First atomic-scale view of inte capsid and host protein cyclop

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A new study offers the first atomic-scale view of an the protein coat that shepherds HIV into the nucleu known as cyclophilin A. This interaction is key to HI

A paper describing the research appears in the jour

Cyclophilin A is found in most tissues of the human inflammatory response, immunity and the folding a it fails to work properly or is overproduced in cells, diseases such as rheumatoid arthritis, asthma, can facilitates some viral infections, including HIV.

"We have known for some time that cyclophilin A pl University of Illinois physics professor Klaus Schulte postdoctoral researcher Juan R. Perilla and Universi Zhang and postdoctoral researcher Chuang Liu.

The HIV capsid somehow tricks this cellular protein transits through the cell and makes its way to the r capsid interacts with a nuclear pore that offers an e virus uses the pore as a channel to inject its geneti commandeer the cell.

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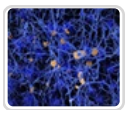
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Studies in cell culture have found that the virus rar cyclophilin disguise. Drugs that interfere with cyclo culture. Such drugs cannot be used in human HIV p immune response.

In the new study, the researchers used a massive c which they developed in a 2013 study. Building this interactions of 64 million atoms, a feat that require supercomputer at the National Center for Supercon

For the new study, the team used Blue Waters as w Ridge National Laboratory to simulate the interactic capsid. The 3-D structure of cyclophilin A was know

"We knew every atom of the underlying capsid, and then we put the cyclophilin on top of that, of which we also knew every atom," Schulten said.

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The simulations revealed that cyclophilin A binds to the capsid in two ways. First, there is the "classic" binding site, one revealed decades earlier in crystallography studies. But in some places, a single cyclophilin A protein also bound the capsid at a second site, forming a bridge between two hexamers. (The HIV capsid is made up of a latt pentamers.) Cyclophilin's bridging behavior occurre capsid, the researchers found.

Further research with NMR spectroscopy, which can corroborated the existence of a second binding site

By varying the amount of cyclophilin A added to the researchers also saw that cyclophilin did not compl concentrations, individual cyclophilin molecules atta others, disrupting their ability to bind.

Laboratory experiments also showed that having to interfered with the virus's ability to infect cells.

"What we think is happening is, where there is no c cell can recognize it and trigger a process that dest capsid is fully occupied by cyclophilin A, it prevents complex. So there is an optimal amount of cyclophi

allows the HIV infection to go forward."

"The HIV capsid has to show some of its surface to docks there properly and can inject its genetic mat "Now, we understand a little bit better the HIV viru defenses. That gives insight into battling the syster

Source:
University of Illinois at Urbana-Champaign

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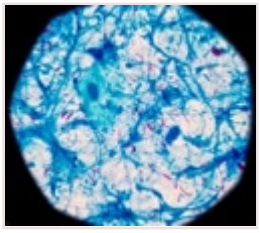

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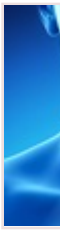

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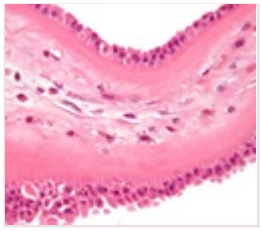

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