孙 涵, 博士

hansun@stanford.com • 出生: 1985年10月 • 性别: 男 • 籍贯: 江苏 盐城

工作经历

高级 计算生物学者 **2020 –**
儿科系, 医学院, 斯坦福大学, **Prof. Anna Gloyn**

博士后 **2015 – 2019**
遗传系, 医学院, 斯坦福大学, **Prof. Lars Steinmetz**

学习经历

博士, 生物信息学 **2009 – 2014**
系统生物学重点实验室, 中科院上海生命科学院, 导师: 李亦学研究员 谢鹭研究员

学士, 软件工程 **2004 – 2008**
华东师范大学

研究课题

- 剪切介导的癌基因激活
- RBM20突变引起的扩张型心肌病
- 糖尿病小鼠模型的遗传和发病机制

学术兴趣

- 疾病遗传学 (癌症, 心脏病, 糖尿病等)
- 生物信息学和生物统计学
- 深度学习在生命科学中的应用

科研技能

- Python, R, C, git, conda, slurm, Linux, and cloud computing (AWS and GCP)
- containerization (docker and singularity) and workflow management (Snakemake and Nextflow)
- Bioinformatics (blast, bwa, samtools, STAR, featureCounts, GATK, plink, seurat, scanpy)
- Biostatistics (hypothesis testing, confidence interval, power calculation, bayesian inference, DESeq2, statsmodels)
- Visualization (matplotlib, seaborn, plotly, ggplot2, shiny for python)
- Machine Learning (scikit-learn) and Deep Learning (Tensorflow and PyTorch)
- Multiomics: Genomics (WGS, WES, genotyping), Transcriptomics (bulk and single cell RNA-Seq, long reads), Proteomics (MS/MS), and Epigenomics (ATAC-Seq, ChIP-Seq). Linkage analysis, QTL, and GWAS.

访学经历

- European Molecular Biology Laboratory (EMBL), Heidelberg, Germany (2014.07 - 2014.10)
- Institute of Immunology, University of Rostock, Rostock, Germany (2013.10 - 2013.12)

专利

- Methods of Treatment, Genetic Screening, and Disease Models for Heart Conditions Associated with RBM20 Deficiency. Francesca Briganti, Lars M. Steinmetz, Han Sun, and Wu Wei. WO 2020/092171.

发表论文

1. **Han Sun**, Huiying Yan, Kathryn Bieging-Rolett, Michelle Nguyen, William F. Mueller, Zhuanfen Cheng, Hong Zeng, Laura Attardi, Wu Wei, and Lars M. Steinmetz et al. "CDKN1A-RAB44 transcript fusion and oncogene activation in cancers.", bioRxiv.

2. Francesca Briganti, **Han Sun**, Wu Wei, Jingyan Wu, Chenchen Zhu, Martin Liss, Ioannis Karakikes et al. "iPSC Modeling of RBM20-Deficient DCM Identifies Upregulation of RBM20 as a Therapeutic Strategy." Cell Reports 32, no. 10 (2020): 108117, **co-first author**.

3. Chenchen Zhu, Jingyan Wu, **Han Sun**, Francesca Briganti, Benjamin Meder, Wu Wei, and Lars M. Steinmetz. "Single-molecule, full-length transcript isoform sequencing reveals disease-associated RNA isoforms in cardiomyocytes." Nature Communications 12, no. 1 (2021): 1-9.

4. Benedikt Rauscher, William F Mueller, Sandra Clauder-Münster, Petra Jakob, M Saiful Islam, **Han Sun**, Sonja Ghidelli-Disse, Markus Boesche, Marcus Bantscheff, Hannah Pflaumer, Paul Collier, Bettina Haase, Songjie Chen, Rene Hoffman, Guangwen Wang, Vladimir Benes, Gerard Drewes, Michael Snyder, Lars M Steinmetz. "Patient-derived gene and protein expression signatures of NGLY1 deficiency", Journal of Biochemistry, 2021

5. Semih Calamak, Menekse Ermis, **Han Sun**, Saiful Islam, Michael Sikora, Michelle Nguyen, Vasif Hasirci, Lars M. Steinmetz, and Utkan Demirci. "A Circulating Bioreactor Reprograms Cancer Cells Toward a More Mesenchymal Niche." Advanced Biosystems 4, no. 2 (2020): 1900139, **co-first author**.

6. Jay W Schneider, Saji Oommen, Muhammad Y Qureshi, Sean C Goetsch, Rhianna S Sundsbak, Wei Guo, Mingming Sun, **Han Sun**, Dennis A Webster, Alex W Coutts, Francesca Briganti, Wu Wei, Lars Steinmetz, Daniel F Carlson, and Timothy J. Nelson et al. "Dysregulated ribonucleoprotein granules promote cardiomyopathy in RBM20 gene-edited pigs", Nature Medicine (2020): 1-13.

7. Arne H. Smits, Frederik Ziebell, Gerard Joberty Nico Zinn, William F. Mueller, Sandra Clauder-Munster, Paola Grandi, Petra Jakob, Anne-Marie Michon, **Hanice Sun**, Karen Tessmer, Tilmann Burckstummer, Marcus Bantscheff, Lars M. Steinmetz, Gerard Drewes, and Wolfgang Huber. "Biological plasticity rescues target activity in CRISPR knock outs.", Nature Methods 2019 Oct 28:1-7.

8. William F. Mueller, Petra Jakob, **Han Sun**, Sandra Clauder-Münster, Sonja Ghidelli-Disse, Diana Ordonez, Markus Boesche, Marcus Bantscheff, Paul Collier, Bettina Haase, Vladimir Benes, Malte Paulsen, Peter Sehr, Joe Lewis, Gerard Drewes, Lars M. Steinmetz. "Loss of N-glycanase 1 Alters Transcriptional and Translational Regulation in K562 Cell Lines." G3: Genes, Genomes, Genetics (2020).

9. Lun Suo, Yu Xiao Zhou, Li Ling Jia, Hai Bo Wu, Jin Zheng, Qi Feng Lyu, Li Hua Sun, **Han Sun**, and Yan Ping Kuang. 2018. "Transcriptome Profiling of Human Oocytes Experiencing Recurrent Total Fertilization Failure." Scientific Reports 8 (1): 17890.

10. **Han Sun**, Chen Chen, Baofeng Lian, Menghuan Zhang, Xiaojing Wang, Bing Zhang, Yixue Li, Pengyuan Yang, and Lu Xie. 2015. "Identification of HPV Integration and Gene Mutation in HeLa Cell Line by Integrated Analysis of RNA-Seq and MS/MS Data." Journal of Proteome Research 14 (4): 1678–86.

11. **Han Sun**, Chen Chen, Meng Shi, Dandan Wang, Mingwei Liu, Daixi Li, Pengyuan Yang, Yixue Li, and Lu Xie. 2014. “Integration of Mass Spectrometry and RNA-Seq Data to Confirm Human Ab Initio Predicted Genes and lncRNAs.” Proteomics 14 (23-24): 2760–68.

12. **Han Sun**, Xiaobin Xing, Jing Li, Fengli Zhou, Yunqin Chen, Ying He, Wei Li, et al. 2013. “Identification of Gene Fusions from Human Lung Cancer Mass Spectrometry Data.” BMC Genomics 14 Suppl 8 (December): S5.

13. Zhen-Hao Liu, Bao-Feng Lian, Qiong-Zhu Dong, **Han Sun**, Jin-Wang Wei, Yuan-Yuan Sheng, Wei Li, et al. 2018. “Whole-Exome Mutational and Transcriptional Landscapes of Combined Hepatocellular Cholangiocarcinoma and Intrahepatic Cholangiocarcinoma Reveal Molecular Diversity.” Biochimica et Biophysica Acta 1864 (6 Pt B): 2360–68.

14. Menghuan Zhang, Hong Li, Ying He, **Han Sun**, Li Xia, Lishun Wang, Bo Sun, et al. 2015. “Construction and Deciphering of Human Phosphorylation-Mediated Signaling Transduction Networks.” Journal of Proteome Research 14 (7): 2745–57.

15. Wei Li, Jian Yu, Baofeng Lian, **Han Sun**, Jing Li, Menghuan Zhang, Ling Li, Yixue Li, Qian Liu, and Lu Xie. 2015. “Identifying Prognostic Features by Bottom-up Approach and Correlating to Drug Repositioning.” PloS One 10 (3): e0118672.

16. Jing Li, Jia Jia, Hong Li, Jian Yu, **Han Sun**, Ying He, Daqing Lv, et al. 2014. “SysPTM 2.0: An Updated Systematic Resource for Post-Translational Modification.” Database: The Journal of Biological Databases and Curation 2014 (April): bau025.

17. Yulin Dai, Shengdi Li, Xiao Dong, **Han Sun**, Chao Li, Zhi Liu, Beili Ying, Guohui Ding, and Yixue Li. 2013. “The de Novo Sequence Origin of Two Long Non-Coding Genes from an Inter-Genic Region.” BMC Genomics 14 (Suppl 8): S6.

18. Li Xia, Tong-Dan Wang, Shao-Ming Shen, Meng Zhao, **Han Sun**, Ying He, Lu Xie, et al. 2013. “Phosphoproteomics Study on the Activated PKCδ-Induced Cell Death.” Journal of Proteome Research 12 (10): 4280–4301.

19. Jian Yu, Xiaobin Xing, Lingyao Zeng, Jiehuan Sun, Wei Li, **Han Sun**, Ying He, et al. 2012. “SyStemCell: A Database Populated with Multiple Levels of Experimental Data from Stem Cell Differentiation Research.” PloS One 7 (7): e35230.

20. Ying He, Menghuan Zhang, Yuanhu Ju, Zhonghao Yu, Daqing Lv, **Han Sun**, Weilan Yuan, et al. 2011. “dbDEPC 2.0: Updated Database of Differentially Expressed Proteins in Human Cancers.” Nucleic Acids Research 40 (D1): D964–71.

21. Xiao Chang, Yun Li, Jie Ping, Xiao-Bin Xing, **Han Sun**, Peng Jia, Chuan Wang, Yuan-Yuan Li, and Yi-Xue Li. 2011. “EcoBrowser: A Web-Based Tool for Visualizing Transcriptome Data of Escherichia Coli.” BMC Research Notes 4 (October): 405.

22. Xiao-Bin Xing, Qing-Run Li, **Han Sun**, Xing Fu, Fei Zhan, Xiu Huang, Jing Li, et al. 2011. “The Discovery of Novel Protein-Coding Features in Mouse Genome Based on Mass Spectrometry Data.” Genomics 98 (5): 343–51.