y, Dai Z<sup>\*</sup>, **Yu G**<sup>\*</sup>. 2022. ggmsa: a visual exploration tool for multiple sequence alignment and associated data. *Briefings in Bioinformatics* 1–12
7. Huang M, Zhang L, Zhou L, Yung WS, Wang Z, Xiao Z, **Wang Q**, Wang X, Li M, Lam H<sup>\*</sup>. 2022. Identification of the accessible chromatin regions in six tissues in the soybean. *Genomics* 114(3), 110364.
6. Yung W<sup>#</sup>, **Wang Q**<sup>#</sup>, Huang M, Wong F-L, Liu A, Ng M, Li K, Sze C, Li M, Lam H<sup>\*</sup>. 2022. Priming-induced alterations in histone modifications modulate transcriptional responses in soybean under salt stress. *The Plant Journal* 190(6): 1575-1590
5. **Wang Q**<sup>#</sup>, Bao X<sup>#</sup>, Chen S<sup>#</sup>, Zhong H<sup>#</sup>, Liu Y, Zhang L, Xia Y, Kragler F, Luo M, Li XD, *et al.* 2021. AtHDA6 functions as an H3K18ac eraser to maintain pericentromeric CHG methylation in Arabidopsis thaliana. *Nucleic Acids Research* 49: 9755–9767
4. Yung W, Li M, Sze C, **Wang Q**, Lam H<sup>\*</sup>. 2021. Histone modifications and chromatin remodelling in plants in response to salt stress. *Physiologia Plantarum*: ppl.13467.
3. Huang M, Zhang L, Zhou L, Wang M, Yung WS, Wang Z, Duan S, Xiao Z, **Wang Q**, Wang X, *et al.* 2021. An expedient survey and characterization of the soybean JAGGED 1 (GmJAG1) transcription factor binding preference in the soybean genome by modified ChIPmentation on soybean protoplasts. *Genomics* 113: 344–355.
2. **Wang Q**<sup>#</sup>, Yung W<sup>#</sup>, Wang Z, Lam H<sup>\*</sup>. 2020. The histone modification H3K4me3 marks functional genes in soybean nodules. *Genomics* 112: 5282–5294.
1. Liu A<sup>#</sup>, Xiao Z<sup>#</sup>, Li M, Wong L, Yung W, Ku Y, **Wang Q**, Wang X, Xie M, Yim AK, *et al.* 2019.

Transcriptomic reprogramming in soybean seedlings under salt stress. *Plant, Cell & Environment* 42: 98–114.