

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 25 th Annual Lorne Proteomics Symposium <i>CiteFuse enables multimodal analysis of CITE-seq data</i>	
2019	2nd Best Oral Presentation Award (\$120 AUD) at the COMBINE Symposium <i>CiteFuse enables multimodal analysis of CITE-seq data</i>	
2019	Winner of Oz Single Cell Challenge 2019 (\$1000 AUD) at Oz Single Cell Conference <i>Network fusion using CITE-seq identifies a rare population of B-cells in metastatic lymph nodes</i>	
2019	Travel Award for EMBL Australia PhD Course at the University of Tasmania, Hobart <i>A two-week intensive and residential course for 60 outstanding PhD students</i>	
2018	2nd Best Poster Presentation Award (\$120 AUD) at the COMBINE Symposium <i>Dynamic Transcriptional Networks in the Progression of Pluripotency Revealed by Integrative Statistical Learning</i>	

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 <i>Multimodal analysis of CITE-seq data with CiteFuse</i> 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 <i>Single Cell RNA-seq Analysis</i> 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 year undergraduate students
- Developed content of **OEO5601/OET5602 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://sydneybioinformatics.github.io/CiteFuse/>
- An **R** package for phosphoproteomic data analysis <https://github.com/PYangLab/PhosR/>

REFEREES

Pengyi Yang PhD

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Group Leader and ARC DECRA Fellow & NHMRC Investigator

School of Mathematics & Statistics, The University of Sydney, NSW 2006, AUSTRALIA

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