

# ZHIYUAN HU

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Nuffield Department of Medicine ◇ Oxford OX3 7BN, UK

## EDUCATION

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**University of Oxford, United Kingdom**

*Oct 2015 - Sep 2019*

**D.Phil in Clinical Medicine**

Thesis title: *Functional genomics studies of cancer and cells of origin: from pan-cancer to single-cell*

Supervisors: Dr Christopher Yau and Prof Ahmed Ahmed

**Peking University, China**

*Sep 2011 - July 2015*

**B.S. in Biological Science**

Undergraduate Honors Program in Biology

Cumulative GPA: 3.86/4.00 (ranking: 1st out of 108)

## WORK EXPERIENCE

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**MRC Weatherall Institute of Molecular Medicine/Nuffield department of Women's & Reproductive Health, University of Oxford**

*Oct 2019 - Present*

**Postdoctoral research assistant**

Research field: *Exploring cancer genome, transcriptome and the initiation of ovarian cancer*

Supervisor: Prof Ahmed Ahmed

## SCHOLARSHIPS AND AWARDS

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AACR-Margaret Foti Scholar-in-Training Award, American Association for Cancer Research *2019*

Travel and Research Fund, St Cross College, University of Oxford *2019*

Poster Prize, CRUK Oxford Centre 2018 Symposium *2018*

NDM Graduate Student Prize, University of Oxford *2017*

CSC-NDM Studentship *2015*

Shen Tong Outstanding Undergraduate Award, Peking University *2015*

China National Scholarship *2014*

Li & Fung Scholarship, Victor and William Fung Foundation *2014*

Arawana Scholarship, Yihai Kerry, Wilmar China *2013*

Robin Li Scholarship, Robin Li Foundation *2012*

## PUBLICATIONS

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**Z. Hu**, M. Artibani, A. Alsaadi, N. Wietek, M. Morotti, L. Santana Gonzalez, S. El-Sahhar, M. KaramiNejadRanjbar, G. Mallett, T. Shi, K. Masuda, Y. Zheng, K. Chong, S. Damato, S. Dhar, R. Garruto Campanile, H. Soleymani majd, V. Cerundolo, T. Sauka-Spengler, C. Yau\*, A. A. Ahmed\*. The repertoire of serous ovarian cancer non-genetic heterogeneity revealed by single-cell sequencing of normal fallopian tube epithelial cells. (Under 2nd round review at *Cancer Cell*) (\* co-corresponding authors)

R. Ma\*, K. P. Capobianco, N. T. Buchanan, **Z. Hu**, J. M. Oakman\*. Etiologic and Treatment Conceptualizations of Disordered Eating Symptoms among Mainland Chinese Therapists. *International Journal of Eating Disorders* (Accepted)

M. P. Menden, D. Wang, M. J. Mason, B. Szalai, K. C. Bulusu, Y. Guan, T. Yu, J. Kang, M. Jeon, R. Wolfinger, T. Nguyen, M. Zaslavskiy, **AstraZeneca-Sanger Drug Combination DREAM Consortium**, I. Sock Jang, Z. Ghazoui, M. Eren Ahsen, R. Vogel, E. Chaibub Neto, T. Norman, E. K. Y. Tang, M. J. Garnett, G. Y. Di Veroli, S. Fawell, G. Stolovitzky, J. Guinney\*, J. R. Dry\* J. Saez-Rodriguez\*. Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. *Nature Communications* **10**, 2674 (2019). <https://www.nature.com/articles/s41467-019-09799-2> (\* co-corresponding authors)

T. Motohara, K. Masuda, M. Morotti, Y. Zheng, S. El-Sahhar, K. Chong, N. Wietek, A. Alsaadi, M. Karaminejadranjbar, **Z. Hu**, M. Artibani, L. Santana Gonzalez, H. Katabuchi, H. Saya and A. Ahmed. An evolving story of the metastatic voyage of ovarian cancer cells: cellular and molecular orchestration of the adipose-rich metastatic microenvironment. *Oncogene*, 38, 2885–2898 (2019).

**Z. Hu**, C. Yau\* and A. Ahmed\*. A pan-cancer genome-wide analysis reveals tumour dependencies by induction of non-sense mediated decay. *Nature Communications* **8**, 15943 (2017). doi: 10.1038/ncomms15943. (\* co-corresponding authors)

## CONFERENCE ABSTRACT

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**Z. Hu**, A. Alsaadi, N. Wietek, L. Santana Gonzlez, C. Yau\* and A. Ahmed\*. Deep single-cell RNA-seq of the putative cell of origin revealed a novel molecular subtype of high-grade serous ovarian cancer with poor prognosis [abstract]. In: *Proceedings of the American Association for Cancer Research Annual Meeting 2019* (Accepted) (\* co-corresponding authors)

## PREPRINT

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**Z. Hu**, M. Artibani, A. Alsaadi, N. Wietek, M. Morotti, L. Santana Gonzalez, S. El-Sahhar, M. KaramiNejadRanjbar, G. Mallett, T. Shi, K. Masuda, Y. Zheng, K. Chong, S. Damato, S. Dhar, R. Garruto Campanile, H. Soleymani majd, V. Cerundolo, T. Sauka-Spengler, C. Yau\*, A. A. Ahmed\*. The repertoire of serous ovarian cancer non-genetic heterogeneity revealed by single-cell sequencing of normal fallopian tube epithelial cells. *BioRxiv*. January 2019: 672626. <http://biorxiv.org/content/early/2019/06/17/672626>

## PATENT

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UK Patent Application No. 1902653.3 Ovarian Cancer Biomarkers. Date of filing: 27 February 2019

## RESEARCH EXPERIENCE

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**Nuffield Department of Medicine, University of Oxford**

*Project: Single-cell RNA sequencing in ovarian cancer*

Oct 2015 - Present

*Oxford, UK*

· Advisors: Prof. Christopher Yau, Prof. Ahmed Ahmed and Prof. Chris Holmes

- Conducted single-cell RNA sequencing with clinical samples of ovarian cancer
- Analysed the single-cell RNA-seq data

**Nuffield Department of Medicine, University of Oxford**

Oct 2015 - May 2017

*Project: Pan-cancer analysis of nonsense-mediated decay in cancer genomes*

*Oxford, UK*

- Advisors: Prof. Christopher Yau and Prof. Ahmed Ahmed
- Conducted a pan-cancer genome-wide analysis of nonsense-mediated decay
- Revealed tumour dependencies on induction of nonsense-mediated decay

**Nuffield Department of Medicine, University of Oxford**

Oct 2015 - Oct 2016

*Project: Prediction of drug synergistic effects with machine learning technique*

*Oxford, UK*

- Advisors: Prof. Ahmed Ahmed and Dr. Christopher Yau
- Constructed a Lasso model based on drug targets and genetic information to explore the prediction power of genetic information
- Wiki URL: <https://www.synapse.org/#!Synapse:syn5705150/wiki/394570>

**Nuffield Department of Medicine, University of Oxford**

July 2014 - August 2014

*Project: Analysis of the metformin effect on cancer single-cell transcriptome*

*Oxford, UK*

- Advisors: Dr. Christopher Yau and Dr. Quin Wills
- Explored co-expression measures for the single-cell RNA sequencing data using R, clustered co-expression measures based on gene sets defined by prior biological knowledge and calculated the centrality based on co-expression network and explored its correlation with the biological importance of genes.

**Center for Quantitative Biology, Peking University**

October 2014 - June 2015

*Project: Phylogenetic analysis of horizontal gene transfer in microbial microevolution* *Beijing, China*

- Advisor: Prof. Huaqiu Zhu
- Developed new methods to detect horizontally transferred genes and analyzed the rate of horizontal gene transfer on the phylogenetic tree.

**Center for Quantitative Biology, Peking University**

June 2013 - October 2014

*Project: Analysis of non-coding regions in horizontal gene transfer*

*Beijing, China*

- Advisor: Prof. Huaqiu Zhu
- Classified the transferred genes based on the Cluster of Orthologous Groups of proteins (COG) database.
- Classified genes by their translation initiation mechanisms to study the characteristic translation regulation of horizontally transferred genes.

## LABORATORY EXPERIENCE

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I have been working in the wet lab for more than three years.

Experienced in handling human/mouse samples, flow cytometry/FACS, Confocal microscope, bulk RNA sequencing, single-cell RNA-seq and *etc.*

Familiar with next-generation sequencing (e.g. whole-exome sequencing) and basic laboratory skills (e.g. RT, PCR, qPCR, electrophoresis, fluorescent staining, cell culturing).

## COMPUTING EXPERIENCE

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Proficient: R, Shell, Git and analysing of next-generation sequencing data

Familiar with: Python, C,

**Z. Hu**, C. Yau and A. Ahmed (2017). masonmd: making sense of nonsense mediated decay. MIT License. doi: 10.5281/zenodo.546698

The R package masonmd (**MA**ke **S**ense **O**f **NMD**) we developed can predict the genomic mutations that can elicit nonsense-mediated decay and may cause loss-of-function of the mutated genes.

## RELEVANT SKILLS

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**Language** English (fluent) and Mandarin Chinese (native)

**Softwares** R, Shell, L<sup>A</sup>T<sub>E</sub>X, Python, Make, C/C++, MATLAB, Fiji *etc.*