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Research

The geographical range of Zika virus (ZIKV) has expanded dramatically in recent decades, accompanied by a spike in Guillain-Barré syndrome and microcephaly. No antiviral drugs or vaccines are available for the treatment or prevention of ZIKV infection. To learn more about ZIKV biology, we used IP-MS and BioID to map host cell protein interactions for each of the 10 ZIKV polypeptides, generating a protein topology network comprising >3000 interactions among >1200 human polypeptides. Depicted here is the ZIKV life cycle in a human cell (*green arrow*), along with a number of newly described interactions between ZIKV proteins (*blue circles*) and host cell organelles. For details, see the article by Coyaud *et al.*, pages 2242–2255.

[S] Online version of this article contains supplemental material. ⌘ Author's Choice

Technological Innovation and Resources

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