



Real-time tracking of influenza A/H3N2 evolution

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Showing 17572 of 17572 genomes sampled between Jan 2001 and Jan 2019 and comprising 10 regions, 163 countries and 95 authors.

The data presented here is intended to rapidly disseminate analysis of important pathogens. Unpublished data is included with permission of the data generators, and does not impact their right to publish. A full list of sequence authors is available via nextstrain.org.

Relevant publications:

[Hadfield et al, Nextstrain: real-time tracking of pathogen evolution, Bioinformatics \(2018\)](#)