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The Role of HIV-1 Protease in Drug Resistance: New Pharmacological and Computational Approaches

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Message from the Guest Editor

Dear Colleagues,

Combined antiretroviral therapy has significantly improved the life expectancy of HIV patients, converting a fatal disease into a manageable chronic infection. Protease inhibitors are the most widely used class of antiviral drugs. They work by binding to the catalytic site of protease, avoiding the production of mature viral particles. Currently, ten different PIs have been approved by the FDA.

Despite progress obtained, drug resistance, caused by a high mutation rate and a high frequency of recombination of HIV, remains a global challenge. In order to overcome this issue, it is important to develop computational methods capable of predicting resistance of HIV-1 mutated protease. This will enable researchers to easily select new molecules, as well as develop new pharmacological approaches which could prevent the development of viral resistance.

This Special Issue aims to establish a collection of papers to provide cutting-edge insight to all interested in this area of research. Therefore, based on your expertise in this field, I would like to invite you to contribute a paper to this Issue.

I look forward to receiving your contributions.



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Special Issue



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Editor-in-Chief

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Message from the Editor-in-Chief

The worldwide impact of infectious disease is incalculable. The consequences for human health in terms of morbidity and mortality are obvious and vast but, when infections of animals and plants are also taken into account, it is hard to imagine any other disease that has such a significant impact on our lives—on healthcare systems, on agriculture and on world economics. *Pathogens* is proud to continue to serve the international community by publishing high quality studies that further our understanding of infection and have meaningful consequences for disease intervention.

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