

Publications

1. Zhou YW, **Zheng Y**, Li C, Sharma A, Tang L. 2024. GRASP: Sample Size Planning for Training Binary Classifiers Using the Area Under the ROC Curve. Submitted to *Statistics in Medicine*.
2. 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.
3. Zheng Z, Gorden PJ, Xia X, **Zheng Y**, Li G. 2022. Whole-genome analysis of *Klebsiella pneumoniae* from bovine mastitis milk in the U.S. *Environmental Microbiology*. 24(3):1183-1199.
4. 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.
5. 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.
6. 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
7. Shen H, Zhang J, Gauger PC, Burrough ER, Zhang J, Harmon K, Wang L, **Zheng Y**, Petznick T, Li G. 2021. Genetic characterization of porcine sapoviruses identified from pigs during a diarrhoea outbreak in Iowa, 2019. *Transboundary and emerging diseases*. 69(3):1246-1255.
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11. Wang M, Zeng Z, Jiang F, **Zheng Y**, Shen H, Macedo N, Sun Y, Sahin O, Li G. 2020b. Role of enterotoxigenic *Escherichia coli* prophage in spreading antibiotic resistance in a porcine-derived environment. *Environmental Microbiology*. 22(12):4974-4984.
12. Wang L, Shen H, **Zheng Y**, Schumacher L, Li G. 2020a. Astrovirus in White-Tailed Deer, United States, 2018. *Emerging Infectious Diseases*. 26(2):374-376.
13. 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.
14. Cook S, Li G, **Zheng Y**, Willand Z, Issel CJ, Cook F. 2019. 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.

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