



Xinxia Peng



Associate Professor

Credentials, degrees and  
diplomates

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### Title:

### Research emphasis:

Dr. Peng developed a variety of analytical approaches to discover novel aspects of pathogen-host interactions. Recently, he combined mRNA and total RNA deep sequencing to discover an early CD4+ T cell transcriptional response to HIV-1 infection, which includes both lncRNAs and nascent transcripts. He led the completion of the domestic ferret genome sequencing project. Currently Dr. Peng leads a multi-institutional team in developing a centralized nonhuman primate (NHP) reference transcriptome resource by deep sequencing complete transcriptomes of multiple NHP species & immune cell subsets. I also served as the lead computational biologist for the NIAID NHP Functional Genomics Core for AIDS Vaccine Research and Development,

### Selected publications:

approaches to more effectively evaluate SIV vaccine induced immune responses and identify immune correlates that predict vaccine efficacy. For this purpose, I have developed a computational strategy for quantifying the allele-specific expression of rhesus complex immune genes like MHC genes. I also associated the expression of human Fc-gamma receptors with their genetic variations by mining the sequencing data from the 1000 genomes project. My experience and expertise therefore qualifies me to assemble and lead an interdisciplinary collaborative team using integrative genomic approach to systematically elucidate the contribution of Fc mediated functions in HIV vaccine discovery and evaluation.

### Application:

- Noncoding RNAs
- 2
- 3
- 4

### Collaboration potential:

- 1
- 2
- 3
- 4