



Hong Zheng

Research Engineer, Med/BMIR-ITI Institute

Bio

INSTITUTE AFFILIATIONS

- Member (Staff), Cardiovascular Institute

Publications

PUBLICATIONS

- **Impaired innate and adaptive immune responses to BNT162b2 SARS-CoV-2 vaccination in systemic lupus erythematosus.** *JCI insight*
Sarin, K. Y., Zheng, H., Chaichian, Y., Arunachalam, P. S., Swaminathan, G., Eschholz, A., Gao, F., Wirz, O. F., Lam, B., Yang, E., Lee, L. W., Feng, A., Lewis, et al
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- **Integrative systems biology reveals NKG2A-biased immune responses correlate with protection in infectious disease, autoimmune disease, and cancer.** *Cell reports*
Chen, D. G., Xie, J., Choi, J., Ng, R. H., Zhang, R., Li, S., Edmark, R., Zheng, H., Solomon, B., Campbell, K. M., Medina, E., Ribas, A., Khatri, et al
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- **Systems immunology of transcriptional responses to viral infection identifies conserved antiviral pathways across macaques and humans.** *Cell reports*
Ratnasiri, K., Zheng, H., Toh, J., Yao, Z., Duran, V., Donato, M., Roederer, M., Kamath, M., Todd, J. M., Gagne, M., Foulds, K. E., Francica, J. R., Corbett, et al
2024; 43 (2): 113706
- **Multi-omics analysis of mucosal and systemic immunity to SARS-CoV-2 after birth.** *Cell*
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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.
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- **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
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- **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.
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- **INTEGRATED MULTI-SCALE MODEL FOR PEDIATRIC BRAIN TUMOR SURVIVAL PREDICTION**
Qiu, Y., Sabran, A., Zheng, H., Gevaert, O.
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- **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.
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- **Genomic data imputation with variational auto-encoders.** *GigaScience*
Qiu, Y. L., Zheng, H. n., Gevaert, O. n.
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- **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.
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- **Establishment and characterization of new tumor xenografts and cancer cell lines from EBV-positive nasopharyngeal carcinoma.** *Nature communications*
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- **A radiogenomic dataset of non-small cell lung cancer.** *Scientific data*
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- **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*
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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.
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- **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*
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