Kai Li, B.S.

Lester and Sue Smith Breast Center | Baylor College of Medicine

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Education

2015 fall	**Missouri State University**	Exchange student
2013 — 2017	**Qingdao University**	B.S. in Biotechnology

Research Experience

2018 — present   **Bioinformatics Programmer**, Lester and Sue Smith Breast Center, Baylor College of Medicine

1. *Developed and maintained NeoFlow for proteogenomic data analysis* (tool development, second author manuscript in Nat. Commun.)
2. *Implemented NeoFlow for several projects in Clinical Proteomic Tumor Analysis Consortium* (informatics analysis, three co-author manuscripts in Cell)
3. *Proteogenomic analysis of three large-scale cancer studies to evaluate different quality control strategies (*informatics analysis, second author manuscript with NeoFlow in Nat. Commun., abstracts selected for poster presentations at domestic conferences)
4. *Developed DeepRescore to improve peptide identification in immunopeptidomic data by deep learning* (tool development, first author manuscript in Proteomics, abstracts selected for oral/poster presentations at international conferences)

2017 — 2018   **Bioinformatician**, Bioinformatics Platform, Mass Spectrometry Department, BGI-Shenzhen

1. *Developed and maintained PDV for integrated proteomic data* visualization(tool development, first author manuscript in Bioinformatics)
2. *Implemented PDV for several projects* (informatics analysis, two co-author manuscripts in Mol. Cell Proteomics)

2016 — 2017   **Bioinformatician (Internship)**, Bioinformatics Platform, Mass Spectrometry Department, BGI-Shenzhen

1. *Developed a graphic user interface tool for Extracted-Ion Chromatogram (XIC) extraction and visualization for large Data-independent acquisition data* (tool development, collaborated with Dr.Tiannan Guo from the laboratory of Dr.Ruedi Aebersold at ETH Zurich)
2. *Explored applications of deep learning in peptide phosphorylation sites prediction* (informatics analysis)

Awards and Honors

2017	Outstanding graduate student of Shandong Province (5%)
2016 — 2017	Third class scholarship (7/71)
2015	Full scholarship to Missouri State University as an exchange student
2015 — 2016	Model student of academic records in Qingdao University (1/19)

Invited Presentations

2020	Oral presentation, American Society for Mass Spectrometry 2020 Annual Meeting, Houston, TX
2019	Poster presentation, Clinical Proteomic Tumor Analysis Consortium 2019 Annual Meeting, National Institutes of Health, Bethesda, MD

Membership and Service

2020	Member, American Society for Mass Spectrometry
2016	Volunteer, The Annual Meeting of the International Conference on Genomics

Technical Skills

Programming Language: Java, R, Python, Shell, NextFlow

Proteomics Software: MaxQuant, MS-GF+, Comet, X!Tandem, pFind

Conference Abstracts

1. ***Kai Li**, Bo Wen, Bing Zhang: Deep learning improves sensitivity and specificity of peptide identification in immunopeptidomics. American Society for Mass Spectrometry 2020 Annual Meeting, Houston, TX, 2020.

2. *Bo Wen, **Kai Li**, Yun Zhang, Bing Zhang: Cancer neoantigen prioritization through sensitive and reliable proteogenomics analysis. American Society for Mass Spectrometry 2020 Annual Meeting, Houston, TX, 2020.

3. *Wen Jiang, **Kai Li**, Bo Wen, Bing Zhang: Deep learning - derived evaluation metrics for benchmarking computational pipelines for the analysis of large-scale phosphoproteomics datasets. American Society for Mass Spectrometry 2020 Annual Meeting, Houston, TX, 2020.

4. *Xinpei Yi, Yuxing Liao, **Kai Li**, Bo Wen, Bing Zhang: CAatlas: an immunopeptidome atlas of human cancer. American Society for Mass Spectrometry 2020 Annual Meeting, Houston, TX, 2020.

Publications

1. **Li, K.**, Jain, A., Malovannaya, A., Wen, B., & Zhang, B. (2020). DeepRescore: Leveraging Deep Learning to Improve Peptide Identification in Immunopeptidomics. Proteomics, 1900334. *IF: 3.3, cited by 1*

2. Wen, B., **Li, K.**, Zhang, Y., & Zhang, B. (2020). Cancer neoantigen prioritization through sensitive and reliable proteogenomics analysis. Nature communications, 11(1), 1-14. *IF: 12.1, cited by 3*

3. Gillette, M. A., Satpathy, S., Cao, S., Dhanasekaran, S. M., Vasaikar, S. V., Krug, K., ... & Krek, A. (2020). Proteogenomic characterization reveals therapeutic vulnerabilities in lung adenocarcinoma. Cell, 182(1), 200-225. *IF: 38.6, cited by 6*

4. Dou, Y., Kawaler, E. A., Zhou, D. C., Gritsenko, M. A., Huang, C., Blumenberg, L., ... & Liu, W. (2020). Proteogenomic characterization of endometrial carcinoma. Cell, 180(4), 729-748. *IF: 38.6, cited by 25*

5. **Li, K.**, Vaudel, M., Zhang, B., Ren, Y., & Wen, B. (2019). PDV: an integrative proteomics data viewer. Bioinformatics, 35(7), 1249-1251. *IF: 5.6, cited by 21*

6. Ren, Z., Qi, D., Pugh, N., **Li, K.**, Wen, B., Zhou, R., ... & Jones, A. R. (2019). Improvements to the rice genome annotation through large-scale analysis of RNA-Seq and proteomics data sets. Molecular & Cellular Proteomics, 18(1), 86-98. *IF: 4.8, cited by 8*

7. Clark, D. J., Dhanasekaran, S. M., Petralia, F., Pan, J., Song, X., Hu, Y., ... & Ma, W. (2019). Integrated proteogenomic characterization of clear cell renal cell carcinoma. Cell, 179(4), 964-983. *IF: 38.6, cited by 47*

8. Wang, X., Codreanu, S. G., Wen, B., **Li, K.**, Chambers, M. C., Liebler, D. C., & Zhang, B. (2018). Detection of proteome diversity resulted from alternative splicing is limited by trypsin cleavage specificity. Molecular & Cellular Proteomics, 17(3), 422-430. *IF: 4.8, cited by 36*

9. Li, B., Li, N., Zhang, L., **Li, K.**, Xie, Y., Xue, M., & Zheng, Z. (2018). Hsa_circ_0001859 regulates ATF2 expression by functioning as an MiR-204/211 sponge in human rheumatoid arthritis. Journal of immunology research, 2018. *IF: 3.3, cited by 11*

10. Huang, C., Chen, L., Li, Y., Savage, S., Schnaubelt, M., Leprevost, F. V., ... & Zhang, B. (2020). Proteogenomics characterization of HPV-negative head and neck squamous cell carcinomas. (Cancer Cell, Under review)

11. Satpathy, S., Beltran, P., Savage, S., ... & Gillette, M. (2020). Systems-wide analysis of proteogenomic variation in lung squamous cell carcinoma. (Cell, Submitted)