

Researchers solve the structure of the Zika virus helicase

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From the article in *Protein & Cell* -- the crystal structure of Zika virus helicase: basis for antiviral drug design. Credit: *Protein & Cell*

A team led by researchers from Tianjin University (P.R. China) has solved the structure of the Zika virus helicase, which is a key target for antiviral development. The research is published in Springer's journal *Protein & Cell*.

The Zika virus can cause microcephaly and other severe birth defects. However, as there are currently no effective vaccines or therapies



available to contain ZIKV infection, ZIKV remains a significant challenge to public health.

All viruses seem to need a helicase for replication. The Zika virus helicase is a motor enzyme which can convert energy from nucleoside triphosphate to unwind double stranded nucleic acids. This is an essential step for viral replication. By targeting Zika virus helicase with small-molecule inhibitors, it might be possible to stop viral <u>replication</u> and prevent disease. The scientists have successfully obtained an image at 1.8 angstroms of this viral enzyme. An angstrom is one ten-billionth (10-10) of a meter. This high-resolution image of the Zika virus key enzyme will help scientists develop drugs to treat the Zika <u>virus</u> disease.

More information: Hongliang Tian et al, The crystal structure of Zika virus helicase: basis for antiviral drug design, *Protein & Cell* (2016). DOI: 10.1007/s13238-016-0275-4

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