## **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 L-A, Cotton A, Hayden RT, Tang L, Yuan X, **Zheng Y,** Thomas PG, Hurwitz JL. 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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- 17. Jiang F, Wu Z, **Zheng Y**, Frana T, Sahin O, Zhang Q, Li G. 2019. Genotypes and antimicrobial susceptibility profiles of hemolytic Escherichia coli from diarrheic piglets. *Foodborne Pathogens and Disease*. 16(2):94-103.
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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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- 35. **Zheng Y**, Xu D, Gu X. 2007. Functional divergence after gene duplication and sequence–structure relationship: a case study of G-protein alpha subunits. *J Exp Zool B Mol Dev Evol* 308(1):85-96.
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