Researchers discover structure of key Ebola protein

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Research led by Iowa State University scientists has them a step closer to finding a way to counter the Ebola virus.

A team led by Gaya Amarasinghe, an assistant professor in biochemistry, biophysics and molecular biology, has recently solved the structure from a key part of the Ebola protein known as VP35.

VP35 interferes with the natural resistance of host cells against viral infections.

"Usually when viruses infect cells, the host immune system can fight to eventually clear the virus. But with Ebola infections, the ability of the host to mount a defense against the invading virus is lost," said Amarasinghe.

This is because the VP35 protein interferes with the host's innate immune pathways that form the first line of defense against pathogens, he said.

In their research directed toward understanding host-viral interactions, Amarasinghe and his research team used a combination of X-ray crystallography and nucleic magnetic resonance spectroscopy to solve the structure using non-infectious protein samples.

A report describing the findings is published this week in the journal Proceedings *of the National Academy of Sciences of the United States of*

America.

Now that the structure from a key part of VP35 is available, this information can be used as a template for anti-viral drug discovery.

"The next step is to use this structure to identify and design drugs that potentially bind with VP35," he said.

If a drug that inhibits VP35 function can be discovered, then the Ebola virus could potentially be neutralized.

"Without functional VP35, the Ebola virus cannot replicate so it is noninfectious," said Amarasinghe.

The Ebola virus can cause hemorrhagic fever that is usually fatal. According to the Center for Disease Control and Prevention, outbreaks have caused more than 1,000 deaths, mostly in Central Africa, since it was first recognized in 1976.

Source: Iowa State University