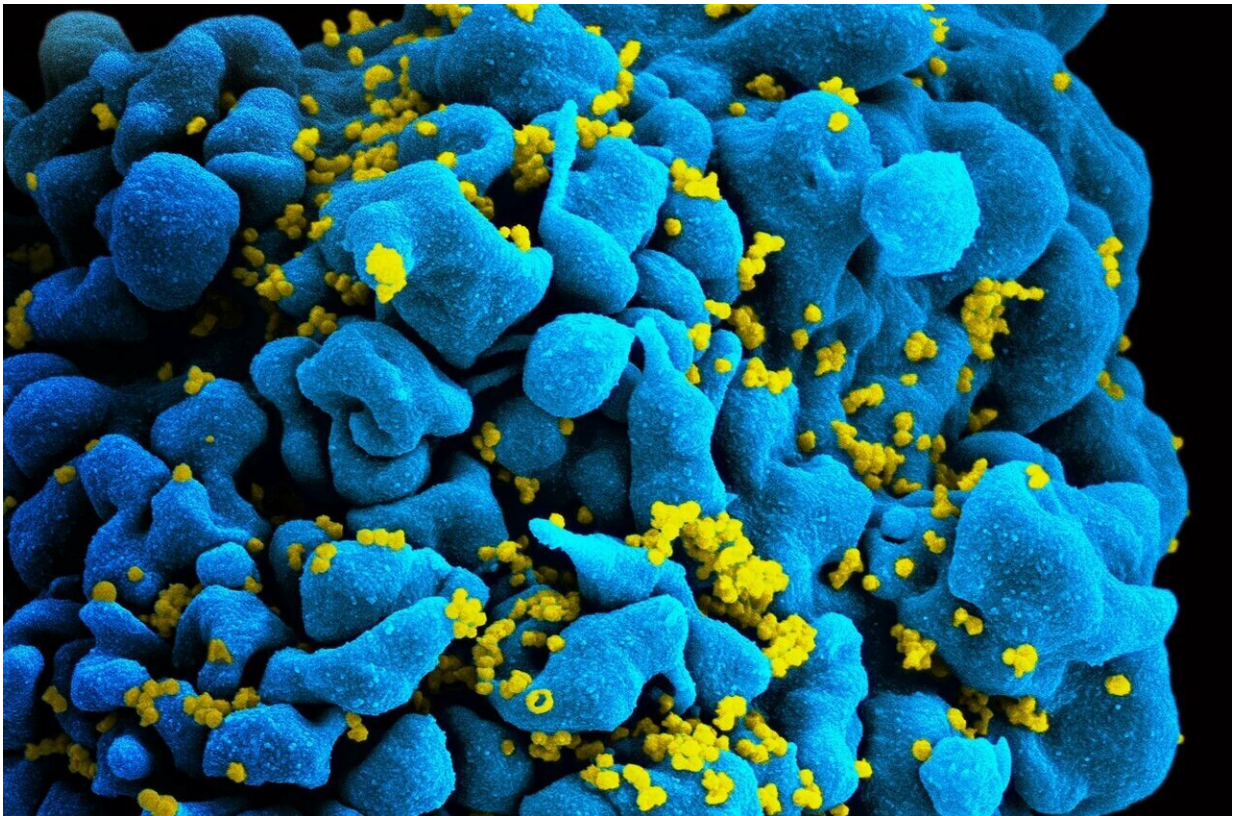


Researchers identify basic mechanisms that regulate HIV expression

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Scanning electromicrograph of an HIV-infected T cell. Credit: NIAID

Despite the positive advances that anti-human immunodeficiency virus (HIV) therapy, commonly called anti-retroviral therapy (ART) or highly active antiretroviral therapy (HAART), has had on the life expectancy of

HIV-positive people, finding a cure for HIV or acquired immunodeficiency syndrome (AIDS) has remained elusive.

"One of the major challenges in curing HIV is that there is a persistent latent reservoir of virus that is not targeted by current antiretroviral treatments and is hidden from immune cells. When treatment is interrupted, this reservoir of the virus allows the HIV to rapidly rebound," explained corresponding author Andrew J. Henderson, Ph.D., professor of medicine and microbiology at Boston University School of Medicine.

In an effort to identify [cellular pathways](#) that influence the establishment, maintenance and reversal of HIV persistence, the researchers conducted studies with yeast to screen a large library of human factors for binding to HIV [deoxyribonucleic acid](#) (DNA) sequences responsible for virus' expression. As a result, they identified several factors as potential regulators and confirmed that a subset of factors did control HIV in infected cells by increasing and decreasing levels of HIV expression.

"Our study identified novel transcription factors that influence HIV and provide an appreciation into [cellular networks](#) that influence activation and repression of different HIV strains," said Henderson.

According to the researchers, understanding the mechanisms that control HIV expression will provide insight into HIV replication, latency and pathogenesis. "By gaining an understanding of the cellular pathways that control HIV, we might be able to target them and alter the behavior of this latent reservoir," Henderson added.

These findings appear online in the journal *PNAS*.

More information: Kyle D. Pedro et al., "A functional screen

identifies transcriptional networks that regulate HIV-1 and HIV-2,"
PNAS (2021). www.pnas.org/cgi/doi/10.1073/pnas.2012835118

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