

USING FUNCTIONAL GENOMICS TO FIND HOST PROTEINS REQUIRED FOR HIV REPLICATION

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HIV-1 exploits multiple host proteins during infection. Each host protein that HIV relies on is a potential viral weakness, that once discovered represents a therapeutic target, both for prophylaxis and treatment. We performed a large-scale siRNA screen to identify host factors required by HIV, and identified more than 200 new, and 38 previously known, HIV-dependency factors (HDFs). Further analysis revealed that the karyopherin, TNPO3, and the nuclear pore protein, RanBP2, are required for HIV-1 nuclear import. This effort begins to illustrate the power with which RNA interference and forward genetics can be used to expose the dependencies of human pathogens such as HIV, and in so doing identify potential targets for therapy.