Postgraduate student:  **Argiro D. Karozou**

Thesis Title:

# 3D molecular modelling study of the H7N9 RNA-dependent RNA polymerase as an emerging pharmacological target

Abstract:

Currently, we live in the verge of a world-wide epidemic of the H7N9 influenza A virus. This strain has turned out to be very virulent for humans and there have been many reported casualties already. This epidemic is uncontrolled as we speak and continuous to spread in many places of the globe. Concordantly, not much is known for the H7N9 strain and this is the major drawback for a scientific strategy to tackle this viral epidemic. Herein, the 3D complex structure of the H7N9 RNA-dependent RNA Polymerase has been established using a repertoire of molecular modelling techniques, including homology modelling, molecular docking and molecular dynamics simulations. Strikingly, it was found that the oligonucleotide cleft and tunnel in the H7N9 RNA-dependent RNA Polymerase is structurally very similar to the corresponding region on the Hepatitis C virus RNA-dependent RNA Polymerase crystal structure. A direct comparison and 3D post-dynamics analysis of the 3D complex of the H7N9 RNA-dependent RNA Polymerase provide invaluable clues and insight regarding the role and mode of action of a series of interacting residues on the latter enzyme. Our study provides a novel and efficiently intergraded platform with structural insights for the H7N9 RNA-dependent RNA Polymerase. We propose that future use and exploitation of these insights may prove invaluable in fight against this lethal, ongoing epidemic.

The results have been published in two journal articles:

- 3D molecular modelling study of the H7N9 RNA-dependent RNA polymerase as an emerging pharmacological target,  Dimitrios Vlachakis, Argiro Karozou, and Sophia Kossida (http://www.hindawi.com/journals/irt/aip/)

- An update on virology and emerging viral epidemics, Dimitrios Vlachakis, Argiro Karozou, Sophia Kossida
(http://www.jmolbiochem.com/index.php/JmolBiochem/issue/view/5/showToc)

SUBJECT AREA: 3D molecular modelling
KEYWORDS: H7N9, influenza A virus, 3D molecular modelling, RNA-dependent RNA polymerase, homology modelling, pharmacological target

Examining Committee

PhD. Sophia Kossida, Investigator (Assist.Prof.Level), BRFAA
PhD. Dimitrios Gunopulos, Associate Professor, Department of Informatics and Telecommunication, University of  Athens
PhD. Antonia Vlahou,  Staff Research Scientist (Prof. Level), BRFAA