

## **Publications**

1. Zhou Y, **Zheng Y**, Li C, Sharma A, Tang L. 2025. Sample size determination for external validation of risk models with binary outcomes using the area under the ROC curve. Submitted to *The Journal of Clinical Epidemiology*.
2. Patel N, Surman SL, Jones BG, Penkert RR, Ringwald-Smith K, DeLucca K, Richardson J, **Zheng Y**, Tang L, Hurwitz JL. 2025. Pediatric Pneumococcus and Hepatitis A Vaccinations With or Without a High-Dose Oral Vitamin A Supplement. Submitted to *Biomolecules*.
3. Allen EK, Penkert RR, Hankins JS, Surman SL, Van de Velde LA, Cotton A, Hayden RT, Tang L, Yuan X, **Zheng Y**, Thomas PG. 2024. Immune Cell Profiles of Patients with Sickle Cell Disease during Parvovirus B19–Induced Transient Red Cell Aplasia. *Vaccines*. 12(9):984.
4. Feraco AM, Zhou Y, **Zheng Y**, Marks LJ, Friedmann A, Weinstein HJ, Link MP, Flerlage JE. 2023. Disease site number was not prognostic in a low-risk Hodgkin lymphoma combined modality trial: revisiting PHC HOD90. *Blood Advances*. 7(21):6665-6667.
5. Zheng Z, Gorden PJ, Xia X, **Zheng Y**, Li G. 2022. Whole-genome analysis of *Klebsiella pneumoniae* from bovine mastitis milk in the US. *Environmental Microbiology*. 24(3):1183-1199.
6. Li G, **Zheng Y**, Wang L, Zhang Y, Shen H. 2022. Whole Genome Sequencing of Porcine Epidemic Diarrhea Virus and Porcine Deltacoronavirus. *Animal Coronaviruses*. 277-286.
7. Shen H, Zhang J, Gauger PC, Burrough ER, Zhang J, Harmon K, Wang L, **Zheng Y**, Petznick T, Li G. 2022. Genetic characterization of porcine sapoviruses identified from pigs during a diarrhoea outbreak in Iowa, 2019. *Transboundary and emerging diseases*. 69(3):1246-1255.
8. Arruda B, Shen H, **Zheng Y**, Li G. 2021. Novel morbillivirus as putative cause of fetal death and encephalitis among swine. *Emerging Infectious Diseases*. 27(7):1858-1866.
9. Hashish A, Sato Y, Li G, **Zheng Y**, Gauger PC, El-Gazzar M. 2021. Near-Complete Genome Sequence of GI-17 Lineage Infectious Bronchitis Virus, Circulating in Iowa. *Microbiology Resource Announcements*. 10(20):e01406-20.
10. Yang C, Wang L, Schwartz K, Burrough E, Groeltz-Thrush J, Chen Q, **Zheng Y**, Shen H, Li G. 2021. Case report and genomic characterization of a novel porcine nodavirus in the United States. *Viruses*. 13(1):73.
11. Gall A, Burrough E, Zhang J, Magstadt D, Yim-Im W, Stevenson G, Derscheid R, Piñeyro P, **Zheng Y**, Li G, Olds J. 2020. Identification and correlation of a novel siadenovirus in a flock of budgerigars (*Melopsittacus undulates*) infected with *Salmonella Typhimurium* in the United States. *Journal of Zoo and Wildlife Medicine*. 51(3):618-630.
12. Wang M, Zeng Z, Jiang F, **Zheng Y**, Shen H, Macedo N, Sun Y, Sahin O, Li G. 2020. Role of enterotoxigenic *Escherichia coli* prophage in spreading antibiotic resistance in a porcine-derived environment. *Environmental Microbiology*. 22(12):4974-4984.
13. Wang L, Shen H, **Zheng Y**, Schumacher L, Li G. 2020. Astrovirus in white-tailed deer, United States, 2018. *Emerging Infectious Diseases*. 26(2):374-376.
14. Cook S, Li G, **Zheng Y**, Willand Z, Issel CJ, Cook F. 2020. Molecular characterization of the major open reading frames (ORFs) and enhancer elements from four geographically distinct north

American equine infectious anemia virus (EIAV) isolates. *Journal of Equine Veterinary Science*. 85:102852.

15. Wang A, Zhang J, Shen H, **Zheng Y**, Feng Q, Yim-Im W, Gauger P, Harmon K, Zhu S, An T-Q, Li G. 2019. Genetic diversity of porcine reproductive and respiratory syndrome virus 1 in the United States of America from 2010 to 2018. *Veterinary Microbiology*. 239:108486.
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20. Yang C, Wang L, Shen H, **Zheng Y**, Gauger P, Chen Q, Zhang J, Yoon K-J, Harmon K, Main R, Li G. 2018. Detection and genomic characterization of new avian-like hepatitis E virus in a sparrow in the United States. *Archives of Virology*. 163:2861-2864.
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27. Zhang J\*, **Zheng Y\***, Xia X-Q, Chen q, Bade S, Yoon K-J, Harmon K, Gauger P, Main R, Li G. 2017. High-throughput whole genome sequencing of Porcine reproductive and respiratory syndrome virus from cell culture materials and clinical specimens using next-generation sequencing technology. *Journal of Veterinary Diagnostic Investigation*. 29:41-50. **\*These authors contributed equally to this work.**
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