The FASEB Journal article fj.11-193466. Published online January 12, 2012

Host gene targets for novel influenza therapies elucidated by high-throughput RNA interference screens

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ABSTRACT

Influenza virus encodes only 11 viral proteins but replicates in a broad range of avian and mammalian species by exploiting host cell functions. Genome-wide RNA interference (RNAi) has proven to be a powerful tool for identifying the host molecules that participate in each step of virus replication. Metaanalysis of findings from genome-wide RNAi screens has shown influenza virus to be dependent on functional nodes in host cell pathways, requiring a wide variety of molecules and cellular proteins for replication. Because rapid evolution of the influenza A viruses persistently complicates the effectiveness of vaccines and therapeutics, a further understanding of the complex host cell pathways coopted by influenza virus for replication may provide new targets and strategies for antiviral therapy. RNAi genome screening technologies together with bioinformatics can provide the ability to rapidly identify specific host factors involved in resistance and susceptibility to influenza virus, allowing for novel disease intervention strategies.