



Hong Zheng

Research Engineer, Med/BMIR-ITI Institute

Bio

INSTITUTE AFFILIATIONS

- Member (Staff), Cardiovascular Institute

Publications

PUBLICATIONS

- **Multi-omics analysis of mucosal and systemic immunity to SARS-CoV-2 after birth.** *Cell*
Wimmers, F., Burrell, A. R., Feng, Y., Zheng, H., Arunachalam, P. S., Hu, M., Spranger, S., Nyhoff, L. E., Joshi, D., Trisal, M., Awasthi, M., Bellusci, L., Ashraf, et al
2023
- **Prediction of HLA genotypes from single-cell transcriptome data.** *Frontiers in immunology*
Solomon, B. D., Zheng, H., Dillon, L. W., Goldman, J. D., Hourigan, C. S., Heath, J. R., Khatri, P.
2023; 14: 1146826
- **Serum proteome analysis of systemic JIA and related lung disease identifies distinct inflammatory programs and biomarkers.** *Arthritis & rheumatology (Hoboken, N.J.)*
Chen, G., Deutsch, G. H., Schulert, G., Zheng, H., Jang, S., Trapnell, B., Lee, P., Macaubas, C., Ho, K., Schneider, C., Saper, V. E., de Jesus, A. A., Krasnow, et al
2022
- **A 6-mRNA host response classifier in whole blood predicts outcomes in COVID-19 and other acute viral infections.** *Scientific reports*
Buturovic, L., Zheng, H., Tang, B., Lai, K., Kuan, W. S., Gillett, M., Santram, R., Shojaei, M., Almansa, R., Nieto, J. A., Munoz, S., Herrero, C., Antonakos, et al
1800; 12 (1): 889
- **NSD1 mutations deregulate transcription and DNA methylation of bivalent developmental genes in Sotos syndrome.** *Human molecular genetics*
Brennan, K., Zheng, H., Fahrner, J. A., Shin, J. H., Gentles, A. J., Schaefer, B., Sunwoo, J. B., Bernstein, J. A., Gevaert, O.
2022
- **Tumor response as defined by iRECIST in gastrointestinal malignancies treated with PD-1 and PD-L1 inhibitors and correlation with survival.** *BMC cancer*
Xie, P., Zheng, H., Chen, H., Wei, K., Pan, X., Xu, Q., Wang, Y., Tang, C., Gevaert, O., Meng, X.
2021; 21 (1): 1246
- **Multi-cohort analysis of host immune response identifies conserved protective and detrimental modules associated with severity across viruses.** *Immunity*
Zheng, H., Rao, A. M., Dermadi, D., Toh, J., Murphy Jones, L., Donato, M., Liu, Y., Su, Y., Dai, C. L., Kornilov, S. A., Karagiannis, M., Marantos, T., Hasin-Brumshtein, et al
2021
- **Artificial intelligence and data science applied to bioengineering** *AIMS BIOENGINEERING*
Espin-Perez, A., Bozkurt, S., Zheng, H., Nivina, A.
2021; 8 (1): 93–94

● **INTEGRATED MULTI-SCALE MODEL FOR PEDIATRIC BRAIN TUMOR SURVIVAL PREDICTION**

Qiu, Y., Sabran, A., Zheng, H., Gevaert, O.
OXFORD UNIV PRESS INC.2020: 440–41

● **A meta-learning approach for genomic survival analysis.** *Nature communications*

Qiu, Y. L., Zheng, H. n., Devos, A. n., Selby, H. n., Gevaert, O. n.
2020; 11 (1): 6350

● **Genomic data imputation with variational auto-encoders.** *GigaScience*

Qiu, Y. L., Zheng, H. n., Gevaert, O. n.
2020; 9 (8)

● **Whole slide images reflect DNA methylation patterns of human tumors.** *NPJ genomic medicine*

Zheng, H. n., Momeni, A. n., Cedoz, P. L., Vogel, H. n., Gevaert, O. n.
2020; 5 (1): 11

● **Benchmark of long non-coding RNA quantification for RNA sequencing of cancer samples.** *GigaScience*

Zheng, H. n., Brennan, K. n., Hernaez, M. n., Gevaert, O. n.
2019; 8 (12)

● **Establishment and characterization of new tumor xenografts and cancer cell lines from EBV-positive nasopharyngeal carcinoma.** *Nature communications*

Lin, W., Yip, Y. L., Jia, L., Deng, W., Zheng, H., Dai, W., Ko, J. M., Lo, K. W., Chung, G. T., Yip, K. Y., Lee, S., Kwan, J. S., Zhang, et al
2018; 9 (1): 4663

● **A radiogenomic dataset of non-small cell lung cancer.** *Scientific data*

Bakr, S., Gevaert, O., Echegaray, S., Ayers, K., Zhou, M., Shafiq, M., Zheng, H., Benson, J. A., Zhang, W., Leung, A. N., Kadoch, M., D Hoang, C., Shrager, et al
2018; 5: 180202

● **Whole-exome sequencing reveals critical genes underlying metastasis in esophageal squamous cell carcinoma.** *The Journal of pathology*

Dai, W., Ko, J. M., Choi, S. S., Yu, Z., Ning, L., Zheng, H., Gopalan, V., Chan, K. T., Lee, N. P., Chan, K. W., Law, S. Y., Lam, A. K., Lung, et al
2017

● **Whole-exome sequencing identifies multiple loss-of-function mutations of NF-kappa B pathway regulators in nasopharyngeal carcinoma** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

Zheng, H., Dai, W., Cheung, A. K., Ko, J. M., Kan, R., Wong, B. W., Leong, M. M., Deng, M., Kwok, T. C., Chan, J. Y., Kwong, D. L., Lee, A. W., Ng, et al
2016; 113 (40): 11283-11288

● **Genetic and epigenetic landscape of nasopharyngeal carcinoma.** *Chinese clinical oncology*

Dai, W., Zheng, H., Cheung, A. K., Lung, M. L.
2016; 5 (2): 16-?

● **Whole-exome sequencing identifies MST1R as a genetic susceptibility gene in nasopharyngeal carcinoma** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

Dai, W., Zheng, H., Cheung, A. K., Tang, C. S., Ko, J. M., Wong, B. W., Leong, M. M., Sham, P. C., Cheung, F., Kwong, D. L., Ngan, R. K., Ng, W. T., Yau, et al
2016; 113 (12): 3317-3322

● **Comparative methylome analysis in solid tumors reveals aberrant methylation at chromosome 6p in nasopharyngeal carcinoma** *CANCER MEDICINE*

Dai, W., Cheung, A. K., Ko, J. M., Cheng, Y., Zheng, H., Ngan, R. K., Ng, W. T., Lee, A. W., Yau, C. C., Lee, V. H., Lung, M. L.
2015; 4 (7): 1079-1090

● **Viral-Inducible Argonaute18 Confers Broad-Spectrum Virus Resistance in Rice by Sequestering A Host MicroRNA** *ELIFE*

Wu, J., Yang, Z., Wang, Y., Zheng, L., Ye, R., Ji, Y., Zhao, S., Ji, S., Liu, R., Xu, L., Zheng, H., Zhou, Y., Zhang, et al
2015; 4

● **RNA-dependent RNA polymerase 6 of rice (*Oryza sativa*) plays role in host defense against negative-strand RNA virus, Rice stripe virus** *VIRUS RESEARCH*

Jiang, L., Qian, D., Zheng, H., Meng, L., Chen, J., Le, W., Zhou, T., Zhou, Y., Wei, C., Li, Y.
2012; 163 (2): 512-519

● **Viral Infection Induces Expression of Novel Phased MicroRNAs from Conserved Cellular MicroRNA Precursors** *PLOS PATHOGENS*

Du, P., Wu, J., Zhang, J., Zhao, S., Zheng, H., Gao, G., Wei, L., Li, Y.
2011; 7 (8)