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## Database developed at UFRGS gathers impacted genes during Zika virus infection

**Work should accelerate the investigations by Brazilian and international research groups related to the disease**

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Researchers at UFRGS created a public non-profit database that gathers the genes whose expression was altered due to Zika infection. Called *Zikavid*, the site compiles data from all the published papers so far that have evaluated gene expression after infection by the Zika virus in animals, cells and other biological samples. The development of the work that resulted in the database was described in an [article published in The Journal of Neurovirology](#) in September 2019.

The database gathers 7,348 genes identified with altered expression after Zika virus infection and 16,984 measurements of gene expression on the RNA or protein level. The information was extracted from 45 articles, tracked from more than 5,000 works on Zika available in the Pubmed database. As explained by [Walter O. Beys da Silva](#), professor at the Faculty of Pharmaceutical Sciences at UFRGS, the entire inspection was done manually. The researchers initially searched for articles related to the virus, by checking their titles and abstracts. When they found a scientific article that contained data on gene expression, they fully read and uploaded it to the system. The process took about a year and involved, in addition to researchers from the Faculty of Pharmaceutical Sciences, researchers from the *Hospital de Clínicas de Porto Alegre* and the Department of Biochemistry at UFRGS.

Zikavid allows the identification and tracking of the most used experimental models for studies of the molecular impact of Zika infection, the origins of the most studied viruses (Brazilian, African or Asian clinical samples, for example), among other factors. The search can be filtered by the names of genes or proteins, the strain of the virus and the type of sample used in the research, such as cell culture, human tissues or tests with lab mice. The availability of these data in a single database should make the research made by Brazilian and international groups, related to pathology, therapy and diagnosis of Zika infection, easier and faster. "For the entire scientific community, this database will certainly speed up the analysis on the impacts of the infection," emphasizes Silva.

In order to maintain its relevance, the database will be updated regularly. As new articles are published, researchers will collect the data and include it in the system. "There will be at least one monthly screening," explains the professor. The group also plans to create analysis tools integrated with the database so that the scientists who use it do not need to export data to other platforms. A study on the content of the database itself is also underway.

### Scientific article

ROSA, Rafael L. et al. *ZIKAVID – Zika virus infection database: a new platform to analyze the molecular impact of Zika virus infection*. *Journal of Neurovirology*, 11 Sept. 2019.

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The Zika virus is mainly transmitted by the bite of the *Aedes aegypti* mosquito - Photo: Ian Jacobs / CC 2.0

