Chun-Jie Liu, Ph.D.

Department of Bioinformatics and Systems Biology

Hubei Bioinformatics & Molecular Imaging Key Laboratory

Huazhong University of Science and Technology (HUST)

Wuhan, Hubei, 430074 P.R. China **Email:** chunjie.sam.liu@gmail.com

Website: https://github.com/chunjie-sam-liu

https://chunjie-sam-liu.life

EDUCATION

2014.09 - 2018.06	Ph.D.	Genetics	HUST
2016.10 - 2017.10	Visiting Scholar	Computational Biology and Bioinformatics	UTHealth
2010.09 - 2014.06	B.S.	Bioinformatics	HUST

RESEARCH EXPIERENCE

2018.06 - Present	Postdoctoral Fellow	HUST	Advisor: An-Yuan Guo
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RESEARCH INTERESTS

Tumor immunotherapy and biomarkers

- ♦ Tumor diagnosis of RNA signatures based on tumor educated platelet.
- ♦ Mining immunotherapy response biomarkers and building prediction model.

Non-coding RNA in cancer

- ♦ Non-coding RNA (snoRNA, tRNA, circRNA) in cancer subtype and prognosis.
- ♦ Data portal of non-coding construction, including LNCRediting and miRNASNP.

Bioinformatic tools

- ♦ Cancer analysis tools, including GSCALite, GEDS and SEGtool.
- ♦ Building genomic and immunogenomic pipelines.

FUNDINGS

2019.06	China Postdoctoral Science Foundation	2019M652623	¥80,000
2016.06	Innovative Interdisciplinary Ph.D. Student Foundation	-	¥50,000

PUBLICATIONS

Contributed equally as first author

1. Gong, J.[†], Liu, C.J. [†], Liu, W., Xiang, Y., Diao, L., Guo, A.Y., Han, L. (2017). LNCediting: a database for

- functional effects of RNA editing in lncRNAs. Nucleic Acids Research, 45(D1), D79-D84.
- 2. Gong, J.[†], Li, Y.[†], <u>Liu, C.J.[†]</u>, Xiang, Y., Li, C., Ye, Y., Zhang, Z., Hawke, D. H., Park, P. K., Diao, L., others, NA (2017). A pan-cancer analysis of the expression and clinical relevance of small nucleolar RNAs in human cancer. *Cell Reports*, 21(7), 1968-1981.
- 3. Zhang, Z.[†], Ruan, H.[†], <u>Liu, C.J.[†]</u>, Ye, Y., Gong, J., Diao, L., Guo, A.Y., Han, L. (2019). tRic: a user-friendly data portal to explore the expression landscape of tRNAs in human cancers. *RNA Biology*, 1-6.
- 4. <u>Liu, C.J.</u>, Hu, F.F., Xia, M.X., Han, L., Zhang, Q., Guo, A.Y. (2018). GSCALite: a web server for gene set cancer analysis. *Bioinformatics*, 34(21), 3771-3772.
- 5. <u>Liu, C.J.</u>, Gao, C., Cong, R., Zhang, Q., Guo, A.Y. (2017). lncRInter: a database of experimentally validated long non-coding RNA interaction. *Journal Of Genetics And Genomics*, 44(5), 265-268.
- 6. Xia, M.[†], <u>Liu, C.J.[†]</u>, Zhang, Q., Guo, A.Y. (2019). GEDS: a gene expression display server for mRNAs, miRNAs and proteins. *Cells*, 8(7), 675.
- 7. Gong, J.[†], <u>Liu, C.J.[†]</u>, Liu, W., Wu, Y., Ma, Z., Chen, H., Guo, A.Y. (2015). An update of miRNASNP database for better SNP selection by GWAS data, miRNA expression and online tools. *Database*, 2015.
- 8. Gao, M.[†], Zhang, S.[†], <u>Liu, C.J.[†]</u>, Qin, Y., Archacki, S., Jin, L., Wang, Y., Liu, F., Chen, J., Liu, Y., others, NA (2016). Whole exome sequencing identifies a novel NRL mutation in a Chinese family with autosomal dominant retinitis pigmentosa. *Molecular Vision*, 22.

Others

- 1. Zhang, H.M., Liu, T., <u>Liu, C.J.</u>, ..., Xue, Y., Guo, A.Y. (2015). AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. *Nucleic Acids Research*, 43(D1), D76-D81.
- Gong, J., Mei, S., <u>Liu, C.J.</u>, Xiang, Y., Ye, Y., Zhang, Z., Feng, J., Liu, R., Diao, L., Guo, A.Y., others, NA (2018). PancanQTL: systematic identification of cis-eQTLs and trans-eQTLs in 33 cancer types. *Nucleic Acids Research*, 46(D1), D971-D976.
- Shi, M.W., Zhang, N.A., Shi, C.P., <u>Liu, C.J.</u>, Luo, Z.H., Wang, D.Y., Guo, A.Y., Chen, Z.X. (2019). SAGD: a comprehensive sex-associated gene database from transcriptomes. *Nucleic Acids Research*, 47(D1), D835-D840.
- 4. Zhang, Q., Liu, W., <u>Liu, C.J.</u>, Lin, S.Y., Guo, A.Y. (2018). SEGtool: a specifically expressed gene detection tool and applications in human tissue and single-cell sequencing data. *Briefings In Bioinformatics*, 19(6),

- 1325-1336.
- 5. Gong, J., Wan, H., Mei, S., Ruan, H., Zhang, Z., <u>Liu, C.J.</u>, Guo, A.Y., Diao, L., Miao, X., Han, L. (2019). Pancan-meQTL: a database to systematically evaluate the effects of genetic variants on methylation in human cancer. *Nucleic Acids Research*, 47(D1), D1066-D1072.
- 6. Ruan, H., Xiang, Y., Ko, J., Li, S., Jing, Y., Zhu, X., Ye, Y., Zhang, Z., Mills, T., Feng, J., <u>Liu. C.J.</u>, NA (2019). Comprehensive characterization of circular RNAs in 1000 human cancer cell lines. *Genome Medicine*, 11(1), 1-14.
- 7. Ye, Y., Xiang, Y., Ozguc, F. M., Kim, Y., <u>Liu, C.J.</u>, Park, P. K., Hu, Q., Diao, L., Lou, Y., Lin, C., others, NA (2018). The genomic landscape and pharmacogenomic interactions of clock genes in cancer chronotherapy. *Cell Systems*, 6(3), 314-328.
- 8. Zhang, Q., Hu, H., Chen, S.Y., <u>Liu, C.J.</u>, Hu, F.F., Yu, J., Wu, Y., Guo, A.Y. (2019). Transcriptome and regulatory network analyses of CD19-CAR-T immunotherapy for B-ALL. *Genomics, Proteomics & Bioinformatics*, 17(2), 190-200.
- 9. Lin, Y., Zhang, Q., Zhang, H.M., Liu, W., Liu, C.J., Li, Q., Guo, A.Y. (2015). Transcription factor and miRNA co-regulatory network reveals shared and specific regulators in the development of B cell and T cell. *Scientific Reports*, 5.
- 10. Zhao, A., Kong, F., <u>Liu, C.J.</u>, Yan, G., Gao, F., Guo, H., Guo, A.Y., Chen, Z., Li, Q. (2017). Tumor cell-derived microvesicles induced not epithelial-mesenchymal transition but apoptosis in human proximal tubular (HK-2) cells: implications for renal impairment in multiple myeloma. *International Journal Of Molecular Sciences*, 18(3), 513.
- 11. Wang, J., Liu, Y., Liu, F., Huang, C., Han, S., Lv, Y., Liu, C.J., Zhang, S., Qin, Y., Ling, L., others, NA (2016). Loss-of-function mutation in PMVK causes autosomal dominant disseminated superficial porokeratosis. *Scientific Reports*, 6(1), 1-9.
- 12. Zhang, Z., Ye, Y., Gong, J., Ruan, H., <u>Liu, C.J.</u>, Xiang, Y., Cai, C., Guo, A.Y., Ling, J., Diao, L., others, NA (2018). Global analysis of tRNA and translation factor expression reveals a dynamic landscape of translational regulation in human cancers. *Communications Biology*, 1(1), 1-11.
- 13. Zhang, Q., Luo, M., Liu, C. J., Guo, A.Y. (2019). CCLA: an accurate method and web server for cancer cell

line authentication using gene expression profiles. Biorxiv, 858456.

AWARDS & FELLOWSHIPS

2018.06	Excellent Ph.D. Student	HUST
2017.11	Second Prize, Bioinformatics young scholars conference	
2017.10	Merit Student	HUST
2017.10	National Graduate Scholarship	Chinese Ministry of Education
2016.06	State Scholarship Fund	China Scholarship Council
2015.10	Merit Student	HUST
2015.10	National Graduate Scholarship	Chinese Ministry of Education
2015.07	Excellent Participant in Dragon Star	HMU
2014-2019	Full scholarship for graduate education	HUST
2014.06	Excellent Participant in High Performance Computing	NUDT
2014.06	Excellent Graduate Student	HUST
2013.11	Silver Medel	iGEM(Asian)
2013.11	Outstanding Student Scholarship	HUST
2013.11	Honorable Mention Prize	HUST
2011.11	Outstanding Student Scholarship	HUST