

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 | 2022.06 - 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 | 2022.06 - 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

11. **Wang Q[#]**, Li M[#], Wu T, Zhan L, Li L, Chen M, Xie W, Xie Z, Hu E, Xu S, Yu G^{*}. 2022. Exploring epigenomic datasets by ChIPseeker. *Current Protocols in Bioinformatics*, 2022. doi: 10.1002/cpz1.585.

10. Xiao Z[#], **Wang Q[#]**, Li M, Huang M, Wang Z, Xie M, Varshney RK, Nguyen HT, Chan T^{*}, Lam H^{*}. 2022. Wildsoydb DataHub : an online platform for accessing soybean multiomic datasets across multiple reference genomes. *Plant Physiol.*, 1-4

9. Feng T[#], Wu T[#], Zhang, Y[#] Zhou L[#], Liu S[#], 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[#], Feng T[#], Xu S, Gao F, Lam TT, **Wang Q**, Wu T, Huang H, Zhan L, Li L, Guan Y, Dai Z^{*}, **Yu G^{*}**. 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^{*}. 2022. Identification of the accessible chromatin regions in six tissues in the soybean. *Genomics* 114(3), 110364.

6. Yung W[#], **Wang Q[#]**, Huang M, Wong F-L, Liu A, Ng M, Li K, Sze C, Li M^{*}, Lam H^{*}. 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[#]**, Bao X[#], Chen S[#], Zhong H[#], Liu Y, Zhang L, Xia Y, Kragler F, Luo M, Li XD^{*}, Lam H^{*}, Zhang S^{*}. 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^{*}. 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, Li M, Lam H^{*}. 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[#]**, Yung W[#], Wang Z, Lam H^{*}. 2020. The histone modification H3K4me3 marks functional

genes in soybean nodules. *Genomics* 112: 5282–5294.

1. Liu A[#], Xiao Z[#], Li M, Wong L, Yung W, Ku Y, **Wang Q**, Wang X, Xie M, Yim AK, Chan T, Lam H^{*}. 2019. Transcriptomic reprogramming in soybean seedlings under salt stress. *Plant, Cell & Environment* 42: 98–114.