Hani Jieun Kim

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EDUCATION

2018 – present	**PhD, Computational Biology**	**The University of Sydney** School of Mathematics and Statistics, Australia
2011 – 2014	**MSc, Biological Sciences**	**Seoul National University** School of Biological Sciences, South Korea
2008 – 2011	**BSc, Biomedical Sciences**	**Imperial College London** Department of Biomedical Sciences, United Kingdom

PROFESSIONAL EXPERIENCE

2015 – 2018	**Academic Publication Trainer and Consultant** Conducted >100 hours of workshops at >30 tertiary tier education institutes and hospitals and live streamed workshops (up to 400 participants) on publication and scientific writing	**Editage** of Cactus Communications
2014 – 2015	**Research Assistant** in molecular biology Developed strong command of molecular biology and cloning techniques (PCR, RT-qPCR, DNA/RNA extraction, WB, and IP) and autoradiography techniques	**Seoul National University**

AWARDS AND SCHOLARSHIPS

2018 – current **Postgraduate Research Scholarship in Computational Biology** from The University of Sydney, Australia
Valued at **$44,500 per annum** (plus annual increase) to cover tuition fees + **$27,082 per annum** (plus annual increase) to cover living expenses

2019 – current **CMRI PhD Top-up Scholarship** from the Children's Medical Research Institute
Valued at **$7,160 per annum** (plus annual increase)

2020 **Student Oral Award ($250 AUD)** at the 25th Annual Lorne Proteomics Symposium
CiteFuse enables multimodal analysis of CITE-seq data

2019 **2nd Best Oral Presentation Award ($120 AUD)** at the COMBINE Symposium
CiteFuse enables multimodal analysis of CITE-seq data

2019 **Winner of Oz Single Cell Challenge 2019 ($1000 AUD)** at Oz Single Cell Conference
Network fusion using CITE-seq identifies a rare population of B-cells in metastatic lymph nodes

2019 **Travel Award for EMBL Australia PhD Course** at the University of Tasmania, Hobart
A two-week intensive and residential course for 60 outstanding PhD students

2018 **2nd Best Poster Presentation Award ($120 AUD)** at the COMBINE Symposium
Dynamic Transcriptional Networks in the Progression of Pluripotency Revealed by Integrative Statistical Learning

PRESENTATIONS

2020	Poster presentation at **The Australian Bioinformatics And Computational Biology Society (virtual)**
2020	Poster presentation at **Charles Perkins Centre EMCR Symposium (virtual)**
2020	Workshop on *Multimodal analysis of CITE-seq data with CiteFuse* at **BioCAsia 2020**
2020	**Invited** oral presentation at **A/Prof Hagen Tigner Laboratory** at Weill Cornell Medicine, New York, USA **(virtual)**
2020	**Invited** oral presentation at **OzSingleCell 2020** Episode on New technologies: Exploring the complexities of genetic regulation in single cells **(virtual)**
2020	Poster presentation at **Cold Spring Harbor Laboratory "Epigenetics & Chromatin" (virtual)**
2020	Poster presentation at **28th Conference on Intelligent Systems for Molecular Biology (virtual)**
2020	Oral presentation at **25th Annual Lorne Proteomics Symposium** in Lorne, Australia
2019	Poster presentation at **The Australian Bioinformatics And Computational Biology Society** in Sydney, Australia
2019	Workshop on *Single Cell RNA-seq Analysis* at **AMSI BioInfoSummer 2019**
2019	Oral presentation at **COMBINE Symposium** in Sydney, Australia
2019	Oral presentation at **10x Genomics User Guide Meeting** in Sydney, Australia
2019	Poster presentation at **EMBL Australia PhD Course** in Tasmania, Australia
2018	Poster presentation at **COMBINE Symposium** in Melbourne, Australia
2018	Poster presentation at **Garvan Signalling Symposium** in Sydney, Australia

PUBLICATIONS

Impact factor (IF)
†Co-first author

Peer-Reviewed Journal Articles

1. Lin, Y., Cao, Y., **Kim, H.**, Salim, A., Speed, T., Lin, D., Yang, P. & Yang, J. (2020) scClassify: sample size estimation and multiscale classification of cells using single and multiple reference. *Molecular Systems Biology*, 16:e9389 **[IF: 9.800]** [link]
2. **Kim, H.**†, Lin, Y.†, Geddes, T., Yang, J. & Yang, P. (2020) CiteFuse enables multi-modal analysis of CITE-seq data. *Bioinformatics* **[IF: 4.531]** [link]
3. **Kim, H.**, Osteil, P., Humphrey, S., Cinghu, S., Oldfield, A., Patrick, E., Wilkie, E., Peng, G., Suo, S., Jothi, R., Tam, P. & Yang, P. (2020) Transcriptional network dynamics during the progression of pluripotency revealed by integrative statistical learning. *Nucleic Acids Research*, 48, 1828–1842. **[IF: 11.147]** [link]
4. Kim, T., Lo, K., Geddes, T., **Kim, H**., Yang, J. & Yang, P. (2019) scReClassify: post hoc cell type classification of single-cell RNA-seq data. *BMC Genomics*, 20, 913. **[IF: 3.501]** [link]
5. Yim, C., Jung, S., **Kim, H**., Jung, Y., Jeong, S. & Kim, H. (2018) Profiling of signal sequence characteristics and requirement of different translocation components. *BBA-Molecular Cell Research*, 1865(11), 1640-1648. **[IF: 4.739]** [link]
6. Jung, S., **Kim, H**., Reithinger, J. & Kim, H. (2014) The Sec62/63 translocon facilitates the C_{out} orientation of membrane proteins. *Journal of Cell Science*, 127(19), 4270-4278. **[IF: 4.517]** [link]
7. Reithinger, J., **Kim, H.** & Kim, H. (2013) Sec62 protein mediates membrane insertion and orientation of moderately hydrophobic signal anchor proteins in the endoplasmic reticulum. *Journal of Biological Chemistry*, 288(25), 18058-18067. **[IF: 4.106]** [link]

Preprints

8. **Kim, H.**†, Kim, T.†, Hoffman, N., Xiao, D., James, D., Humphrey, S. & Yang, P. (2020) PhosR enables processing and functional analysis of phosphoproteomic data. *bioRxiv, under review in Cell Reports* **[IF: 7.700]** [link]
9. **Kim, H.**†, Kim, T., Oldfield, A. & Yang, P. (2020) Integrative Analysis Reveals Histone Demethylase LSD1/KDM1A Associates with RNA Polymerase II Pausing. *bioRxiv, submitted to Genome Biology* **[IF: 12]** [link]

TEACHING

- Tutored **DATA2002 Data Analytics: Learning from Data** (2020 Semester 2) for second and third year undergraduate students
- Developed content of **OLEO5601/OLET5602 Computational Analysis for Omics Data**, a Higher Degree Research Open Learning Environment (HDR OLE) course for graduate students
- Tutored **AMED3002 Interrogating Biomedical and Health Data** (2020 Semester 1) for third year undergraduate students
- Tutored **STAT5003 Computational Statistical Methods** (2019 Semester 2) for graduate students

RESEARCH SUPERVISION

- Carissa Chan, Honours student (2020), School of Life and Environmental Sciences, The University of Sydney (contribution to supervision by Dr Pengyi Yang)

PEER REVIEW & PROFESSIONAL SERVICE
Web of Science ResearcherID: ABC-3112-2020

- Reviewed for Journal of Bioinformatics and Computational Biology (1)
- Reviewed for BMC Genomics (1)

- Committee member of COMBINE, a student-run Australian organisation for researchers in computational biology and bioinformatics
   Sponsorship coordinator, fundraised over **$1000 AUD** worth of sponsorships

SOFTWARE

- An **R** package for multi-modal analysis of CITE-seq data https://sydneybiox.github.io/CiteFuse/
- An **R** package for phosphoproteomic data analysis https://github.com/PYangLab/PhosR/

REFEREES

Pengyi Yang PhD
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