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Selected Scholarly Contributions [Data Provided by **SCOPUS**]

[Reassortment networks for investigating the evolution of segmented viruses](#)

IEEE/ACM Transactions on Computational Biology and Bioinformatics, 7 (2), pp. 288-298, 2010.

[Selection for resistance to oseltamivir in seasonal and pandemic H1N1 influenza and widespread co-circulation of the lineages](#)

International Journal of Health Geographics, 9, art. no. 13, 2010.

[Tracking the geographical spread of avian influenza \(H5N1\) with multiple phylogenetic trees](#)

Cladistics, 26 (1), pp. 1-13, 2010.

[Evolution of drug resistance in multiple distinct lineages of H5N1 avian influenza](#)

Infection, Genetics and Evolution, 9 (2), pp. 169-178, 2009.

[GRASSIUS: A platform for comparative regulatory genomics across the grasses](#)

Plant Physiology, 149 (1), pp. 171-180, 2009.

[Large-scale phylogenetic analysis on current HPC architectures](#)

Scientific Programming, 16 (2-3), pp. 255-270, 2008.

[Large-scale phylogenetic analysis of emerging infectious diseases](#)

Lecture Notes in Mathematics, 1922, pp. 39-76, 2008.

[Evolution of genomes, host shifts and the geographic spread of SARS-CoV and related coronaviruses](#)

Cladistics, 24 (2), pp. 111-130, 2008.

[Genomic analysis and geographic visualization of H5N1 and SARS-CoV.](#)

AMIA ... Annual Symposium proceedings / AMIA Symposium. AMIA Symposium, p. 975, 2007.

[Quasispecies of bovine enteric and respiratory coronaviruses based on complete genome sequences and genetic changes after tissue culture adaptation](#)

Virology, 363 (1), pp. 1-10, 2007.

[Genome analysis linking recent European and African influenza \(H5N1\) viruses](#)

Emerging Infectious Diseases, 13 (5), pp. 713-718, 2007.

[Genomic analysis and geographic visualization of the spread of avian influenza \(H5N1\).](#)

Systematic biology, 56 (2), pp. 321-329, 2007.

[Large scale genotype-phenotype correlation analysis based on phylogenetic trees](#)

Bioinformatics, 23 (7), pp. 785-788, 2007.

[Complete genomic sequences, a key residue in the spike protein and deletions in nonstructural protein 3b of US strains of the virulent and attenuated coronaviruses, transmissible gastroenteritis virus and porcine respiratory coronavirus](#)

Virology, 358 (2), pp. 424-435, 2007.